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138060	ATCEA4S36388

Table 3

Seq No.	Seq.ID	Unigen e_location	Principle	ESTs_aligned	EST_pc_t_identities	gensca_n_prediction	gensca_n_weighted_score	ncbi_ids	nap_id_entities	nap_scores	blastx_pscores	genbank_descriptions
138061	ATU000001	ATL8C5 209:30 0..225 1	gap2	ATCEA4 C25038 1, ATCEA4 C17221 1_1	100, 98	ATL8C5 209:39 4..225 1	0.98	g114268	100	2469	2.1e-237	L- ASORB ATE OXIDAS E HOMOLO G PRECUR SOR (ASCOR BASE) [Brass ica napus]
138062	ATU000002	ATL8C5 320:24 11..52 34	gap2	ATCEA4 S910, ATCEA4 S1155, ATCEA4 C11734 1_1	100, 99, 93	ATL8C5 320:24 32..52 34	0.97	g4507071	100	1042	4.1e-127	SWI/SN F related, matrix associated, actin dependent regula tor of chroma tin, subfam ily a, member 3 [Homo sapien s]
138063	ATU000003	ATL8C4 7892:7 5..410 6	gap2	ATCEA4 S4231	100	ATL8C4 7892:7 5..410 6	0.96	g3036816	100	4296	0.0	(AL022 373) myosin -like protei

138064	ATU000 004	ATL8C4 5063:1 209..1 55	gap2	ATCEA4 C6137 1, ATCEA4 S1734	100, 99	ATL8C4 5063:1 064..1 55	0.94	g17067 38	100	691	3.6e- 65	FLAVON OL 3- SULFOT RANSFE RASE (F3- ST) [Flave ria bident is]	n [Arabi dopsis thalia na]
138065	ATU000 005	ATL8C2 1658:2 12..18 09	gap2	ATCEA4 C33385 1, ATCEA4 C61441 1	100, 93	ATL8C2 1658:2 77..18 09	0.93	g45875 26	100	1164	9.7e- 111	(AC007 060) Strong simila rity to F19I3. 2 []	
138066	ATU000 006	ATL8C9 867:75 7..364 8	gap2	ATCEA4 S855, ATCEA4 S31482	100, 92	ATL8C9 867:75 7..364 8	0.93	g45386 24	100	1686	1.6e- 170	(AJ133 502) hypothe tical protei n [Nicot iana tabacu m]	
138067	ATU000 007	ATL8C1 0254:1 533..3 914	gap2	ATCEA4 S33371 , ATCEA4 S33780 , ATCEA4 S27907 , ATCEA4 S25947	100, 100, 90, 84	ATL8C1 0254:1 533..3 550	0.91	g44540 43	100	1118		(AI035 394) putati ve recept or kinase [Arabi dopsis thalia na]	

138068	ATU000 008	ATL8C1 5562:9 06..52 56	gap2	ATCEA4 S14038 , ATCEA4 S15394 , ATCEA4 C10823 1, ATCEA4 C33316 1, ATCEA4 S30349	100, 99, 98, 96, 90	ATL8C1 5562:2 170..5 148	0.89	g42622 36, g49143 71, g48368 97	100, 100, 67	870, 543, 211	2.8e- 89, 7.1e- 49, 1.6e- 21	(AC006 200) putati ve ribose 5- phosph ate isomer ase [Arabi dopsis thalia na]; (AC007 584) unknow n protei n [Arabi dopsis thalia na]; (AC007 369) Hypoth etical protei n [Arabi dopsis thalia na]
138069	ATU000 009	ATL8C1 2717:1 06..17 19	gap2	ATCEA4 C22782 1, ATCEA4 S25897	100, 83	ATL8C1 2717:1 92..17 16	0.87	g37023 32	100	1100	2.2e- 84	(AC005 397) unknow n protei n [Arabi dopsis thalia na]
138070	ATU000	ATL8C3	gap2	ATCEA4	100	ATL8C3	0.87	g37460	100,	547,	2.1e-	(AC005

010	4186:4 134..1 557			C81252 _1			4186:3 949..1 649		60, g30634 49	35	284	42, 4.3e- 20	311) unknown protein [Arabi dopsis thalia na]; (AC003 981) F22013 .11 [Arabi dopsis thalia na]
138071	ATU000 011	ATL8C3 6192:1 ..2345	gap2	ATCEA4 S1330, ATCEA4 C57159 _1, ATCEA4 S30666	100, 98, 85		ATL8C3 6192:1 28..23 45	0.87	g42205 27	100	847	8.2e- 72	(AL035 356) putati ve protei n [Arabi dopsis thalia na]
138072	ATU000 012	ATL8C3 6642:7 65..30 96	gap2	ATCEA4 S2671, ATCEA4 C25956 _1, ATCEA4 C11729 7_1, ATCEA4 C25956 _2	100, 97, 92, 84		ATL8C3 6642:7 67..30 96	0.86	g21790 9	100	785	4.2e- 52	(D1404 4) glycol ate oxidas e [Cucur bita sp.]
138073	ATU000 013	ATL8C2 5693:1 49..96 0	gap2	ATCEA4 C39704 _1	100		ATL8C2 5693:1 63..93 6	0.85	g48368 87	100	627	3.2e- 60	(AC007 260) lcl pr t_seq No defini tion

138074	ATU000014	ATL8C33457:3684..1	gap2	ATCEA4S2102,ATCEA4C5970_1,ATCEA4C5970_2,ATCEA4C63511_1	100,98,96,95	ATL8C33457:3663..465	0.84	g3879145, g459890, g1914685	100,100,42	263,270,316	6.9e-23, 7.1e-17, 3.2e-27	line found [Arabidopsis thaliana] (Z93386) predicted using GeneFinder; Similarity to Human placenta (DIFF33) protein (TR:Q13530); cDNA EST YK198a11.5 comes from this gene [Caenorhabditis elegans]; (L29441) overexpressed in testicular
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138075	ATU000 015	ATL8C1 826:24 77..26 1	gap2	ATCEA4 C8244_1, ATCEA4 S27716	100, 86	ATL8C1 826:24 77..26 1	0.84	g24971 84	100	178	2.6e- 14	VESICLE TRANSPORT V-SNARE PROTEIN VTI1 [Saccharomyces cerevisiae]
138076	ATU000 016	ATL8C1 7732:7 163..4 413	gap2	ATCEA4 C2395_1, ATCEA4 C24408_1, ATCEA4 S30456, ATCEA4 S10009, ATCEA4 S17833	100, 93, 91, 88, 85	ATL8C1 7732:7 163..4 559	0.82	g30233 29	100	688	1.7e- 66	3-DEHYDROQUINATE SYNTHASE [Salmonella typhimurium]
138077	ATU000 017	ATL8C2 2945:1 707..5 262	gap2	ATCEA4 S816	100	ATL8C2 2945:1 987..5 262	0.82	g45394 14	100	2452	1.5e- 241	(Al049524) putative

138078	ATU000 018	ATL8C3 6834:1 ..4345	gap2	ATCEA4 S25927 , ATCEA4 C1227_1, ATCEA4 C28988_1	100, 99, 99	ATL8C3 6834:7 ..4345	0.82	g35229 42	100	1334	7.5e- 144	subtilisin-like protease [Arabis dopsis thaliana]
138079	ATU000 019	ATL8C2 0696:6 61..46 31	gap2	ATCEA4 C18426 1, ATCEA4 S2295, ATCEA4 C45401 1, ATCEA4 S4456	100, 100, 97, 96	ATL8C2 0696:6 87..46 17	0.82	g11706 06, g42396 96	100, 90	539, 262	2.7e- 49, 1.9e- 13	ADENYLATE KINASE , CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) [AJ132767) hypothetical protein [Arabis dopsis thaliana]
138080	ATU000 020	ATL8C2 4660:1 95..44 17	gap2	ATCEA4 S13887	100	ATL8C2 4660:1 95..44 17	0.81	g24355 11, g24355 18	100, 100	828, 677	9.0e- 89, 1.6e- 37	(AF024504) contains

138081	ATU000021	ATL8C1 3534:2 870..1 16	gap2	ATCEA4 S700	100	ATL8C1 3534:2 181..1 58	0.80	g4519671	100	272	4.6e-17	(AB017693) transfactor [Nicotiana tabacum]
138082	ATU000022	ATL8C4 44:1.. 4582	gap2	ATCEA4 S13861 , ATCEA4 C75193 1, ATCEA4	100, 97, 92	ATL8C4 44:177 ..4582	0.80	g4678216, g746510	100, 37	413, 309	3.0e-41, 7.8e-19	(AC007134) hypothetical protein [Arabi

138083	ATU000 023	ATL8C1 5866:6 026..1	gap2	ATCEA4 C15951 1, ATCEA4 S26149 , ATCEA4 C9213_1, ATCEA4 S30530 , ATCEA4 C14360_1	100, 99, 98, 96, 94	ATL8C1 5866:5 941..2 722, ATL8C1 5866:1 819..2 9	0.79, 0.79	g46307 48, g22135 94	100, 37	1862, 305	2.8e- 190, 1.2e- 28	dopsis thalia nal; (U2351 7) simila r to ubiqui tin conjug ating enzyme [Caeno rhabdi tis elegan s]
138084	ATU000 024	ATL8C3 1186:3 84..47 31	gap2	ATCEA4 C18654 1, ATCEA4 C19508 2, ATCEA4	100, 98, 88, 86, 86	ATL8C3 1186:4 78..47 31	0.78	g45393 14	100	2842	1.2e- 293	(AL035 679) kinesi n like protei n [Arabi

138085	ATU000 025	ATL8C3 6577:1 ..5697	gap2	S23384 , ATCEA4 S3239, ATCEA4 S3155 ATCEA4 S12559	100	ATL8C3 6577:3 6..569 7	0.78	g21911 69	100	1513	1.8e- 154	(AF007 270) Simila r to shaggy relate d. protei n kinase . Belong s to the CDC2/C DKX subfam ily [Arabi dopsis thalia na]
138086	ATU000 026	ATL8C2 6598:2 177..6 59	gap2	ATCEA4 S10403 , ATCEA4 S1694	100, 98	ATL8C2 6598:2 069..6 59	0.77	g18061 44	100	1535	1.2e- 129	(X9731 6) cdc2Ms E [Medic ago sativa l.
138087	ATU000 027	ATL8C1 8818:1 27..41 05	gap2	ATCEA4 S919, ATCEA4 C35222 1, ATCEA4 C16243 1	100, 100, 85	ATL8C1 8818:7 35..41 05	0.72	g45393 06	100	3588	0.0	(AL049 480) pumili o-like protei n [Arabi dopsis thalia

138088	ATU000 028	ATL8C3 7182:2 499..3 90	gap2	ATCEA4 S13656 , ATCEA4 C22954 _1	100, 98	ATL8C3 7182:2 061..3 90	0.67	g49144 26, g45672 81	100, 100	279, 339	na]	(AL050 351) putati ve protei n [Arabi dopsis thalia na]; (AC006 841) unknow n protei n [Arabi dopsis thalia na]
138089	ATU000 029	ATL8C3 1644:1 ..3074	gap2	ATCEA4 S1814, ATCEA4 S31844 , ATCEA4 C71697 _1, ATCEA4 S11333 , ATCEA4 S19089 , ATCEA4 C7947 _ 1	100, 98, 97, 95, 95, 93	ATL8C3 1644:7 4..395 , ATL8C3 1644:8 45..30 09	0.66, 0.89	g32832 20	100	1350	2.9e- 143	(AF061 241) splici ng factor hPRP17 [Homo sapien s]
138090	ATU000 030	ATL8C4 1647:8 54..1	gap2	ATCEA4 S9985, ATCEA4 C11223 _2, ATCEA4 C11223	100, 99, 99, 96, 83	ATL8C4 1647:8 13..13 2	0.56	g41668 1	100	656	3.7e- 59	ATP SYNTHA SE DELTA CHAIN, CHLORO PLAST

138091	ATU000 031	ATL8C2 363:29 86..34 4	gap2	ATCEA4 S10737 , ATCEA4 S15286 ATCEA4 S32192 , ATCEA4 S32193	100, 99	ATL8C2 363:29 24..12 27	0.41	g22905 32, g48952 24	100, 30	1396, 127	3.3e- 145, 2.5e- 05	PRECUR SOR [Nicot iana tabacu m] (U9474 8) AN11 [Petun ia x hybrid al; (AC007 660) putati ve revers e transc riptas e [Arabi dopsis thalia na] (AB016 803) orf509 e; simila r to putres cine oxidas e from Microc occus rubens [Deino coccus radiod urans] , (AF001
138092	ATU000 032	ATL8C1 9376:4 566..1 283	gap2	ATCEA4 S14012 , ATCEA4 C18831 1, ATCEA4 S26306	100, 97, 90			g34260 15, g39129 27, g12938 35	100, 47, 33	313, 251, 328	4.1e- 21, 1.7e- 28, 5.4e- 32	

138093	ATU000 033	ATL8C2 2472:1 678..8 01	gap2	ATCEA4 S13949 , ATCEA4 S26744	100, 100							g28946 01	100	786	1.5e- 62	(AL021 889) putati ve protei n [Arabi dopsis thalia na]	308) hypoth etical protei n [Arabi dopsis thalia na]; (U5696 5) C15H9. 5 gene produc t [Caeno rhabdi tis elegan s]
138094	ATU000 034	ATL8C4 8440:1 358..2 40	gap2	ATCEA4 C8177 1	100							g30333 95	100	390	1.9e- 44	(AC004 238) putati ve zinc- finger protei n [Arabi dopsis thalia na]	
138095	ATU000 035	ATL8C4 4028:1 280..3	gap2	ATCEA4 S14433 ,	100, 99, 94,	ATL8C4 4028:1 214..7	1.00					g13978 0	99	281	1.1e- 20	WOUND- INDUCE D [Arabi dopsis thalia na]	

138099	ATU000 039	ATL8C1 7337:2 018..5 70	gap2	ATCEA4 S11857 , ATCEA4 S12452	100, 82				g34137 08	100	417	1.7e- 41	na] (AC004 747) hypoth etical protei n [Arabi dopsis thalia na]
138100	ATU000 040	ATL8C1 685:35 14..49 57	gap2	ATCEA4 S12463	100				g42205 25	100	411	1.4e- 39	(AL035 356) putati ve tRNA isopen tenylt ransfe rase [Arabi dopsis thalia na]
138101	ATU000 041	ATL8C3 342:17 7..128 8	gap2	ATCEA4 C19348 1, ATCEA4 S25870 , ATCEA4 S11654	100, 98, 98				g23168 0	100	414	3.7e- 42	CALMOD ULIN- LIKE PROTEI N [Arabi dopsis thalia na]
138102	ATU000 042	ATL8C2 1598:5 65..19 29	gap2	ATCEA4 S34550 , ATCEA4 C62320 1	100, 94	ATL8C2 1598:6 57..19 21	0.93		g13261 63	99	440	4.7e- 41	(U5470 4) stress relate d protei n PvSRP [Phase olus vulgar is]

138103	ATU000 043	ATL8C3 6798:1 ..2526	gap2	ATCEA4 S1254	100	ATL8C3 6798:1 00..17 97	0.88	g35488 19, 945389 29	99, 38	240, 97	4.3e-24, 1.3e-06	(AC005 313) putative hetero geneou s nuclea r ribonu cleopr otein [Arabi dopsis thalia na]; (AL049 483) putati ve nuclei c acid bindin g protei n [Arabi dopsis thalia na]
138104	ATU000 044	ATL8C1 6403:2 76..19 49	gap2	ATCEA4 S13717 , ATCEA4 S3380, ATCEA4 S17819	100, 100, 82	ATL8C1 6403:2 76..19 49	0.85	g73190 8	99	235	2.1e-17	HYPOTH ETICAL 17.1 KD PROTEI N IN BET1-PAN1 INTERG ENIC REGION [Sacch aro myc es cerevi

138105	ATU000 045	ATL8C3 9279:8 37..11 3	gap2	ATCEA4 C18330 _1	100	ATL8C3 9279:8 30..50 6	0.82	g72874 9	99	269	1.3e- 20	siae] TAPETU M- SPECIF IC PROTEI N A9 PRECUR SOR [Brass ica napus] (AE000 715) hypoth etical protei n [Aquif ex aeolic us]
138106	ATU000 046	ATL8C2 2866:1 110..2 692	gap2	ATCEA4 S13600 , ATCEA4 C77937 _1	100, 98	ATL8C2 2866:1 110..2 567	0.80	g29834 76	99	317	8.8e- 29	(AE000 715) hypoth etical protei n [Aquif ex aeolic us]
138107	ATU000 047	ATL8C2 1239:1 ..2966	gap2	ATCEA4 C91030 _2, ATCEA4 C46484 _1, ATCEA4 S19464	100, 93, 93	ATL8C2 1239:2 49..14 71, ATL8C2 1239:1 961..2 966	0.76, 0.92	g44551 74	99	640	1.6e- 51	(AL035 521) putati ve protei n [Arabi dopsis thalia na] (Z9733 7) S- linalo ol syntha se homolo g [Arabi dopsis thalia na]; (Z9733
138108	ATU000 048	ATL8C2 4831:6 527..3 60	gap2	ATCEA4 S2327, ATCEA4 S3103, ATCEA4 S1839	100, 99, 82	ATL8C2 4831:6 527..5 43	0.62	g22448 58, g22448 59	99, 65	469, 1377	8.3e- 33, 1.8e- 125	(Z9733 7) S- linalo ol syntha se homolo g [Arabi dopsis thalia na]; (Z9733

138109	ATU000 049	ATL8C3 4328:4 837..2 999	gap2	ATCEA4 S1650	100	ATL8C3 4328:4 837..2 999	0.59	g45126 68	99	339	2.4e- 19	7) hypoth etical protein [Arabi dopsis thalia na]
138110	ATU000 050	ATL8C4 902:11 37..19 09	gap2	ATCEA4 C35001 1, ATCEA4 C31752 3_	100, 97			g47047 30	99	475	1.4e- 46	(AF121 355) peroxi redoxi n TPx1 [Arabi dopsis thalia na]
138111	ATU000 051	ATL8C1 4810:1 855..5 35	gap2	ATCEA4 S25771 , ATCEA4 C15670 7, ATCEA4 C15670 6, ATCEA4 C15670 5, ATCEA4 S11271 , ATCEA4 S12660	100, 99, 99, 98, 88, 84			g81966	99	130	3.0e- 08	hypoth etical protein n 91 - garden pea chloro plast [Pisum sativu m]

138112	ATU000 052	ATL8C4 7988:3 21..24 80	gap2	ATCEA4 C29075 2, ATCEA4 C40880 1, ATCEA4 C3138 1, ATCEA4 S24186 , ATCEA4 S30396	100, 96, 96, 91, 87				g82201	99	389	2.4e-16	hypothetical protein 131 - common tobacco chloroplast [Nicotiana tabacum]
138113	ATU000 053	ATL8C3 6440:1 041..7 40	gap2	ATCEA4 S34654	100				g26422 15	99	155	1.3e-11	(AF030386) NOI protein [Arabidopsis thaliana]
138114	ATU000 054	ATL8C2 027:70 8..114	gap2	ATCEA4 S14075 , ATCEA4 S789	100, 95				g13512 67	99	173	1.6e-13	TROPONIN C, ISOFORM 41C [Drosophila melanogaster]
138115	ATU000 055	ATL8C2 2033:1 ..1764	gap2	ATCEA4 C31196 1	100	ATL8C2 2033:9 7..154 6			g30055 76	97	2015	2.0e-197	(AF047718) putative high affinity tyrosine transporter; GmNRT2 [Glycine max]

138116	ATU000 056	ATL8C1 6282:6 03..23 52	gap2	ATCEA4 C9550_1, ATCEA4 S33269	100, 93					947752 96	97	160	3.2e- 16	ne max] (AJ238 631) putati ve MINE protei n [Chlor ella protot hecoide es]
138117	ATU000 057	ATL8C3 7683:1 683..4 0	gap2	ATCEA4 C26941_1, ATCEA4 C34481_1	100, 97					g44553 57	96	945	5.5e- 90	(AL035 524) putati ve protei n [Arabi dopsis thalia na]
138118	ATU000 058	ATL8C3 1661:1 ..1093	gap2	ATCEA4 S4404	100	ATL8C3 1661:6 1878:1 1..109 0	0.72			g46782 10	95	448	4.5e- 40	(AC007 134) hypoth etical protei n [Arabi dopsis thalia na]
138119	ATU000 059	ATL8C1 1878:1 ..855	gap2	ATCEA4 S1789, ATCEA4 C16628_1, ATCEA4 S32367	100, 99, 88	ATL8C1 1878:1 51..57 4	0.79			g29822 43	94	245	5.7e- 16	(AF051 204) hypoth etical protei n [Picea marian a]
138120	ATU000	ATL8C1	gap2	ATCEA4	100	ATL8C1	0.77			g58526	94	321	1.6e-	HYPOXA

	060	9069:1 204..4 4		S13397		9069:1 098..4 4		4				22	NTHINE - GUANIN E PHOSPH ORIBOS YLTRAN SFERAS E (HGERT) (HGERT ASE) [Bacil lus subtil is]
138121	ATU000 061	ATL8C4 9877:1 ..1192	gap2	ATCEA4 S24	100	ATL8C4 9877:1 14..86 8	0.73	g36084 12	94	930	2.0e- 98		(AF079 355) protei n phosph atase- 2c [Mesem bryant hemum crysta llinum]
138122	ATU000 062	ATL8C4 9952:1 792..7 39	gap2	ATCEA4 C20296 _1	100	ATL8C4 9952:1 644..7 86	0.56	g44328 42	93	482	1.9e- 54		(AC006 283) hypoth etical protei n [Arabi dopsis thalia na]
138123	ATU000 063	ATL8C1 2094:5 631..1	gap2	ATCEA4 S809, ATCEA4 S31299	100, 88	ATL8C1 2094:5 548..1 25	0.94	g46783 39	92	5971	0.0		(AL049 658) putati ve protei

138124	ATU000 064	ATL8C3 8350:2 390:3 58	gap2	ATCEA4 S26090 , ATCEA4 C2246_1	100, 97	ATL8C3 8350:2 308:6 17	0.90	g40068 71	92	1662	3.8e-139	n [Arabi dopsis thalia na] (Z9970 7) patati n-like protei n [Arabi dopsis thalia na]
138125	ATU000 065	ATL8C1 6977:1 ..3379	gap2	ATCEA4 S1725, ATCEA4 S2265	100, 99	ATL8C1 6977:6 9..329 2	0.86	g26233 01	91	952	1.1e-67	(AC002 409) putati ve kinase [Arabi dopsis thalia na]
138126	ATU000 066	ATL8C3 1202:7 84..1	gap2	ATCEA4 C3982_5, ATCEA4 C3982_3, ATCEA4 S18079	100, 98, 89	ATL8C3 1202:4 21..32 0	0.78	g13507 36	91	189	1.5e-12	60S RIBOSO MAL PROTEI N L37 [Lycop ersico n escule ntum] (AL035 602) hypoth etical protei n [Arabi dopsis thalia na]
138127	ATU000 067	ATL8C5 43:117 3..1	gap2	ATCEA4 S2699	100	ATL8C5 43:108 6..787	0.72	g44690 17	91	869	5.8e-57	(AL035 602) hypoth etical protei n [Arabi dopsis thalia na]

138128	ATU000 068	ATL8C1 4900:9 66...91	gap2	ATCEA4 S32183 , ATCEA4 S7112	100, 99	ATL8C1 4900:8 64...93	1.00	g45396 09	90	226	1.6e- 22	(AL049 522) WD repeat protei n [Schiz osacch aromyc es pombe]
138129	ATU000 069	ATL8C1 4780:5 346...5 63	gap2	ATCEA4 C44237 1, ATCEA4 C42353 1, ATCEA4 C11660 0 1, ATCEA4 S9536, ATCEA4 C56620 1, ATCEA4 S8233, ATCEA4 S34432 , ATCEA4 C12669 8 1, ATCEA4 S35823	100, 99, 97, 96, 95, 90, 89, 86, 84	ATL8C1 4780:5 199...1 354	0.78	g23166 0	90	3608	1.7e- 305	HYPOTH ETICAL 226 KD PROTEI N (ORF 1901) []
138130	ATU000 070	ATL8C1 3035:4 896...1 610	gap2	ATCEA4 S11304 , ATCEA4 C19518 1, ATCEA4 C17935 1, ATCEA4	100, 100, 98, 91, 87	ATL8C1 3035:3 709...1 878	0.97	g46790 28	89	936	2.9e- 107	(AF077 207) HSPC02 1 [Homo sapien s]

138134	ATU000 074	ATL8C4 5760:7 229..2 260	gap2	ATCEA4 C22096 1, ATCEA4 S23839	100, 95	ATL8C4 5760:5 715..2 260	0.93	g43097 34	86	1635	8.0e- 141	(AC006 439) putati ve 26S proteo some regula tory subuni t 8 [Arabi dopsis thalia na]
138135	ATU000 075	ATL8C8 43:215 5..13	gap2	ATCEA4 C39414 1, ATCEA4 S11571 , ATCEA4 S11679	100, 98, 83	ATL8C8 43:208 0..13	0.86	g32818 68	85	2612	5.8e- 252	(AL031 004) putati ve protei n [Arabi dopsis thalia na]
138136	ATU000 076	ATL8C3 6984:1 ..1232	gap2	ATCEA4 C8348 1, ATCEA4 S29924	100, 91	ATL8C3 6984:6 1..111 6	0.67	g21300 04	85	256	3.4e- 20	squamo sa- promot er bindin g protei n 2 - garden snapdr agon [Antir rhinum majus]

138137	ATU000 077	ATL8C3 9558:1 269..3 02	gap2	ATCEA4 C27645 _1	100	ATL8C3 9558:1 103..3 53	0.62	g48369 28	85	582	2.5e- 60	(AC006 085) Simila r to protei n kinase s [Arabi dopsis thalia na]
138138	ATU000 078	ATL8C1 7377:1 ..869	gap2	ATCEA4 S894, ATCEA4 S5995	100, 86	ATL8C1 7377:5 9..856	0.56	g38688 57	85	1007	4.8e- 106	(AB013 886) RAV1 [Arabi dopsis thalia na]
138139	ATU000 079	ATL8C3 7123:1 722..8 07	gap2	ATCEA4 C12379 _1	100			g28275 58	85	595		(AL021 635) putati ve DNA bindin g protei n [Arabi dopsis thalia na]
138140	ATU000 080	ATL8C4 5637:1 ..504	gap2	ATCEA4 C70706 _1	100	ATL8C4 5637:3 ..402	0.85	g29959 53	84	137	0.013	(AF053 565) glutar edoxin I [Mesem bryant hemum crysta llinum]
138141	ATU000 081	ATL8C9 785:1. .3246	gap2	ATCEA4 C33178 _1,	100, 88, 84	ATL8C9 785:6. .3238	0.80	g47592 80	84	2452	9.3e- 273	U5 snRNP- specif

138142	ATU000 082	ATL8C1 695:23 88..93 4	gap2	ATCEA4 S1996, ATCEA4 S9061	100	ATL8C1 695:23 88..11 54	0.66	g33342 44	84	630	1.9e- 54	ic protei n, 116 kD [Homo sapien s]
138143	ATU000 083	ATL8C4 6537:1 55..26 04	gap2	ATCEA4 S7775, ATCEA4 C8526 1	100, 98	ATL8C4 6537:1 55..25 00	0.68	g28277 15	82	3565	0.0	(AL021 684) recept or protei

138144	ATU000 084	ATL8C4 8916:1 ..1766	gap2	ATCEA4 C21663 1, ATCEA4 C99026 1	100, 97						g30333 92	82	2685	3.4e- 263	n kinase - like protei n [Arabi dopsis thalia na]
138145	ATU000 085	ATL8C4 9015:1 781..2 65	gap2	ATCEA4 S33086 , ATCEA4 S14122	100, 99	ATL8C4 9015:1 550..5 70	0.82				g29824 51	81	1261	2.8e- 115	(AL022 223) putati ve protei n [Arabi dopsis thalia na]
138146	ATU000 086	ATL8C2 6015:6 73..23 53	gap2	ATCEA4 C8568 2, ATCEA4 C8568 1, ATCEA4	100, 100, 99, 97, 91	ATL8C2 6015:7 53..22 13	0.62				g44552 76	81	1323	2.7e- 138	(AL035 527) peptid e transp orter- like

138147	ATU000087	ATL8C4 8934:1 ..1939	gap2	ATL8C4 8934:1 ..1939	ATL8C4 8934:1 88..16 55	0.75	g27022 72	80	871	1.8e- 106	(AC003 033) hypoth etical protein [Arabi dopsis thalia na]
138148	ATU000088	ATL8C4 0666:1 ..3199	gap2	ATL8C4 0666:1 ..3199	ATL8C4 0666:5 6..319 9	0.44	g22526 32	80	1390	5.5e- 128	(U9597 3) Barley Mlo protein isolat [Arabi dopsis thalia na]
138149	ATU000089	ATL8C3 5627:1 478..2 844	gap2	ATL8C3 5627:1 478..2 844	ATL8C3 5627:1 990..2 716	0.83	g42042 63	79	782	7.3e- 79	(AC005 223) 40409 [Arabi dopsis thalia na]
138150	ATU000090	ATL8C4 6561:2 450..1	gap2	ATL8C4 6561:2 450..1	ATL8C4 6561:1 990..8 18	0.75	g27603 18, g48368 85	79, 77	281, 323	4.5e- 24, 1.3e- 25	(AC002 130) F1N21. 2 [Arabi

138151	ATU000 091	ATL8C3 03:296 ..1984	gap2	ATCEA4 S14072 , ATCEA4 C13084 1, ATCEA4 S7321	100, 99, 86	ATL8C3 03:304 ..1832	0.61	g11727 04	79	669	1.1e- 76	dopsis thalia na]; (AC007 260) Hypoth etical protei n [Arabi dopsis thalia na]
138152	ATU000 092	ATL8C2 3883:2 410..1	gap2	ATCEA4 C50752 1, ATCEA4 C14037 1	100, 88	ATL8C2 3883:2 345..1 0	0.80	g30803 93	78	1418	1.7e- 144	(AL022 603) NADH dehydr ogenas e like protei n [Arabi dopsis thalia na]
138153	ATU000 093	ATL8C4 3992:2 605..1	gap2	ATCEA4 C17888 1, ATCEA4 S32188	100, 94	ATL8C4 3992:2 605..2 4	0.63	g45080 69	78	847	(AC005 882) 12246 [Arabi dopsis	

138154	ATU000 094	ATL8C2 4608:1 ..2230	gap2	ATCEA4 C18362 1, ATCEA4 S22400 , ATCEA4 S22399	100, 91, 83	ATL8C2 4608:1 593..1 03	0.52	g30212 85	78	686	4.9e- 44	thalia nal (AL022 347) hypoth etical protei n [Arabi dopsis thalia nal]
138155	ATU000 095	ATL8C2 4165:1 121..2 528	gap2	ATCEA4 S13624	100	ATL8C2 4165:1 121..2 480	0.90	g62960 0	77	1760	3.3e- 181	1- aminoc yclopr opane- 1- carbox ylate syntha se (EC 4.4.1. 14) - wild cabbag e [Brass ica olerac ea]
138156	ATU000 096	ATL8C2 9755:1 094..9 2	gap2	ATCEA4 S2198	100	ATL8C2 9755:1 006..9 2	0.82	g30637 11	77	466	2.1e- 45	(AL022 537) hypoth etical protei n [Arabi dopsis thalia nal]
138157	ATU000 097	ATL8C1 7735:1 14..48 72	gap2	ATCEA4 C4322- 1, ATCEA4 S2120,	100, 97, 95	ATL8C1 7735:1 353..4 837	0.69	g45875 71, g32420 77	77, 38	607, 151	3.6e- 36, 1.4e- 12	(AC006 550) Belong s to the.

138158	ATU000 098	ATL8C2 879:16 21..1	gap2	ATCEA4 C85180 1, ATCEA4 C35730 1	100, 99	ATL8C2 879:16 06..16 3	0.64	g10869 00	77	316	3.5e- 21	PF 010 27 Unchar acteri zed protei n family UPF000 5 with 7 transm embran e domain s. [Arabi dopsis thalia na]; (AJ003 119) protei n phosph atase 2C [Arabi dopsis thalia na] (U4127 8) contai ns simila rity to G beta repeat s (PROSI TE:PS0 0670) of the
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138159	ATU000 099	ATL8C4 5568:4 125..2 40	gap2	ATCEA4 C89393 1, ATCEA4 C894_1 , ATCEA4 C21011 1, ATCEA4 S10264	100, 97, 91, 82	ATL8C4 5568:4 054..3 40	0.49	g17032 00	77	1343	1.3e- 99	beta- transd ucin family [Caeno rhabdi tis elegan s]
138160	ATU000 100	ATL8C2 9256:1 27..15 44	gap2	ATCEA4 S5637	100	ATL8C2 9256:2 13..14 28	0.95	g44067 89	76	1459	1.4e- 158	(AC006 532) putati ve glutam ate decarb oxylas e [Arabi dopsis thalia na]
138161	ATU000 101	ATL8C1 6715:1 ..2374	gap2	ATCEA4 S6296, ATCEA4 S36318	100, 87	ATL8C1 6715:8 8..237 4	0.90	g25762 55	76	961	1.5e- 86	(AJ001 729) TH65 protei n [Arabi dopsis thalia na]
138162	ATU000 102	ATL8C1 0850:3 790..9	gap2	ATCEA4 S8311, ATCEA4	100, 94, 84	ATL8C1 0850:3 555..9	0.93	g23846 96	75	151	1.7e- 12	(AF013 216) acyl-

	17		17	S10508 , ATCEA4 S10788		100, 98	ATL8C2 0683:1 96..12 59	0.82	g32876 93	75	1509	1.3e- 159	CoA oxidase [Myxococcus xanthus]
138163	ATU000 103	ATL8C2 0683:8 2..138 1	gap2	ATCEA4 S6373, ATCEA4 C22329 _1									(AC003 979) Simila r to LIM17 gene produc t gb 165 3769 from the genome of Synech ocysti s sp. gb D90 916. [Arabi dopsis thalia na]
138164	ATU000 104	ATL8C5 0002:1 376..1	gap2	ATCEA4 C38379 1, ATCEA4 C18881 _1		100, 99	ATL8C5 0002:1 271..1 53	0.76	g31281 68	75	902	2.5e- 86	(AC004 521) putati ve carbox yl- termin al peptid ase [Arabi dopsis thalia na]
138165	ATU000	ATL8C1	gap2	ATCEA4		100	ATL8C1	0.64	q72877	75	518	5.6e-	ACTIVA

105	8843:1 406..1		C28653 _1		8843:1 406..8 8	7	58	TOR 1 36 KD SUBUNIT (REPLICATION FACTOR C 36 KD SUBUNIT) (A1 36 KD SUBUNIT) (RF-C 36 KD SUBUNIT) (RFC36) [Homo sapiens]			
138166	ATU000 106	ATL8C2 6631:2 342..1	gap2	ATCEA4 C18201 _1	100	ATL8C2 6631:2 103..6 41	0.97	g14018 5	269	7.5e- 29	PROBAB LE GYP7 PROTEIN [Yarrowia lipolytica]
138167	ATU000 107	ATL8C2 8333:1 242..1	gap2	ATCEA4 C10642 8_1, ATCEA4 C27213 _1, ATCEA4 S11667	100, 98, 97	ATL8C2 8333:1 242..2 68	0.95	g47387 4	1164	1.7e- 123	(U08285) a membrane- associated salt-inducible protein [Nicotiana]

138168	ATU000 108	ATL8C1 0943:3 136..1	gap2	ATCEA4 C6032_ 1, ATCEA4 C15210 1, ATCEA4 C11699 7 1	100, 96, 96	ATL8C1 0943:3 048..4 3	0.88	g14958 04	74	2150	1.1e- 203	tabacu m] (X9640 6) 13- lipoxy genase [Solan um tubero sum]
138169	ATU000 109	ATL8C4 858:23 99..1	gap2	ATCEA4 S1235, ATCEA4 S7713, ATCEA4 S32666	100, 92, 87	ATL8C4 858:22 48..37 8	0.84	g39994 0	74	1999	1.5e- 215	MITOCH ONDRIA L HEAT SHOCK 70 KD PROTEI N PRECUR SOR [Phase olus vulgar is]
138170	ATU000 110	ATL8C1 7319:1 771..1	gap2	ATCEA4 C21187 1, ATCEA4 C9405_ 1	100, 97			g22448 39	74	747	8.5e- 76	(Z9733 7) hypoth etical protei n [Arabi dopsis thalia na]
138171	ATU000 111	ATL8C1 2344:1 ..1261	gap2	ATCEA4 S916, ATCEA4 C29155 _1	100, 88	ATL8C1 2344:4 7..120 5	0.98	g48952 61	73	958	1.1e- 97	(AC007 658) putati ve serine /threo nine protei n kinase , 5'

138172	ATU000 112	ATL8C4 700:10 02..1	gap2	ATCEA4 S13359 , ATCEA4 C19590 _1	100, 96	ATL8C4 700:95 3..143	0.79	g54442 1	73	166	0.17	partia 1 [Arabi dopsis thalia na]
138173	ATU000 113	ATL8C3 1511:2 849..9 4	gap2	ATCEA4 S12524 , ATCEA4 S6692, ATCEA4 C50815 2, ATCEA4 S33144	100, 95, 94, 82	ATL8C3 1511:2 652..9 4	0.76	g22528 62	73	493	2.0e- 41	GLYCIN E-RICH RNA- BINDIN G PROTEI N 1 [Sorgh um bicolo r]
138174	ATU000 114	ATL8C1 2992:4 32..30 04	gap2	ATCEA4 S1137	100	ATL8C1 2992:4 32..29 12	0.66	g47551 99	73	299	2.6e- 14	(AC007 018) hypoth etical protei n [Arabi dopsis thalia na]
138175	ATU000 115	ATL8C8 011:18 29..1	gap2	ATCEA4 S13961 , ATCEA4 S2859, ATCEA4 C27631	100, 99, 94, 91, 87	ATL8C8 011:17 85..34 7	0.56	g30045 65	73	1694	2.7e- 168	(AC003 673) putati ve protei n kinase

138176	ATU000 116	ATL8C1 9751:1 090...3 871	gap2	1, ATCEA4 S33865 , ATCEA4 C28868 1	100, 97, 90, 84							g38853 41	73	916	2.5e- 97	[Arabi dopsis thalia na]
138177	ATU000 117	ATL8C3 8152:1 059...1	gap2	ATCEA4 S3256, ATCEA4 S30602	100, 86	ATL8C3 8152:1 029...9	0.81					g40564 60	72	1554	1.2e- 157	(AC005 990) Contai ns simila rity to gb L26 505 Met30p from Saccha romyce s cerevi siae. ESTs gb F14 133, gb T46 217, gb AA4 04758 and gb Z37 647 come from

138178	ATU000 118	ATL8S1 6762:3 74..1	gap2	ATCEA4 C33049 2, ATCEA4 C33049 1_	100, 98	ATL8S1 6762:3 56..14	0.79	g17235 68	72	76	4.9e- 05	HYPOTH ETICAL 10.7 KD PROTEI N C17C9. 09C IN CHROMO SOME I [Schiz osacch aromyc es pombe]
138179	ATU000 119	ATL8C3 5250:1 ..1656	gap2	ATCEA4 S23794 , ATCEA4 C20508 1_	100, 97	ATL8C3 5250:1 19..15 27	0.90	g25018 50	71	1140	1.9e- 116	(AF012 823) GDP dissoc iation inhibi tor [Nicot iana tabacu m]
138180	ATU000 120	ATL8C2 5738:1 915..1	gap2	ATCEA4 C20570 1, ATCEA4 C89353 1_	100, 97	ATL8C2 5738:1 784..1 57	0.69	g33416 97	71	391	7.0e- 36	(AC003 672) hypoth etical protei n [Arabi dopsis thalia na]
138181	ATU000 121	ATL8C1 4844:9 ..806	gap2	ATCEA4 S31599	100	ATL8C1 4844:5 49..68	0.51	g40975 87	70	108	9.8e- 08	(U6492 6) NTGP5

					ATCEA4 C2169_1			6									e-rich protein isolog [Arabi dopsis thalia na]
138186	ATU000 126	ATL8C3 1659:7 78..17 11	gap2	ATCEA4 C13667 _1	100						69	g25586 60	175	8.2e- 19	(AC002 354) No defini tion line found [Arabi dopsis thalia na]		
138187	ATU000 127	ATL8C4 7018:1 861..5 476	gap2	ATCEA4 C21846 1, ATCEA4 C89626 _1	100, 94		ATL8C4 7018:3 669..4 848	0.91			68	g33425 56	557	4.4e- 43	(AF077 528) import in alpha [Arabi dopsis thalia na]		
138188	ATU000 128	ATL8C1 8065:2 92..18 93	gap2	ATCEA4 C15330 1, ATCEA4 S691, ATCEA4 S1845	100, 99, 98		ATL8C1 8065:3 55..18 66	0.74			68	g30804 33	874	2.4e- 93	(AL022 605) putati ve gamma- glutam yltran sferas e [Arabi dopsis thalia na]		
138189	ATU000 129	ATL8C1 4911:1 ..1297	gap2	ATCEA4 S6751, ATCEA4 C9382	100, 96						68	g44671 51	1705	7.9e- 124	(AL035 540) putati ve		

138193	ATU000 133	ATL8C1 1681:1 886..1	gap2	ATCEA4 S9216, ATCEA4 S2786	100, 96					g12554 30, g37381 70	67, 42	203, 143	7.6e- 14, 8.3e- 12	subsp. tricho carpal (U5315 5) No defini tion line found [Caeno rhabdi tis elegan s]; (AL031 856) putati ve involv ement in cell wall struct ure or biosyn thesis , by simila rity to N3265 yeast [Schiz osacch aromyc es pombe]
138194	ATU000 134	ATL8C1 2157:1 ..845	gap2	ATCEA4 C50015 1, ATCEA4 S6577	100, 87					g30804 11	66	319	2.6e- 26	(AL022 604) putati ve protei n [Arabi

138195	ATU000 135	ATL8C3 2174:3 099..1 114	gap2	ATCEA4 C4728 1, ATCEA4 C92043 _1	100, 94	ATL8C3 2174:2 916..1 309	0.97	g45593 33	65	587	6.1e- 48	dopsis thalia na] (AC007 087) unknown n protei n [Arabi dopsis thalia na]
138196	ATU000 136	ATL8C2 4323:2 674..3 33	gap2	ATCEA4 S1103, ATCEA4 C34727 _1	100, 97	ATL8C2 4323:2 586..3 33	0.90	g29247 77	65	1750	3.4e- 175	(AC002 334) putati ve recept or protei n kinase [Arabi dopsis thalia na]
138197	ATU000 137	ATL8C3 5004:2 302..1	gap2	ATCEA4 S11809	100	ATL8C3 5004:2 239..1 8	0.74	g28277 15	65	802	1.2e- 70	(AL021 684) recept or protei n kinase - like protei n [Arabi dopsis thalia na]
138198	ATU000 138	ATL8C2 7592:7 746..4 801	gap2	ATCEA4 S2459, ATCEA4 C23677 2,	100, 99, 98, 86	ATL8C2 7592:7 746..5 155	0.70	g31356 69	65	398		(AF064 084) prenyl cystei ne

138199	ATU000 139	ATL8C4 7840:1 ..921	gap2	ATCEA4 C26032 1, ATCEA4 S21056	100					g44903 05	65	1053	9.3e- 99	(AL035 678) putati ve protei n [Arabi dopsis thalia na]	carbox yl methyl transf erase [Homo sapien s]
138200	ATU000 140	ATL8C2 6981:1 ..2216	gap2	ATCEA4 C25516 1, ATCEA4 C8920_1	100, 97	ATL8C2 6981:1 24..21 29	0.73			g33193 57	64	1729	1.1e- 131	(AF077 407) contai ns simila rity to phosph oenolp yruvat e syntha se (ppsA) (GB:AE 001056) [Arabi dopsis thalia na]	(AF077 407) contai ns simila rity to phosph oenolp yruvat e syntha se (ppsA) (GB:AE 001056) [Arabi dopsis thalia na]
138201	ATU000 141	ATL8C1 991:11 9..100 7	gap2	ATCEA4 S1248	100	ATL8C1 991:14 9..896	0.73			g25826 39	64	976	5.6e- 89	(AJ002 414) hnRNP- like protei n	(AJ002 414) hnRNP- like protei n

138202	ATU000 142	ATL8C3 9404:1 ..1602	gap2	ATCEA4 S3232, ATCEA4 C6296_2, ATCEA4 S1095, ATCEA4 C6296_1, ATCEA4 S35482	100, 97, 96, 94, 93	ATL8C3 9404:1 09..15 88	0.75	g42621 47	63	823	1.2e- 51	[Arabi dopsis thalia na] (AC005 275) putati ve homolo g of transp ort inhibi tor respon se 1 [Arabi dopsis thalia na]
138203	ATU000 143	ATL8C2 5102:1 352..1 11	gap2	ATCEA4 C29933 1, ATCEA4 S12833	100, 98	ATL8C2 5102:1 262..1 11	0.73	g31281 86	63	78	3.1e- 09	(AC004 521) hypoth etical protei n [Arabi dopsis thalia na]
138204	ATU000 144	ATL8C1 509:87 ..1608	gap2	ATCEA4 S30118	100	ATL8C1 509:14 1..146 7	0.41	g42181 22	63	555	4.8e- 64	(AL035 353) putati ve protei n [Arabi dopsis thalia na]
138205	ATU000 145	ATL8C3 5406:1 ..3764	gap2	ATCEA4 C14853 9 1, ATCEA4 C11909	100, 97, 91			g36034 73, g48369 17	63, 37	213, 599	9.3e- 17, 2.2e- 59	(AF090 698) elicit or- respon

138206	ATU000 146	ATL8C4 6053:3 540..1	gap2	ATCEA4 S4698, ATCEA4 S8405	100, 89	ATL8C4 6053:3 151..2 44	0.89	g24657 38	62	508	4.4e- 47	sive gene-3 [Oryza sativa]; (AC007 153) 80099 [Arabi dopsis thalia nal (AF022 186) cell divisi on protei n [Cyani dium caldar ium]
138207	ATU000 147	ATL8C3 1802:1 551..1	gap2	ATCEA4 C74672 _1	100	ATL8C3 1802:1 163..8 1	0.84	g22447 80	62	1282	1.4e- 117	(Z9733 5) hypoth etical protei n [Arabi dopsis thalia nal (Z6936 0) Simila rity to Yeast hypoth etical protei n 00926 (PIR
138208	ATU000 148	ATL8C3 4378:2 30..90 3	gap2	ATCEA4 C16982 _1	100	ATL8C3 4378:2 54..88 9	0.43	g38763 64	62	99	0.091	

138209	ATU000 149	ATL8C2 7037:2 25..1	gap2	ATCEA4 C42637 _1	100	ATL8C2 7037:2 02..13	0.91	g26187 00	61	169	5.8e- 12	(AC002 510) unknown protein [Arabi dopsis thalia na]	Acc. No. S50412) [Caeno rhabdi tis elegan s]
138210	ATU000 150	ATL8C2 2169:1 914..4 2	gap2	ATCEA4 S8133	100	ATL8C2 2169:1 912..7 2	0.82	g22447 85	61	877	5.8e- 75	(Z9733 5) hypoth etical protei n [Arabi dopsis thalia na]	Acc. No. S50412) [Caeno rhabdi tis elegan s]
138211	ATU000 151	ATL8C4 7935:1 ..2764	gap2	ATCEA4 S25977 , ATCEA4 C34992 _1	100, 99	ATL8C4 7935:1 31..26 63	0.79	g25064 70	61	1848	8.8e- 174	ALPHA- 1,4 GLUCAN PHOSPH ORYLAS E, L ISOFOR M PRECUR SOR (STARC H PHOSPH ORYLAS E L) [Vicia	Acc. No. S50412) [Caeno rhabdi tis elegan s]

138212	ATU000 152	ATL8C4 5585:1 164..7 2	gap2	ATCEA4 C37640 _1	100	ATL8C4 5585:1 076..9 8	0.63	g27696 42	61	1480	3.7e- 146	faba[(Z9721 5) nine- cis- epoxyc aroten oid dioxyg enase [Lycop ersico n escule ntum] (AL035 678) putati ve protei n [Arabi dopsis thalia na]
138213	ATU000 153	ATL8C2 4227:1 45..21 33	gap2	ATCEA4 S2848, ATCEA4 S11717 , ATCEA4 C35178 _1	100, 96, 96	ATL8C2 4227:1 89..20 73	0.54	g44903 14	61	861	1.4e- 75	2- OXOGLU TARATE /MALAT E TRANSL OCATOR PRECUR SOR [Spina cia olerac ea]
138214	ATU000 154	ATL8C8 579:13 71..1	gap2	ATCEA4 S6042	100	ATL8C8 579:12 09..11 25	0.48	g24995 35	61	810	1.1e- 62	(AC007 354) Simila r to gb U54 559 eIF3-
138215	ATU000 155	ATL8C1 1466:1 00..13 35	gap2	ATCEA4 S5515, ATCEA4 C4443_1	100, 98	ATL8C1 1466:1 10..12 42	0.80	g48742 64	60	725	2.0e- 74	

138216	ATU000 156	ATL8C4 746:37 11..26 0	gap2	ATCEA4 C6789_1, ATCEA4 S20271 , ATCEA4 C14416 5_1	100, 94 98, 94	ATL8C4 746:29 64..46 0	0.77	g29824 58	60	1226	6.1e- 105	p40 subunit from Homo sapiens and is a member of the PF1013 98 Mov34 family . ESTs gb N96 623 and gb N07 519 come from this gene. [Arabi dopsis thalia na]
138217	ATU000 157	ATL8C2 1772:1 066..1	gap2	ATCEA4 S8580, ATCEA4 C89530 1, ATCEA4 S33006	100, 92, 90, 84			g16846 47	60	97	0.0025	(Z8298 7) unknown, highly similar to

138218	ATU000 158	ATL8C4 8411:1 296..1	gap2	ATCEA4 S14037 , ATCEA4 S13873	100, 99	ATL8C4 8411:1 151..1 14	0.80	g28092 32	59	1331	5.1e- 100	(AC002 560) F21B7. 1 [Arabi dopsis thalia na]	E. coli YecD hypoth etical 21.8 KD protei n in asps 5'regi on and to isocho rismat ase [Bacil lus subtil is]
138219	ATU000 159	ATL8C4 623:71 8..1	gap2	ATCEA4 C13278 _1	100	ATL8C4 623:67 2..79	0.77	g48952 30	59	965	2.0e- 99	(AC007 660) unknown protei n [Arabi dopsis thalia na]	(Z9733 7) hypoth etical protei n [Arabi
138220	ATU000 160	ATL8C4 5947:1 973..1	gap2	ATCEA4 C5963_1, ATCEA4 S31896 , ATCEA4	100, 96, 96	ATL8C4 5947:1 754..7 2	0.68	g22448 41	59	691	1.4e- 69	(Z9733 7) hypoth etical protei n [Arabi	(Z9733 7) hypoth etical protei n [Arabi

138221	ATU000 161	ATL8C2 5471:1 ..1869	gap2	ATCEA4 C34834 1, ATCEA4 S29812	100, 99					g41153 73	59	802	3.1e- 76	dopsis thalia nal (AC005 967) recept or- like protei n kinase [Arabi dopsis thalia nal
138222	ATU000 162	ATL8C1 3322:2 307..3 12	gap2	ATCEA4 S4888, ATCEA4 C15597 _1	100, 99	ATL8C1 3322:2 270..3 12	0.94			g38757 70	58	103	0.015	(Z6829 7) Simila rity to Human splico some- associ ated protei n SAP62 (PIR Acc. No. A47655); cDNA EST EMBL:C 08866 comes from this gene; cDNA EST yk247a 3.3

138223	ATU000 163	ATL8C3 4975:2 024..1	gap2	ATCEA4 C17169 1, ATCEA4 C8033_1	100, 99	ATL8C3 4975:1 943..9 0	0.87	948683 75	58	486	5.1e- 41	comes from this gene; CDNA EST yk247a 3.5 comes from this gene; CDNA EST yk371. .. [] (AF139 807) nod factor bindin g lectin - nucleo tide phosph ohydro lase [Dolic hos biflor us]
138224	ATU000 164	ATL8C2 9712:1 ..1539	gap2	ATCEA4 S29543 , ATCEA4 S13637	100, 95			933096 20	58	1838	6.1e- 185	(AF074 916) resist ance to Pseudo monas syring ae protei n 5 [Arabi

138225	ATU000 165	ATL8C4 5596:1 478..1	gap2	ATCEA4 S924	100	ATL8C4 5596:1 360..3 7	0.90	g45896 10	57	232	3.1e- 21	dopsis thalia na]
138226	ATU000 166	ATL8C2 6730:1 ..783	gap2	ATCEA4 C9558_ 1, ATCEA4 S15004	100, 82	ATL8C2 6730:4 4..715	0.69	g29700 51	57	516	1.9e- 55	(AB012 110) ARG10 [Vigna radiat a]
138227	ATU000 167	ATL8C2 0934:1 652..2 87	gap2	ATCEA4 S13871 , ATCEA4 C15093 _1	100, 99	ATL8C2 0934:1 645..2 87	0.63	g22450 37	57	363	6.4e- 12	(Z9734 2) nuclea r antige n homolo g [Arabi dopsis thalia na]
138228	ATU000 168	ATL8C2 4275:1 853..1 03	gap2	ATCEA4 C5161_ 1, ATCEA4 C18819 _1	100, 98	ATL8C2 4275:1 618..6 03	0.48	g45805 75	57	1660	4.7e- 161	(AF082 176) auxin respon se factor 9 [Arabi dopsis thalia na]
138229	ATU000 169	ATL8C3 3194:1 ..2264	gap2	ATCEA4 C8022_ 1	100	ATL8C3 3194:2 23..21	0.95	g21453 56	56	1270	1.3e- 116	(Y1112 2) HD- Zip

138230	ATU000 170	ATL8C1 9856:1 035..1	gap2	ATCEA4 S2193	100	ATL8C1 9856:1 030..3 0	0.91	g22450 80	56	419	7.7e- 40	protein [Arabi dopsis thalia na]
138231	ATU000 171	ATL8C2 6298:1 ..2272	gap2	ATCEA4 C21765 1, ATCEA4 C16880 1	100, 91	ATL8C2 6298:7 96..21 61	0.83	g25225 34	56	779	5.9e- 75	(AF027 302) TNF- alpha stimul ated ABC protein [Homo sapien s]
138232	ATU000 172	ATL8C1 2763:1 435..1 085	gap2	ATCEA4 S13248	100	ATL8C1 2763:1 325..1 085	0.79	g48951 89	56	138	9.8e- 09	(AC007 661) unknow n protein [Arabi dopsis thalia na]
138233	ATU000 173	ATL8C4 8559:2 193..1	gap2	ATCEA4 C80247 1, ATCEA4 C11209 1	100, 98	ATL8C4 8559:2 193..5 1	0.70	g22621 00	56	945	1.0e- 77	(AC002 343) unknow n protein

138234	ATU000 174	ATL8C3 1266:3 053..4 9	gap2	ATCEA4 S26567 , ATCEA4 S3002	100, 93	ATL8C3 1266:2 955..3 02	0.67	g36081 55	56	2514	2.9e- 255	[Arabi dopsis thalia na] (AC005 314) putati ve RNA helica se [Arabi dopsis thalia na]
138235	ATU000 175	ATL8C4 4337:6 3..385 0	gap2	ATCEA4 S29561	100			g42638 31	56	3511	0.0	(AC006 067) putati ve revers e transc riptas e [Arabi dopsis thalia na]
138236	ATU000 176	ATL8C3 2481:1 ..952	gap2	ATCEA4 S2893	100	ATL8C3 2481:1 08..95 2	0.84	g38737 07	55	247	9.3e- 20	(Z7310 2) Simila rity to B.subt ilis DNAJ protei n (SW:DN AJ_BAC SU); cDNA EST yk437a 1.5 comes

138237	ATU000 177	ATL8C3 5859:1 099..1	gap2	ATCEA4 S32609 , ATCEA4 C11533 9_2, ATCEA4 C11533 9_1	100, 98, 94	ATL8C3 5859:1 099..4 61	0.63	922447 97	55	150	9.7e- 09	(Z9733 6) hypoth etical protein [Arabi dopsis thalia na]	from this gene [Caeno rhabdi tis elegan s]
138238	ATU000 178	ATL8C7 875:1. .4621	gap2	ATCEA4 S32892 , ATCEA4 C26011 1, ATCEA4 C52584 1, ATCEA4 C50506 1, ATCEA4 S23504	100, 99, 99, 95, 85	ATL8C7 875:50 3..459 8	0.63	973084 3	55	571	1.2e- 47	SHUTTL E CRAFT PROTEI N [Droso phila melano gaster]	
138239	ATU000 179	ATL8C1 5993:3 80..13 12	gap2	ATCEA4 S119	100			947536 55	55	1113	4.4e- 118	(AL049 751) pectat e lyase like protei n [Arabi dopsis thalia na]	
138240	ATU000	ATL8C3	gap2	ATCEA4	100	ATL8C3	0.86	948503	54	986	3.6e-	(AC007	

180	505:21 8..845		C20841 _1		505:28 7..802	83			101	357) Contai ns simila rity to []
138241	ATU000 181	gap2	ATCEA4 S1212, ATCEA4 C28651 _1	100, 99	ATL8C9 723:69 8..35	0.76	g29110 49	54	948	4.5e- 90 (AL021 961) glucos yltran sferas e - like protei n [Arabi dopsis thalia na]
138242	ATU000 182	gap2	ATCEA4 C2011_ 1, ATCEA4 S27432	100, 98	ATL8C1 9255:2 85..41 9	0.74	g40975 57	54	333	3.8e- 34 (U6491 1) ATFP8 [Arabi dopsis thalia na]
138243	ATU000: 183	gap2	ATCEA4 C6316_ 1, ATCEA4 S29593 , ATCEA4 C49888 1	100, 98, 98	ATL8C3 7277:1 382..1 52	0.70	g49030 18	54	1459	(AB027 507) ACE [Arabi dopsis thalia na]
138244	ATU000 184	gap2	ATCEA4 S3430	100	ATL8C1 1293:3 28..28 89	0.46	g44067 57	54	568	2.5e- 70 (AC006 836) putati ve integr al membra ne protei n A3

138245	ATU000 185	ATL8C2 16:1.. 750	gap2	ATCEA4 C32009 _1	100						g44067 59	54	204	1.1e- 06	[Arabi dopsis thalia na] (AC006 836) hypoth etical protei n [Arabi dopsis thalia na]
138246	ATU000 186	ATL8C3 2564:2 660..1	gap2	ATCEA4 S1147, ATCEA4 S34178 , ATCEA4 S33234 , ATCEA4 S24349 , ATCEA4 S24350	100, 93, 92, 86, 84	ATL8C3 2564:2 520..9 44	0.97				g22448 35	53	204	5.2e- 16	(Z9733 7) protei n kinase homolo g [Arabi dopsis thalia na]
138247	ATU000 187	ATL8C3 6256:1 252..1	gap2	ATCEA4 S2249	100	ATL8C3 6256:1 252..5 1	0.89				g34026 97	53	1875	1.5e- 181	(AC004 261) putati ve phosph atidyl inosit ol-4- phosph ate 5- kinase [Arabi dopsis thalia na]
138248	ATU000 188	ATL8C2 5663:1 ..1619	gap2	ATCEA4 S609	100	ATL8C2 5663:6 4..140	0.87				g22135 94	53	276	1.7e- 32	(AC000 348) T7N9.1

								2									4
138249	ATU000 189	ATL8C1 8542:4 919..1	gap2	ATCEA4 S11810 , ATCEA4 S11300 , ATCEA4 S13699 , ATCEA4 S11825 , ATCEA4 S34944	100, 98, 97, 95, 91	ATL8C1 8542:4 789..3 29	0.82	g44903 30	53	5981	0.0	(AL035 656) splici ng factor -like protei n [Arabi dopsis thalia na]					
138250	ATU000 190	ATL8C1 6689:2 593..3 387	gap2	ATCEA4 C4567 1	100			g22447 52	53	714	4.6e- 73	(Z9733 5) hypoth etical protei n [Arabi dopsis thalia na]					
138251	ATU000 191	ATL8C2 5295:1 ..1572	gap2	ATCEA4 S5600	100	ATL8C2 5295:6 0..155 1	0.77	g30634 45	52	1317	1.7e- 127	(AC003 981) F22013 .7 [Arabi dopsis thalia na]					
138252	ATU000 192	ATL8C2 0875:3 090..5 12	gap2	ATCEA4 S31409 , ATCEA4 C15669 1, ATCEA4 S29881	100, 99, 96, 87, 82	ATL8C2 0875:2 855..5 12	0.69	g28298 96	52	1073	1.3e- 110	(AC002 311) highly simila r to auxin- regula ted					

138253	ATU000 193	ATL8C3 5866:1 255..1 835	gap2	ATCEA4 S1001	100					g30804 15	52	814	2.4e- 71	protein GH3, gp X60 033 18 591 [Arabi dopsis thalia na]
138254	ATU000 194	ATL8C1 362:39 73..1	gap2	ATCEA4 S478	100					g31766 89	52	4593	0.0	(AC003 671) Contai ns simila rity to ubiqui tin carbox yl- termin al hydrol ase 14 gb Z35 927 from S. cerevi siae. [Arabi dopsis

138255	ATU000 195	ATL8C1 9724:6 10..1	gap2	ATCEA4 C6273_1	100					g14029 00	52	467	9.2e- 45	thalia na] (X9832 2) peroxi dase [Arabi dopsis thalia na]
138256	ATU000 196	ATL8C4 7490:1 ..755	gap2	ATCEA4 S12623 , ATCEA4 C653_1 , ATCEA4 S14615 , ATCEA4 S35142 , ATCEA4 S36071	100, 95, 89, 88, 87	ATL8C4 7490:1 03..69 1	0.79			g25703 42	51	538	3.8e- 38	(U9092 9) glyoxa lase II cytopl asmic isozyme [Arabi dopsis thalia na]
138257	ATU000 197	ATL8C3 7637:1 ..2108	gap2	ATCEA4 S3914	100	ATL8C3 7637:3 6..195 0	0.70			g28092 58	51	1568	2.3e- 152	(AC002 560) F21B7. 27 [Arabi dopsis thalia na]
138258	ATU000 198	ATL8C7 822:63 7..1	gap2	ATCEA4 C22755 _1	100	ATL8C7 822:31 5..27	0.58			g31933 31	51	109	1.6e- 08	(AF069 299) No defini tion line found [Arabi dopsis thalia na]
138259	ATU000	ATL8C1	gap2	ATCEA4	100,					g41281	51	120	5.6e-	(U7527

199	5006:6 09..90			C14934 1, ATCEA4 C14934 2_	99					97			11	3) acyl- CoA bindin g protei n [Arabi dopsis thalia na]
138260	ATU000 200	ATL8C1 9680:1 561..1	gap2	ATCEA4 S1577, ATCEA4 C21887 _1_	100, 97					g47589 18	51	472	2.1e- 45	phosph atidyl inosit ol glycan , class B [Homo sapien s]
138261	ATU000 201	ATL8C1 5249:6 7..133 6	gap2	ATCEA4 S30802 , ATCEA4 S12570	100, 99		ATL8C1 5249:1 59..11 18	0.84	g10766 34	50	384	1.8e- 32	n- serine /threo nine kinase NPK15 - common tobacc o [Nicot iana tabacu m]	
138262	ATU000 202	ATL8C4 4998:1 451..1	gap2	ATCEA4 C4688_3, ATCEA4 C4688_1	100, 98		ATL8C4 4998:1 373..4 4	0.73	g10551 30	50	152	5.0e- 13	(U3999 8) coded for by C. elegan s cDNA yk92b1	

138263	ATU000 203	ATL8C9 575:64 6..158	gap2	ATCEA4 C15345 1, ATCEA4 S36008	100, 93	ATL8C9 575:60 2..334	0.56	g45394 08	50	345	2.3e- 25	(AL049 524) putati ve alpha NAC [Arabi dopsis thalia
												1.3; coded for by C. elegant s cDNA yk92b1 1.5; coded for by C. elegant s cDNA yk78c2 .5; coded for by C. elegant s cDNA cm9a8; coded for by C. elegant s cDNA yk66h8 .3; coded for by C. elegant s cDNA yk78c2 .3 ... []

138264	ATU000 204	ATL8C8 21:74. .903	gap2	ATCEA4 C15207 71, ATCEA4 S31653	100, 83	ATL8C8 21:411 ..536	0.56	g35598 05	50	524	2.7e- 53	na] (AJ006 787) putati ve phytoc helati n synthe tase [Arabi dopsis thalia na]
138265	ATU000 205	ATL8C4 1903:5 45..35 00	gap2	ATCEA4 C44151 1, ATCEA4 S13709 , ATCEA4 S8242	100, 100, 90	ATL8C4 1903:7 28..32 91	0.52	g11755 22	50	33	0.39	ANKYRI N REPEAT - CONTAI NING PROTEI N YAR1 [Sacch aromyc es cerevi siae]
138266	ATU000 206	ATL8S1 0589:1 ..609	gap2	ATCEA4 C31812 1, ATCEA4 C5669_ 1	100, 98	ATL8S1 0589:4 8..251	0.43	g17063 36	50	508	5.8e- 51	UROPOR PHYRIN OGEN DECARB OXYLAS E [Synec hocyst is sp.]
138267	ATU000 207	ATL8C3 1618:5 448..1 729	gap2	ATCEA4 C35221 1, ATCEA4 C12339 31, ATCEA4 S4046	100, 97, 94			g38735 50	50	70	0.92	(AL033 534) serine -rich protei n [Schiz osacch

138268	ATU000 208	ATL8C1 904:1. .826	gap2	ATCEA4 C9101_ 1	100					g16193 00	50	225	2.8e- 23	aromyc es pombel] (X9526 9) LRR protei n [Lycop ersico n escule ntum]
138269	ATU000 209	ATL8C1 2677:2 566..1	gap2	ATCEA4 C45288 _1, ATCEA4 C45288 _2	100, 98	ATL8C1 2677:2 344..3 10	0.93	g48952 20	49	1150	2.5e- 85	(AC007 660) unknow n protei n [Arabi dopsis thalia na]		
138270	ATU000 210	ATL8C2 0617:2 973..7 645	gap2	ATCEA4 S27241 , ATCEA4 C12248 2_1	100, 97	ATL8C2 0617:2 973..7 546	0.83	g22889 85	49	448	1.3e- 42	(AC002 335) hypoth etical protei n [Arabi dopsis thalia na]		
138271	ATU000 211	ATL8C2 3006:1 37..98 9	gap2	ATCEA4 S11026	100	ATL8C2 3006:6 78..85 4	0.73	g45392 93	49	1002	2.9e- 89	(AL049 480) putati ve membra ne transp orter [Arabi dopsis thalia na]		

138272	ATU000 212	ATL8C4 7198:1 620..1	gap2	ATCEA4 S8249	100	ATL8C4 7198:1 583..1 49	0.66	g32692 90	49	1772	5.2e- 177	(AL030 978) putati ve recept or like kinase [Arabi dopsis thalia na]
138273	ATU000 213	ATL8C2 2091:1 ..2782	gap2	ATCEA4 S1796	100	ATL8C2 2091:1 664..2 740	0.57	g24628 22	49	140	6.7e- 15	(AF000 657) hypoth etical protei n [Arabi dopsis thalia na]
138274	ATU000 214	ATL8C4 3353:8 97..1	gap2	ATCEA4 S27384 , ATCEA4 S1565	100, 99			g42630 50	49	119		(AC005 142) putati ve noduli n [Arabi dopsis thalia na]
138275	ATU000 215	ATL8C2 2718:1 ..580	gap2	ATCEA4 C12288 9_1	100			g22451 31	49	149	2.4e- 10	(Z9734 4) hypoth etical protei n [Arabi dopsis thalia na]
138276	ATU000 216	ATL8C3 7916:3 31..11	gap2	ATCEA4 S735, ATCEA4	100, 99			g32928 29	49	559	1.4e- 41	(AL031 018) putati

138277	ATU000 217	33		S745	100	ATL8C2 832:13 24..32 3	0.96	g38595 94	48	729	3.9e- 57	ve protei n [Arabi dopsis thalia na]
			gap2	ATCEA4 S330								(AF104 919) contai ns simila rity to riboso mal protei n L7Ae (Pfam: PF0124 8, E=0.00 17, N=1) [Arabi dopsis thalia na]
138278	ATU000 218		gap2	ATCEA4 C4036_1, ATCEA4 C7375_1	100, 82	ATL8C4 160:65 2..19	0.88	g21911 55	48	138	4.4e- 16	(AF007 269) contai ns weak simila rity with bacter ial SECA protei ns. [Arabi dopsis thalia na]

138279	ATU000 219	ATL8C1 0531:1 605..1	gap2	ATCEA4 C37664 _1	100	ATL8C1 0531:1 605..2 8	0.82	g27919 00	48	655		(AJ000 057) PP7 [Arabi dopsis thalia na]
138280	ATU000 220	ATL8C3 4557:1 ..674	gap2	ATCEA4 S26559 , ATCEA4 S5339, ATCEA4 S1495	100, 86, 84	ATL8C3 4557:1 16..64 1	0.65	g43143 78	48	647	2.4e- 66	(AC006 232) putati ve lipase [Arabi dopsis thalia na]
138281	ATU000 221	ATL8C3 000:1. .2324	gap2	ATCEA4 S11785	100	ATL8C3 000:26 ..1666	0.58	g46783 07	48	1013	2.9e- 73	(AL049 655) vacuol ar protei n sortin g-like protei n [Arabi dopsis thalia na]
138282	ATU000 222	ATL8C5 835:21 8..346 2	gap2	ATCEA4 S8134, ATCEA4 S34974	100, 83	ATL8C5 835:21 8..346 2	0.58	g36680 95	48	126		(AC004 667) hypoth etical protei n [Arabi dopsis thalia na]
138283	ATU000 223	ATL8C5 245:54 8..131 1	gap2	ATCEA4 S33671 , ATCEA4 C4803	100, 97, 96	ATL8C5 245:11 69..12 41	0.44	g29824 32	48	125	2.9e- 09	(AL022 224) putati ve protei

138284	ATU000 224	ATL8C3 5178:7 73..11 2	gap2	ATCEA4 C33741 _1	100					g30045 56	48	227	5.2e- 24	n [Arabi dopsis thalia na] (AC003 673) hypoth etical protei n [Arabi dopsis thalia na]
138285	ATU000 225	ATL8C2 5656:1 ..1045	gap2	ATCEA4 S4253, ATCEA4 S3377	100, 93	ATL8C2 5656:2 37..10 43	0.95			g37383 38	47	948	4.4e- 101	(AC005 170) putati ve polyga lactur onase [Arabi dopsis thalia na]
138286	ATU000 226	ATL8C4 5143:1 ..1309	gap2	ATCEA4 S11652 , ATCEA4 C94625 _1, ATCEA4 S26698	100, 97, 88	ATL8C4 5143:8 8..682	0.95			g33778 19	47	226	3.5e- 14	(AF076 275) No defini tion line found [Arabi dopsis thalia na]
138287	ATU000 227	ATL8C1 2766:9 98..1	gap2	ATCEA4 S5422	100	ATL8C1 2766:9 42..58 1	0.93			g36000 50	47	195	2.7e- 22	(AF080 120) contai ns simila rity to Ap2 domain

138288	ATU000 228	ATL8C2 3191:1 ..1476	gap2	ATCEA4 S13828 , ATCEA4 C20886 1, ATCEA4 S8576	100, 97, 95	ATL8C2 3191:2 41..12 26	0.65	g34786 37	47	546	1.1e- 38	(AC005 546) R29425 1 [Homo sapien s]
138289	ATU000 229	ATL8C1 5492:1 ..1992	gap2	ATCEA4 S16005 , ATCEA4 C9726_1	100, 98	ATL8C1 5492:1 635..6 1	0.55	g45805 31	47	725	6.4e- 88	(AF036 309) scarec row- like 14 [Arabi dopsis thalia na]
138290	ATU000 230	ATL8C4 1380:1 388..1	gap2	ATCEA4 S2318, ATCEA4 S31131	100, 87	ATL8C4 1380:1 329..1 46	1.00	g26321 03	46	1083	1.1e- 97	(Z9875 9) arginy l-tRNA synthe tase [Arabi dopsis thalia na]
138291	ATU000 231	ATL8C3 9530:1 161..1	gap2	ATCEA4 S32604 , ATCEA4 S28516	100, 87	ATL8C3 9530:1 127..1 0	0.96	g23448 89	46	238	4.2e- 16	(AC002 388) unknow n protei n [Arabi dopsis thalia na]

138292	ATU000 232	ATL8C8 003:1. .799	gap2	ATCEA4 C8059_1, ATCEA4 S3592	100, 100	ATL8C8 003:20 3..771	0.73	g31525 76	46	427	4.5e- 34	na] (AC002 986) Simila r to liver- specif ic transp ort protei n gb L27 651 from Rattus norvie gicus. [Arabi dopsis thalia na]
138293	ATU000 233	ATL8C1 9762:5 69..1	gap2	ATCEA4 S14054	100	ATL8C1 9762:1 55..11	0.56	g37759 95	46	413	3.3e- 19	(AJU10 461) RNA helica se [Arabi dopsis thalia na]
138294	ATU000 234	ATL8C4 5227:1 110..1 548	gap2	ATCEA4 S33644	100			g10408 77	46	366	2.6e- 27	(U3046 0) expans in S2 precu sor [Cucum is sativu s]
138295	ATU000 235	ATL8C1 889:31 90..20 7	gap2	ATCEA4 S3359, ATCEA4 S17771	100, 89, 85	ATL8C1 889:31 87..31 6	0.95	g25010 11	45	732	6.6e- 67	ISOLEU CYL- TRNA SYNTH

138296	ATU000 236	ATL8C4 7002:1 019..1	gap2	ATCEA4 C26976 _1	100	ATL8C4 7002:8 69..19	0.95	g45394 23	45	913	1.7e- 85	(AL049 171) pyroph osphat e- depend ent phosph ofruct o-1- kinase [Arabi dopsis thalia na]
138297	ATU000 237	ATL8C2 7315:1 ..2662	gap2	ATCEA4 C4912_1, ATCEA4 C12122 8_1	100, 88	ATL8C2 7315:5 58..26 62	0.92	g23350 96	45	236		(AC002 339) hypoth etical protei n [Arabi dopsis thalia na]
138298	ATU000 238	ATL8C3 4896:4 832..5 79	gap2	ATCEA4 C6383_1, ATCEA4 C27373 _1	100, 95	ATL8C3 4896:4 443..2 422	0.92	g24925 12	45	553	3.5e- 57	CELL DIVISI ON PROTEI N FTSH HOMOLO G 3 [Synec

138299	ATU000 239	ATL8C1 0978:1 ..1151	gap2	ATCEA4 C23077 _2	100	ATL8C1 0978:1 19..11 51	0.87	g45389 39	45	560	8.3e-31	(AL049 483) Col-0 casein kinase I-like protein [Arabidopsis thaliana]
138300	ATU000 240	ATL8C1 2481:5 15..83 4	gap2	ATCEA4 C43001 _1	100	ATL8C1 2481:7 37..56 8	0.75	g25058 76	45	106	3.0e-08	(Y1277 6) MYB- related protein [Arabidopsis thaliana]
138301	ATU000 241	ATL8C3 5888:1 173..2 12	gap2	ATCEA4 S27054 , ATCEA4 S30734	100, 91	ATL8C3 5888:1 154..4 70	0.73	g32490 88	45	140	8.2e-15	(AC004 473) Contai ns simila rity to goliat h protein gb M97 204 from D. melano gster. [Arabidopsis dopsis]

138307	ATU000 247	ATL8C2 7453:6 23..1	gap2	ATCEA4 S8226	100, 98, 95	ATL8C2 7453:6 23..24 9	0.54	g45078 73	44	144		von Hippel - Lindau bindin g protei n 1 [Homo sapien s]
138308	ATU000 248	ATL8C3 8465:3 34..82 7	gap2	ATCEA4 C6037 - 1	100			g36953 88	44	116	2.7e- 11	(AF096 371) No defini tion line found [Arabi dopsis thalia na]
138309	ATU000 249	ATL8C1 2269:1 032..1	gap2	ATCEA4 S193	100	ATL8C1 2269:9 52..15 0	0.98	g31281 92	43	622	1.2e- 58	(AC004 521) axi 1- like protei n [Arabi dopsis thalia na]
138310	ATU000 250	ATL8C4 9750:1 010..3 926	gap2	ATCEA4 S159	100	ATL8C4 9750:1 010..1 072, ATL8C4 9750:2 238..3	0.74, 0.70	g28298 92	43	534	6.5e- 54	(AC002 311) putati ve pectin estera se

138311	ATU000 251	ATL8C9 870:1. .1208	gap2	ATCEA4 C9211_1	100		775					g21911 31	43	464	1.9e- 39	[Arabi dopsis thalia na]
138312	ATU000 252	ATL8C7 12:546 ..1	gap2	ATCEA4 C9396_1	100		ATL8C7 12:511 ..111	0.93				g26421 58	41	446	4.1e- 46	(AC003 000) hypoth etical protei n [Arabi dopsis thalia na]
138313	ATU000 253	ATL8C1 339:96 9..1	gap2	ATCEA4 C12405 1, ATCEA4 S1338	100, 90		ATL8C1 339:82 6..36	0.75				g33675 76	41	355	2.2e- 37	(AL031 135) NAM / CUC2 - like protei n [Arabi dopsis thalia na]
138314	ATU000 254	ATL8C4 4158:5 79..13 8	gap2	ATCEA4 S24405 , ATCEA4 C934_1 , ATCEA4 C934_2 ,	100, 98, 87, 87		ATL8C4 4158:5 01..14 2	0.59				g16686 7	41	282	4.0e- 15	(J0521 6) riboso mal protei n S11 (proba ble start

138315	ATU000 255	ATL8S1 9021:5 63..16 0	gap2	ATCEA4 S715	100					g29795 66	41	89	6.8e- 10	codon at bp 67) [Arabi dopsis thalia na]
138316	ATU000 256	ATL8S9 647:79 ..547	gap2	ATCEA4 C512_1	100					g14028 94	41	285	6.9e- 30	(X9686 7) adenin e phosph oribos yltran sferas e [Arabi dopsis thalia na]
138317	ATU000 257	ATL8C3 5069:1 526..1	gap2	ATCEA4 S8161, ATCEA4 C6770_2	100, 88	ATL8C3 5069:1 420..1 52	0.96			g16537 67	40	538	4.0e- 45	(D9091 6) oligop eptida se A [Synec hocyst is sp.]
138318	ATU000 258	ATL8C3 5440:2 116..1	gap2	ATCEA4 C9197_1	100	ATL8C3 5440:1 547..4 52	0.85			g33554 80	40	195	7.6e- 16	(AC004 218) Medica go noduli

138319	ATU000 259	ATL8C4 8528:1 ..2785	gap2	ATCEA4 S3098, ATCEA4 C1541_1, ATCEA4 S32866, ATCEA4 S19909, ATCEA4 S35694, ATCEA4 S31438, ATCEA4 S35745, ATCEA4 S7034, ATCEA4 S31316, ATCEA4 S13786, ATCEA4 S5110, ATCEA4 S19094, ATCEA4 S31742, ATCEA4	100, 99, 96, 95, 94, 93, 89, 89, 88, 87, 87, 86, 86, 84	ATL8C4 8528:2 693..1 904, ATL8C4 8528:5 04..15 00	0.72, 0.53	g30565 88	40	1232	1.3e- 127	n N21- like protei n [Arabi dopsis thalia na] (AC004 255) T1F9.9 [Arabi dopsis thalia na]
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138320	ATU000 260	ATL8C9 676:13 52..1	gap2	S17127 ATCEA4 S2466, ATCEA4 C23715 _1	100, 96	ATL8C9 676:11 74..61 9	0.65	g44903 05	40	565	7.3e- 31	(AL035 678) putati ve protei n [Arabi dopsis thalia na]
138321	ATU000 261	ATL8C4 1843:1 ..621	gap2	ATCEA4 C27038 _1	100			g45126 59	40	700	4.5e- 63	(AC006 931) putati ve protei n kinase [Arabi dopsis thalia na]
138322	ATU000 262	ATL8C2 6066:1 105..1	gap2	ATCEA4 C3639 _1	100	ATL8C2 6066:1 007..2 6	0.92	g33778 02	39	1324	9.5e- 141	(AF075 597) Simila r to sucros e syntha se; T2H3.8 [Arabi dopsis thalia na]
138323	ATU000 263	ATL8C1 1503:1 ..749	gap2	ATCEA4 S30207 , ATCEA4 S31114	100, 91	ATL8C1 1503:5 6..648	0.90	g22449 98	39	386	1.8e- 35	(Z9734 1) simila rity to probab le transc riptio nal

138324	ATU000 264	ATL8C1 6948:1 733..1	gap2	ATCEA4 C26982 _1	100	ATL8C1 6948:1 524..4 33	0.82	g38602 51	39	1342	9.5e- 72	adaptor ADA2 [Arabi dopsis thalia na] (AC005 824) putati ve permea se [Arabi dopsis thalia na]
138325	ATU000 265	ATL8C4 8839:1 588..7 0	gap2	ATCEA4 C9875_ 1, ATCEA4 C6244_ 1	100, 83	ATL8C4 8839:1 258..6 23	0.80	g45672 73	39	1109	8.4e- 83	(AC006 841) putati ve vacuol ar proton ATPase subuni t [Arabi dopsis thalia na]
138326	ATU000 266	ATL8C4 5722:1 780..4 17	gap2	ATCEA4 S29376 , ATCEA4 C12436 7_1	100, 96	ATL8C4 5722:1 780..6 39	0.74	g46462 03	39	225	8.9e- 18	(AC007 230) Belong s to PF1000 26 Eukary otic aspart yl protea se family [Arabi

138327	ATU000 267	ATL8S1 128:63 7..1	gap2	ATCEA4 S4404	100	ATL8S1 128:54 3..23	0.74	g42181 44, g47411 85	39, 36	248, 199	1.5e- 23, 5.0e- 18	dopsis thalia na]
138328	ATU000 268	ATL8C4 9673:1 839..3 599	gap2	ATCEA4 S3341, ATCEA4 S2263	100, 83	ATL8C4 9673:1 969..3 528	0.67	g32015 41	39	315	2.3e- 23	(AJ005 077) TCTR2 protei n [Lycop ersico n escule ntum]
138329	ATU000 269	ATL8C4 3605:9 3..732	gap2	ATCEA4 S2902	100	ATL8C4 3605:9 3..536	0.63	g44540 06	39	445	(AL035 396) hypoth etical protei n [Arabi dopsis thalia na]	

138333	ATU000 273	ATL8C4 5891:1 ..886	gap2	ATCEA4 C4441_3, ATCEA4 S5564, ATCEA4 S5566, ATCEA4 S18488 , ATCEA4 S12376	100, 93	ATL8C4 5891:6 7..870	0.68	g29245 09	38	834	3.6e- 82	(AL022 023) subtil isin protei nase- like [Arabi dopsis thalia nal]
138334	ATU000 274	ATL8C3 8487:1 ..1395	gap2	ATCEA4 C49239 1, ATCEA4 C12903 8 1, ATCEA4 C11780 1 1	100, 94, 92	ATL8C3 8487:2 19..13 50	0.52	g35402 19	38	1089	2.9e- 114	(D8768 6) KIAA00 17 protei n [Homo sapien s]
138335	ATU000 275	ATL8C4 3109:1 ..856	gap2	ATCEA4 S3526, ATCEA4 C22163 1_	100, 98	ATL8C4 3109:1 80..10 6	0.49	g33285 87	38	123	1.2e- 07	(AE001 292) CMP-2- keto- 3- deoxyo ctulos onic acid synthe tase [Chlam ydia

138336	ATU000 276	ATL8C3 0401:1 715..1 971	gap2	ATCEA4 S4283	100					g30565 85	38	122	7.3e- 05	(AC004 255) T1F9.6 [Arabi dopsis thalia na]	tracho matis]
138337	ATU000 277	ATL8C4 9129:1 07..75 8	gap2	ATCEA4 C4578- 2, ATCEA4 C4578- 1, ATCEA4 C4578- 4	100, 89, 82	ATL8C4 9129:1 07..67 6	0.98			g22845 5	37	626	1.6e- 57	Gln synthe tase [Arabi dopsis thalia na]	Gln synthe tase [Arabi dopsis thalia na]
138338	ATU000 278	ATL8C1 2721:2 244..1	gap2	ATCEA4 S2144, ATCEA4 S25303	100, 97	ATL8C1 2721:2 190..6 10	0.85			g38853 34	37	882	5.7e- 81	(AC005 623) putati ve argona ute protei n [Arabi dopsis thalia na]	(AC005 623) putati ve argona ute protei n [Arabi dopsis thalia na]
138339	ATU000 279	ATL8C1 8953:3 361..1 83	gap2	ATCEA4 C2069- 1	100	ATL8C1 8953:2 823..8 02	0.78			g35488 05	37	80	6.2e- 05	(AC005 313) unknow n protei n [Arabi dopsis thalia na]	(AC005 313) unknow n protei n [Arabi dopsis thalia na]
138340	ATU000 280	ATL8C4 2350:1 ..991	gap2	ATCEA4 C4315- 2, ATCEA4	100, 94	ATL8C4 2350:1 12..68 9	0.78			g30804 27	37	554	1.3e- 51	(AL022 604) putati ve	(AL022 604) putati ve

138341	ATU000 281	ATL8S2 6033:5 44..1	gap2	ATCEA4 C18570 _1	100	ATL8S2 6033:5 43..89	0.74	g33353 53	37	495	5.9e- 48	prote n [Arabi dopsis thalia na]
138342	ATU000 282	ATL8C4 00:1.. 3229	gap2	ATCEA4 S26118 , ATCEA4 C7540 _1	100, 94	ATL8C4 00:61.. .3206	0.71	g27730 42	37	378	1.7e- 22	(AF038 440) phosph olipas e D2 [Homo sapien s]
138343	ATU000 283	ATL8C7 944:1.. .1435	gap2	ATCEA4 C81406 _1	100			g22451 01	37	362	3.2e- 28	(Z9734 3) hypoth etical protei n [Arabi dopsis thalia na]
138344	ATU000 284	ATL8C1 6978:7 39..1	gap2	ATCEA4 S11959 , ATCEA4	100, 90, 85			g24941 44	37	849	1.6e- 79	(AC002 329) predic ted

138345	ATU000 285	ATL8C4 7596:1 ..1948	gap2	ATCEA4 C8909_1, ATCEA4 C12158 4_1	100, 94	ATL8C4 7596:2 20..71 1, ATL8C4 7596:1 708..1 216	0.97, 0.73	g28092 46	36	435	6.2e- 39	leucin e-rich protei n [Arabi dopsis thalia na]
138346	ATU000 286	ATL8S7 59:1.. 510	gap2	ATCEA4 S28940 , ATCEA4 C13615 6_1	100, 97	ATL8S7 59:222 ..137	0.92	g37383 02	36	291	3.3e- 28	(AC005 309) tubby- like protei n [Arabi dopsis thalia na]
138347	ATU000 287	ATL8C1 3289:6 37..1	gap2	ATCEA4 S30133	100	ATL8C1 3289:3 34..97	0.82	g22451 13	36	761	4.4e- 59	(Z9734 3) glycer ol-3- phosph ate permea se homolo g [Arabi dopsis thalia na]
138348	ATU000 288	ATL8C2 4305:1 ..1936	gap2	ATCEA4 S2992, ATCEA4 S12390	100, 99, 85	ATL8C2 4305:7 63..17 86	0.77	g47339 58	36	148	8.8e- 13	(AC007 294) unknown protei

138352	ATU000 292	ATL8C4 0871:1 092..9 9	gap2	ATCEA4 C31570 1, ATCEA4 C25628 1, ATCEA4 S7400	100, 97, 91	ATL8C4 0871:1 001..1 31	0.85	g17084 64	35	585	3.5e- 63	GDA1- UTR2 INTERG ENIC REGION [Sacch aromyc es cerevi siae]
138353	ATU000 293	ATL8C3 8961:1 ..757	gap2	ATCEA4 S14342 , ATCEA4 C28257 _1	100, 96	ATL8C3 8961:2 24..12 4	0.71	g22528 71	35	466	2.9e- 24	(AF013 294) No defini tion line found [Arabi dopsis thalia na]
138354	ATU000 294	ATL8C6 971:33 19..22	gap2	ATCEA4 S204	100	ATL8C6 971:32 14..22	0.68	g41857 38	35	395	6.3e- 34	(AF079 998) putati

138355	ATU000 295	ATL8C1 1181:2 689..1	gap2	ATCEA4 S3917, ATCEA4 C9309_1	100, 98	ATL8C1 1181:2 536..2 25	0.45	g37639 26	35	496	1.9e- 15	(AC004 450) unknown protein [Arabi dopsis thalia na]
138356	ATU000 296	ATL8C3 368:32 17..20	gap2	ATCEA4 S406, ATCEA4 S4975	100, 95	ATL8C3 368:29 65..20	0.45	g30565 93	35	1249	2.3e- 114	(AC004 255) T1F9.1 4 [Arabi dopsis thalia na]
138357	ATU000 297	ATL8C3 201:47 74..1	gap2	ATCEA4 C7684_1, ATCEA4 S2618	100, 99			g45443 72	35	1833	7.8e- 153	(AC006 920) putative reverse transc riptase [Arabi dopsis thalia na]
138358	ATU000 298	ATL8C3 5634:1 12..67 6	gap2	ATCEA4 C17307 _1	100			g32490 86	35	386	6.2e- 18	(AC004 473) Contains simila

138359	ATU000 299	ATL8C2 7480:6 93..1	gap2	ATCEA4 S11725 , ATCEA4 C3575_1	100, 98	ATL8C2 7480:6 20..15 8	1.00	g43357 58	34	299				rity to 21 KD subuni t of the Arp2/3 protei n comple x (ARC21) gb AF0 06086 from Homo sapien s. EST gb Z37 222 comes [Arabi dopsis thalia nal (AC006 284) unknow n protei n [Arabi dopsis thalia nal (AL031 525) 26s protea se regula tory subuni
138360	ATU000 300	ATL8S1 9752:1 ..415	gap2	ATCEA4 C5510_2	100			g35601 70	35	179	1.9e- 13			(AL031 525) 26s protea se regula tory subuni

138361	ATU000 301	ATL8C2 9276:9 03..1	gap2	ATCEA4 C2523_1	100					g18482 14	35	169	1.1e- 13	(Y1121 0) uracil phosph oribos yltran sferase [Nicot iana tabacu m]	t S10b [Schiz osacch aromyc es pombe]
138362	ATU000 302	ATL8C1 0558:2 174..1 469	gap2	ATCEA4 C11483 _1	100					g30368 06	34	109		(AL022 373) glycin e-rich protei n [Arabi dopsis thalia na]	
138363	ATU000 303	ATL8C1 5455:7 30..22 4	gap2	ATCEA4 S23827	100					g10162 70	34	162	2.2e- 14	(U3512 3) p- glycop rotein [Urech is caupo]	
138364	ATU000 304	ATL8C4 5157:1 306..1 671	gap2	ATCEA4 C35783 _1, ATCEA4 S31440	100, 84					g62956 1	34	159	4.3e- 09	SRG1 protei n - Arabid opsis thalia na [Arabi dopsis thalia]	

138365	ATU0000 305	ATL8C3 9261:1 ..333	gap2	ATCEA4 C212_1	100						g31842 87	34	172	4.4e- 15	na] (AC004 136) revers e- transc riptas e-like protei n [Arabi dopsis thalia na]
138366	ATU0000 306	ATL8C4 8919:1 ..1021	gap2	ATCEA4 S30485	100						g28275 20	34	1499	9.3e- 154	na] (AL021 633) recept or kinase - like protei n [Arabi dopsis thalia na]
138367	ATU0000 307	ATL8C3 389:1. .277	gap2	ATCEA4 S34340	100						g37023 35	34	116	1.5e- 07	na] (AC005 397) putati ve DNA bindin g protei n [Arabi dopsis thalia na]
138368	ATU0000 308	ATL8C2 3531:8 19..1	gap2	ATCEA4 S1625	100	ATL8C2 3531:6 79..29	0.82				g45126 55	33	172	2.7e- 13	na] (AC007 048) putati ve protei n phosph

138369	ATU000 309	ATL8C3 2656:1 ..1229	gap2	ATCEA4 S3581, ATCEA4 C62590 _1	100, 97	ATL8C3 2656:1 34..11 14	0.75	g22811 15	33	858	6.8e- 79	atase 2C [Arabi dopsis thalia na]
138370	ATU000 310	ATL8C2 1197:3 313..1	gap2	ATCEA4 S954	100	ATL8C2 1197:3 313..1 52	0.74	g45393 24	33	486	1.1e- 26	(AL035 679) kinesi n like protei n [Arabi dopsis thalia na]
138371	ATU000 311	ATL8C1 2578:1 479..2 708	gap2	ATCEA4 S2173, ATCEA4 S604, ATCEA4 S1828	100, 98, 87	ATL8C1 2578:1 551..2 644	0.68	g40337 63	33	329	3.2e- 22	IMPORT IN BETA-3 SUBUNI T (KARYO PHERIN BETA-3 SUBUNI T) (RAN- BINDIN G PROTEI N 5) [Homo

138372	ATU000 312	ATL8C1 8761:1 ..501	gap2	ATCEA4 C17080 _1	100	ATL8C1 8761:5 9..213	0.59	g26538 79	33	244	7.7e- 14	sapien s] (AF026 389) adenyl cyclas e [Nicot iana tabacu m]
138373	ATU000 313	ATL8C1 289:1. .390	gap2	ATCEA4 S33347 , ATCEA4 C58277 _1	100, 92			g11729 74	33	197	3.7e- 11	CHLORO PLAST 50S RIBOSO MAL PROTEI N L16 [Vigna unguic ulata]
138374	ATU000 314	ATL8C5 402:29 9..1	gap2	ATCEA4 S12637	100			g38591 16	33	225	3.1e- 24	(AF031 609) unknow n [Oryza sativa]
138375	ATU000 315	ATL8C1 2324:1 589..1	gap2	ATCEA4 S12717	100			g46782 88	33	143	5.7e- 14	(AL049 660) putati ve protei n [Arabi dopsis thalia na]
138376	ATU000 316	ATL8C1 7892:1 508..1	gap2	ATCEA4 S2061, ATCEA4 S24071	100, 94	ATL8C1 7892:1 267..1 77	0.93	g44688 12	32	1375		(AL035 601) putati ve protei n

138377	ATU000 317	ATL8C4 8046:5 28..1	gap2	ATCEA4 S415	100							g36000 30	32	359	1.8e- 28	[Arabi dopsis thalia na] (AF080 119) contai ns simila rity to ankyri n repeat s (Pfam: ank.hm m, score: 13.93, 14.93 and 27.78) [Arabi dopsis thalia na]
138378	ATU000 318	ATL8S3 0124:5 89..14 3	gap2	ATCEA4 S27473	100							g37023 26	32	117	7.9e- 09	(AC005 397) hypoth etical protei n [Arabi dopsis thalia na]
138379	ATU000 319	ATL8C3 8390:6 06..1	gap2	ATCEA4 C56914 1, ATCEA4 C56914 2	100, 91							g22450 62	32	182	9.3e- 19	(Z9734 2) hypoth etical protei n [Arabi dopsis thalia na]

138380	ATU000 320	ATL8C2 8624:1 ..1060	gap2	ATCEA4 C44870 1, ATCEA4 S9921	100, 91					g28276 63	32	132	3.6e- 08	thalia nal (AL021 637) membra ne- associ ated salt- induci ble- like protei n [Arabi dopsis thalia nal]
138381	ATU000 321	ATL8C3 9254:1 ..661	gap2	ATCEA4 C8669 1	100	ATL8C3 9254:5 6..661	0.88			g46487 3	31	89	2.7e- 05	TRANSC RIPTIO N FACTOR IIIA (FACTO R A) (TFIII A) [Rana pipien s]
138382	ATU000 322	ATL8C2 659:79 0..1	gap2	ATCEA4 S25154	100	ATL8C2 659:70 4..210	0.88			g33866 00	31	92	3.1e- 06	(AC004 665) putati ve glycop rotein [Arabi dopsis thalia nal]
138383	ATU000 323	ATL8C1 7884:1 962..5 2	gap2	ATCEA4 C21651 1, ATCEA4 C23909	100, 99	ATL8C1 7884:1 906..3 53	0.77			g10016 78	31	56		(D6400 2) ribose 5- phosph

138384	ATU000 324	ATL8C2 4641:2 768..1	gap2	ATCEA4 S5347	100	ATL8C2 4641:2 647..6 0	0.67	g36883 50	31	251	3.1e- 19	ate isomer ase [Synec hocyst is sp.] (AL030 996) dJ1189 B24.4 (novel PUTATI VE protei n simila r to hypoth etical protei ns S. pombe C22F3. 14C and C. elegan s C16A3. 8) [Homo sapien s]
138385	ATU000 325	ATL8C1 7302:2 429..1	gap2	ATCEA4 S613, ATCEA4 S4630, ATCEA4 S5627, ATCEA4 S23	100, 98, 97, 86	ATL8C1 7302:2 429..1 21	0.66	g37216 26	31	513	1.0e- 47	(AB017 480) chloro plast FtsH protea se [Nicot iana tabacu m]
138386	ATU000	ATL8C1	gap2	ATCEA4	100,	ATL8C1	0.42	g30637	31	499	1.7e-	(AL022

	326	3757:1 ..1232		C17144 _1, ATCEA4 C20007 _1	95	3757:8 5..706		06			14	537) putati ve protei n [Arabi dopsis thalia na]
138387	ATU000 327	ATL8C2 5280:1 ..588	gap2	ATCEA4 S8235	100			g29567 60	31	349	2.8e- 29	(AL022 104) probab le atp- depend ent transp orter [Schiz osacch aromyc es pombe]
138388	ATU000 328	ATL8C7 95:336 ..1385	gap2	ATCEA4 S3327, ATCEA4 S1856, ATCEA4 S29477	100, 97, 93			g26620 48	31	318	2.3e- 37	(AB000 970) recept or kinase 1 [Brass ica rapa]
138389	ATU000 329	ATL8C4 4746:1 ..564	gap2	ATCEA4 C25982 _1	100	ATL8C4 4746:1 25..50 5	0.97	g33193 56	30	566	2.3e- 60	(AF077 407) contai ns simila rity glycos yl hydrol ases [Arabi dopsis thalia

138390	ATU000 330	ATL8C1 0031:2 436..1	gap2	ATCEA4 C21241 1, ATCEA4 C33138 1, ATCEA4 S17072	100, 99, 87	ATL8C1 0031:1 321..5 05	0.91	g45574 45	30	97	1.5e- 06	RCC1- like G exchan ging factor RLG [Homo sapien s]
138391	ATU000 331	ATL8C8 462:24 22..12 5	gap2	ATCEA4 S6031, ATCEA4 C14830 2, ATCEA4 C48474 1, ATCEA4 S16658	100, 99, 95, 95	ATL8C8 462:24 19..49 5	0.89	g59613 4	30	100	0.23	(U1747 4) autoan tigen [Homo sapien s]
138392	ATU000 332	ATL8C4 9498:1 ..2187	gap2	ATCEA4 S12, ATCEA4 S11863 , ATCEA4 C31635 1	100, 98, 86	ATL8C4 9498:2 18..21 79	0.86	g44328 54	30	149	1.3e- 10	(AC006 300) hypoth etical protei n [Arabi dopsis thalia na]
138393	ATU000 333	ATL8C4 673:31 9..1	gap2	ATCEA4 C32938 1	100			g45673 06	30	337	3.7e- 19	(AC005 956) hypoth etical protei n [Arabi dopsis thalia na]
138394	ATU000 334	ATL8C4 7342:5 15..1	gap2	ATCEA4 S13849 , ATCEA4	100, 97, 93	ATL8C4 7342:4 00..22 9	1.00					

		830..2 772		1		800..2 841								hypothetical protein [Arabidopsis thaliana]
138408	ATU000 348	ATL8C2 1272:1 947..8 1	gap2	ATCEA4 S26280 , ATCEA4 S26463 , ATCEA4 S27342 , ATCEA4 S16648 , ATCEA4 S18647 , ATCEA4 S23981	100, 99, 98, 85, 84, 82	ATL8C2 1272:9 26..81	0.98							
138409	ATU000 349	ATL8S2 3650:4 98..12 5	gap2	ATCEA4 S3071, ATCEA4 C30939 1, ATCEA4 S19477	100, 97, 89	ATL8S2 3650:4 61..26 8	0.98							
138410	ATU000 350	ATL8C1 5335:6 02..22 69	gap2	ATCEA4 S36303	100	ATL8C1 5335:6 17..20 49	0.98							
138411	ATU000 351	ATL8C3 6523:1 ..449	gap2	ATCEA4 S3318	100	ATL8C3 6523:6 2..449	0.98							
138412	ATU000 352	ATL8C2 3335:3 371..4 55	gap2	ATCEA4 S8286, ATCEA4 S31354 ,	99, 95, 93, 86	ATL8C2 3335:3 371..5 73	0.98	g46462 18	100	1861	9.1e- 175	(AC007 290) putative GTP-		

138418	ATU000 358	ATL8C3 2678:1 345..2 997	gap2	ATCEA4 C74029 1, ATCEA4 S25463	99, 88	ATL8C3 2678:1 398..2 778	0.97	g16528 07	100	257	7.0e- 26	na] (D9090 8) hypoth etical protei n [Synec hocyst is sp.]
138419	ATU000 359	ATL8C2 8489:2 681..1 117	gap2	ATCEA4 C17071 1, ATCEA4 C19224 1	99, 93	ATL8C2 8489:2 123..1 367	0.97	g45393 59	100	330	7.7e- 20	(AL049 525) putati ve protei n [Arabi dopsis thalia na]
138420	ATU000 360	ATL8C9 032:1. .244	gap2	ATCEA4 S3272	100	ATL8C9 032:47 ..244	0.97					
138421	ATU000 361	ATL8C4 5082:1 516..2 310	gap2	ATCEA4 S769, ATCEA4 C7326_1	100, 96	ATL8C4 5082:1 610..2 310	0.97					
138422	ATU000 362	ATL8C2 4409:1 ..393	gap2	ATCEA4 S13852	100	ATL8C2 4409:1 30..39 3	0.97					
138423	ATU000 363	ATL8C4 8228:1 ..931	gap2	ATCEA4 S3003, ATCEA4 C29858 1, ATCEA4 S22593	100, 98, 96	ATL8C4 8228:1 90..92 7	0.97					
138424	ATU000 364	ATL8C4 2696:1 ..822	gap2	ATCEA4 C35179 1, ATCEA4	100, 93	ATL8C4 2696:1 19..56 4	0.97					

138425	ATU000 365	ATL8C1 0721:5 67..70 9	gap2	S2143 ATCEA4 S32289 , ATCEA4 C13321 1, ATCEA4 S34119 , ATCEA4 S2494	100, 99, 97, 90	ATL8C1 0721:5 84..69 6	0.97								
138426	ATU000 366	ATL8C3 3390:5 18..31 97	gap2	ATCEA4 C33660 3, ATCEA4 S1067, ATCEA4 C33660 1, ATCEA4 C13774 1, ATCEA4 C33660 2, ATCEA4 S26731 , ATCEA4 S35457 , ATCEA4 S19943	99, 99, 97, 96, 94, 85, 84, 82	ATL8C3 3390:6 08..28 89	0.97	944540 51	100	939	1.5e- 86	(AL035 394) putati ve polyga lactur onase [Arabi dopsis thalia na]			
138427	ATU000 367	ATL8C4 6347:1 ..469	gap2	ATCEA4 S7598	100	ATL8C4 6347:4 9..469	0.97								
138428	ATU000 368	ATL8C1 086:1. .245	gap2	ATCEA4 C49_1	100	ATL8C1 086:12 0..245	0.97								
138429	ATU000 369	ATL8C4 2043:3 040..2 336	gap2	ATCEA4 S2064	100	ATL8C4 2043:3 040..2 358	0.97								

	22					17												oyl CoA reduct ase [Popul us balsam ifera subsp. tricho carpa]
138437	ATU000 377	ATL8C1 1805:1 659..3 78	gap2	ATCEA4 S1309, ATCEA4 S1463	100, 91	ATL8C1 1805:1 657..4 85	0.96											
138438	ATU000 378	ATL8C2 0013:8 45..64 2	gap2	ATCEA4 S36091	100	ATL8C2 0013:7 86..64 2	0.96											
138439	ATU000 379	ATL8C3 5523:2 160..1	gap2	ATCEA4 C678_1	100	ATL8C3 5523:2 160..3 73	0.96											
138440	ATU000 380	ATL8C4 1896:1 829..3 1	gap2	ATCEA4 S5503	100	ATL8C4 1896:1 829..3 1	0.96											
138441	ATU000 381	ATL8C4 5580:4 50..1	gap2	ATCEA4 C17575 _1	100	ATL8C4 5580:4 05..27 0	0.96											
138442	ATU000 382	ATL8C4 0517:1 32..16 17	gap2	ATCEA4 S394, ATCEA4 S26172 , ATCEA4 S10113	100, 98, 82	ATL8C4 0517:1 38..16 17	0.96											
138443	ATU000 383	ATL8C4 7604:1 ..609	gap2	ATCEA4 C18913 _1	100	ATL8C4 7604:1 11..35 6	0.95											
138444	ATU000 384	ATL8C3 1205:1	gap2	ATCEA4 S10544	99	ATL8C3 1205:1	0.95	g37460 65	100	1040	1.9e- 90						(AC005 311)	

138452	ATU000 392	ATL8C3 6801:1 256..1 65	gap2	ATCEA4 S1811, ATCEA4 S27020	100, 97	ATL8C3 6801:1 062..1 65	0.95									WALL PROTEI N 1 PRECUR SOR [Glyci ne max]; (AF075 597) contai ns simila rity to Nicoti ana alata pistil extens in- like protei n (GB:U4 5958) [Arabi dopsis thalia na]
138453	ATU000 393	ATL8C7 897:15 57..20 4	gap2	ATCEA4 S4634, ATCEA4 C21433 1, ATCEA4 C47969 1	100, 91, 82	ATL8C7 897:15 50..20 4	0.95									
138454	ATU000 394	ATL8C3 7506:1 39..32	gap2	ATCEA4 S11171 ,	99, 93	ATL8C3 7506:1 497..3	0.95	g48357 71	100	791						(AC007 202) Simila

		57		ATCEA4 C1961_1		116	0.95	g44551 58	100	1146	1.8e- 106	r to []
138455	ATU000 395	ATL8C2 2249:3 917..1 170	gap2	ATCEA4 S27614 , ATCEA4 S5129, ATCEA4 C12116 8_1, ATCEA4 C44069 1, ATCEA4 S27566	99, 95, 90, 88, 87	ATL8C2 2249:3 909..1 400	0.95	g44551 58	100	1146	1.8e- 106	(AL021 687) kinase -like protei n [Arabi dopsis thalia na]
138456	ATU000 396	ATL8C7 472:69 ..934	gap2	ATCEA4 S5233, ATCEA4 S11415	100, 86	ATL8C7 472:69 ..802	0.95					
138457	ATU000 397	ATL8C1 1795:3 63..34 24	gap2	ATCEA4 S3205, ATCEA4 S1038	99, 98	ATL8C1 1795:3 63..34 24	0.95	g16520 57	100	911	1.9e- 79	(D9090 2) hypoth etical protei n [Synec hocyst is sp.]
138458	ATU000 398	ATL8C1 2138:2 842..6 4	gap2	ATCEA4 C7396_1	100	ATL8C1 2138:2 607..6 4	0.95					
138459	ATU000 399	ATL8S1 6934:1 ..521	gap2	ATCEA4 C866_2 , ATCEA4 C866_1	100, 85	ATL8S1 6934:2 49..52 1	0.94					
138460	ATU000 400	ATL8C8 844:14 20..12 7	gap2	ATCEA4 S4824	100	ATL8C8 844:13 45..12 7	0.94					
138461	ATU000	ATL8C2	gap2	ATCEA4	100,	ATL8C2	0.94					

	401	0771:1 735..3 868		C6095_1, ATCEA4 C32035 1	97	0771:2 542..3 868						
138462	ATU000 402	ATL8C1 4793:4 49..16 05	gap2	ATCEA4 S4025	100	ATL8C1 4793:5 32..16 05	0.94					
138463	ATU000 403	ATL8C2 7273:1 06..91 1	gap2	ATCEA4 C33815 _1	100	ATL8C2 7273:3 15..91 1	0.94					
138464	ATU000 404	ATL8C3 6089:3 63..26 29	gap2	ATCEA4 S13920 , ATCEA4 C74666 1	100, 100	ATL8C3 6089:4 38..24 64	0.94					
138465	ATU000 405	ATL8C3 7883:4 10..1	gap2	ATCEA4 C75319 2	100	ATL8C3 7883:3 36..88	0.94					
138466	ATU000 406	ATL8C4 8377:2 119..9 40	gap2	ATCEA4 S13900	100	ATL8C4 8377:2 119..9 40	0.94					
138467	ATU000 407	ATL8C1 8398:6 39..1	gap2	ATCEA4 S10792 , ATCEA4 S14493 , ATCEA4 S86	100, 99, 99	ATL8C1 8398:6 35..11	0.94					
138468	ATU000 408	ATL8C1 2732:2 25..12 45	gap2	ATCEA4 S4384	100	ATL8C1 2732:1 245..2 25	0.94					
138469	ATU000 409	ATL8C1 8064:3 239..1 595	gap2	ATCEA4 S30487	99	ATL8C1 8064:3 168..1 595	0.94	g44067 59	100	911	5.8e- 79	(AC006 836) /hypoth etical protei n

138470	ATU000 410	ATL8C4 409:16 7..563 3	gap2	ATCEA4 S419, ATCEA4 S1013	100, 95	ATL8C4 409:16 7..563 3	0.94							[Arabi dopsis thalia na]
138471	ATU000 411	ATL8C1 2380:2 8..149 3	gap2	ATCEA4 C33099 1, ATCEA4 S33794 , ATCEA4 S32952	99, 94, 89	ATL8C1 2380:8 5..108 9	0.94	g28945 99	100	1178	2.6e- 118	(AL021 889) putati ve protei n [Arabi dopsis thalia na]		
138472	ATU000 412	ATL8C1 6971:8 125..2 550	gap2	ATCEA4 S26418 , ATCEA4 C13616 1, ATCEA4 S26419	99, 99, 98	ATL8C1 6971:7 890..2 550	0.93	g45220 09	100	2124	1.3e- 178	(AC007 069) unknow n protei n [Arabi dopsis thalia na]		
138473	ATU000 413	ATL8S7 136:49 7..1	gap2	ATCEA4 C23476 1, ATCEA4 S1425	100, 95	ATL8S7 136:49 7..37	0.93							
138474	ATU000 414	ATL8C4 8032:1 963..3 41	gap2	ATCEA4 S1816	100	ATL8C4 8032:1 580..3 41	0.93							
138475	ATU000 415	ATL8C9 636:61 8..325	gap2	ATCEA4 C30125 1	100	ATL8C9 636:58 7..325	0.93							
138476	ATU000 416	ATL8C3 5738:2 299..1	gap2	ATCEA4 S173, ATCEA4 S13060	100, 99, 98, 97	ATL8C3 5738:2 147..1 6	0.93							

138477	ATU000 417	ATL8C4 9752:1 ..1909	gap2	ATCEA4 C69477 1, ATCEA4 C3265_3	100, 98, 96, 89	ATL8C4 9752:3 ..1797	0.93									
138478	ATU000 418	ATL8C5 451:25 99..16 1	gap2	ATCEA4 S1359, ATCEA4 C72839 1, ATCEA4 S30968 , ATCEA4 S17167	100, 97	ATL8C5 451:23 41..16 6	0.93									
138479	ATU000 419	ATL8C5 010:26 ..1251	gap2	ATCEA4 S813	100	ATL8C5 010:26 ..1251	0.93									
138480	ATU000 420	ATL8C4 7737:7 20..1	gap2	ATCEA4 S3344, ATCEA4 S17722	100, 98	ATL8C4 7737:6 55..15 9	0.93									
138481	ATU000 421	ATL8C1 4369:7 45..32	gap2	ATCEA4 S29969	100	ATL8C1 4369:4 85..32	0.92									
138482	ATU000 422	ATL8C3 785:34 41..22 59	gap2	ATCEA4 S29765 , ATCEA4 S36388 , ATCEA4 S31822	100, 96, 91	ATL8C3 785:33 80..24 27	0.92									
138483	ATU000 423	ATL8C6 396:22 6..269	gap2	ATCEA4 S3218	100	ATL8C6 396:22 6..269	0.92									

138498	ATU000 438	ATL8C5 817:38 67..35 0	gap2	ATCEA4 C29271 _1	99	ATL8C5 817:38 67..18 91	0.90	g44540 43	100	1181			hydrol ases family 9 (Pfam: glycos yl_hyd ro5.hm m, score: 88.03) [Arabi dopsis thalia na]
138499	ATU000 439	ATL8C1 8742:9 5..158 3	gap2	ATCEA4 C2147 _11	99	ATL8C1 8742:9 5..158 3	0.90	g45860 38	100	1105	3.8e- 106		(AC007 109) putati ve heat shock protei n [Arabi dopsis thalia na]
138500	ATU000 440	ATL8C4 7446:3 685..5 434	gap2	ATCEA4 C6174 _1, ATCEA4 C32334 _1, ATCEA4	99, 98, 87, 84	ATL8C4 7446:3 743..5 187	0.90	g19162 90	100	322	9.8e- 13		(U8987 6) ALY [Mus muscul us]

448	0197:3 130..1		S13790 , ATCEA4 S10655	98	0197:3 130..1 73							
138509	ATU000 449	gap2	ATCEA4 C4232_1	100	ATL8C1 8303:1 3..281	0.89						
138510	ATU000 450	gap2	ATCEA4 S12274 , ATCEA4 C33455 _1, ATCEA4 S13030 , ATCEA4 C84793 _1	100, 97, 97, 94	ATL8C2 4264:2 18..24 96	0.89						
138511	ATU000 451	gap2	ATCEA4 C27548 _1	100	ATL8C1 0811:3 446..5 644	0.89						
138512	ATU000 452	gap2	ATCEA4 S686, ATCEA4 S1540, ATCEA4 C10751 4_1, ATCEA4 S13460 , ATCEA4 S3732	100, 99, 99, 94, 93	ATL8C4 5440:2 01..45 03	0.89						
138513	ATU000 453	gap2	ATCEA4 S10520	100	ATL8C2 3830:2 61..21 92	0.89						
138514	ATU000 454	gap2	ATCEA4 S133	100	ATL8C2 0681:1 376..1 943	0.89						
138515	ATU000	gap2	ATCEA4	99	ATL8C2	0.89	945389	100	762	4.1e-	(AL049	

455	2376:7 49..21 91	S1766	99, 99	2376:8 01..17 91	0.89	g45673 01	100	2534	5.4e- 217	63	488) major intrin sic protei n (MIP)- like [Arabi dopsis thalia na]
138516	ATU000 456	gap2	ATCEA4 S3998, ATCEA4 S3812	ATL8C4 2955:2 870..4 29	0.89	g45673 01	100	2534	5.4e- 217		(AC005 956) putati ve protei n kinase [Arabi dopsis thalia na]
138517	ATU000 457	gap2	ATCEA4 C20799 1, ATCEA4 C26345 _1	ATL8C3 2613:2 120..3 632	0.89	g42205 12	100	1007	7.0e- 102		(AL035 356) putati ve pectat e lyase [Arabi dopsis thalia na]
138518	ATU000 458	gap2	ATCEA4 C28908 1, ATCEA4 S19491	ATL8C3 9638:9 4..162 1	0.88	ATL8C3 9638:1 11..16 21					
138519	ATU000 459	gap2	ATCEA4 S1231	ATL8C4 9285:6 94..11 9	0.88	ATL8C4 9285:6 94..25 7					
138520	ATU000	gap2	ATCEA4	ATL8C1	0.88	ATL8C1					

	460	5867:1 704..3 727		C31004 _1		5867:1 704..3 727							
138521	ATU000 461	ATL8C3 5741:1 719..1	gap2	ATCEA4 C5671_1, ATCEA4 S24632 , ATCEA4 C33635 _2, ATCEA4 S7883	100, 92, 91, 86	ATL8C3 5741:1 719..1 72	0.88						
138522	ATU000 462	ATL8C3 6493:2 022..1	gap2	ATCEA4 C17_2, ATCEA4 S34603	99, 83	ATL8C3 6493:1 347..5 9	0.88	g42622 32	100	968	8.1e- 67	(AC006 200) putati ve riboso mal protei n L7 [Arabi dopsis thalia na]	
138523	ATU000 463	ATL8C1 5712:1 21..27 29	gap2	ATCEA4 S26191 , ATCEA4 C86946 _1, ATCEA4 S32386	100, 96, 91	ATL8C1 5712:1 21..25 18	0.88						
138524	ATU000 464	ATL8C4 10:442 3..126 5	gap2	ATCEA4 C3672_1, ATCEA4 S36127	99, 95	ATL8C4 10:431 0..126 5	0.88	g22258 77	100	1395	3.2e- 113	(AB002 406) TIP49 [Rattu s norveg icus]	
138525	ATU000 465	ATL8C4 9313:1 925..1	gap2	ATCEA4 C69929 _1,	99, 95	ATL8C4 9313:1 370..2	0.88	g26606 77	100	756	4.7e- 80	(AC002 342) unknow	

138532	ATU000 472	ATL8C3 5558:2 7..108 4	gap2	S213, ATCEA4 S25923 , ATCEA4 S2379, ATCEA4 S17006	100, 99	ATL8C3 5558:2 7..869	0.87												
138533	ATU000 473	ATL8C4 0914:3 34..1	gap2	ATCEA4 S594 ATCEA4 S13935	100	ATL8C4 0914:3 34..22 4	0.87												
138534	ATU000 474	ATL8C4 4902:5 9..353 4	gap2	ATCEA4 S955	100	ATL8C4 4902:5 9..353 4	0.87												
138535	ATU000 475	ATL8C1 0073:1 72..28 56	gap2	ATCEA4 S2758, ATCEA4 C21290 1, ATCEA4 C70594 2, ATCEA4 S32680 , ATCEA4 C14002 1, ATCEA4 C70594 1, ATCEA4 S25526 , ATCEA4 S22657	100, 99, 98, 96, 94, 92, 85, 84	ATL8C1 0073:1 74..23 81	0.87												
138536	ATU000	ATL8S1	gap2	ATCEA4	100	ATL8S1	0.86												

476	2844:4 6..497	gap2	S3340		2844:4 6..445	0.86	g31579 43	100	194	4.8e- 13	(AC002 131) Contai ns simi larity to BAP31 protei n gb X81 816 from Mus muscul us. [Arabi dopsis thalia na]
138537	ATU000 477	gap2	ATCEA4 S30945	99	ATL8C4 7782:1 938..7 67	0.86	g31579 43	100	194	4.8e- 13	(AC002 131) Contai ns simi larity to BAP31 protei n gb X81 816 from Mus muscul us. [Arabi dopsis thalia na]
138538	ATU000 478	gap2	ATCEA4 S4676	100	ATL8C1 9711:4 78..13 50	0.86					
138539	ATU000 479	gap2	ATCEA4 S6187	100	ATL8C2 7496:1 030..4 44	0.86					
138540	ATU000 480	gap2	ATCEA4 S732	100	ATL8C4 0108:1 2..454	0.86					
138541	ATU000 481	gap2	ATCEA4 S6450, ATCEA4 C70280 _1	99, 94	ATL8C9 50:20. .3197	0.86	g49144 21	100	1260	9.3e- 120	(AL050 352) putati ve protei n [Arabi dopsis thalia na]
138542	ATU000	gap2	ATCEA4	99	ATL8C3	0.86	g22448	100	1362	9.1e-	(Z9733

482	868:89 2..347 7	868:89 2..279 1	S11365	ATL8C1 287:65 5..417 2	ATL8C1 287:77 7..417 2	0.85	g45394 59	100	1750	4.8e- 162	99	7) hypoth etical protei n [Arabi dopsis thalia na]
138543	ATU000 483	ATL8C1 287:65 5..417 2	gap2	ATCEA4 C30652 2, ATCEA4 S32679 , ATCEA4 C15742 1, ATCEA4 C30652 1, ATCEA4 S20154 , ATCEA4 S19460	99, 95, 93, 90, 83, 82	ATL8C1 287:77 7..417 2	0.85	g45394 59	100	1750	4.8e- 162	(AL049 500) putati ve protei n [Arabi dopsis thalia na]
138544	ATU000 484	ATL8C1 136:27 9..640	gap2	ATCEA4 S29753	100	ATL8C1 136:27 9..567	0.85					
138545	ATU000 485	ATL8C4 7541:3 10..33 03	gap2	ATCEA4 C8402- 1, ATCEA4 S24550 , ATCEA4 S10453	99, 97, 86	ATL8C4 7541:4 21..28 59	0.85	g46783 32	100	1803	5.5e- 185	(AL049 658) putati ve peptid e transp orter [Arabi dopsis thalia na]
138546	ATU000 486	ATL8C3 3724:1 799..2 4	gap2	ATCEA4 S775	100	ATL8C3 3724:1 715..2 4	0.85					

138547	ATU000 487	ATL8C8 299:23 92..53	gap2	ATCEA4 S6234, ATCEA4 C44639 _1	99, 98	ATL8C8 299:21 88..53	0.85	g31282 34	100	841	3.5e- 87	(AC004 077) hypoth etical protei n [Arabi dopsis thalia na]
138548	ATU000 488	ATL8C1 9277:5 98..44 72	gap2	ATCEA4 S12457 , ATCEA4 S1211, ATCEA4 S217, ATCEA4 S2773, ATCEA4 S10965 , ATCEA4 C64211 _1, ATCEA4 C64211 _2, ATCEA4 S6145	100, 99, 98, 97, 96, 94, 93, 90	ATL8C1 9277:6 54..42 72	0.85					
138549	ATU000 489	ATL8C3 9872:9 1..230 2	gap2	ATCEA4 S1713	100	ATL8C3 9872:2 89..23 02	0.85					
138550	ATU000 490	ATL8C2 7002:6 70..1	gap2	ATCEA4 C41311 _1, ATCEA4 C3571 _1	100, 97	ATL8C2 7002:5 48..63 0	0.85					
138551	ATU000 491	ATL8C8 349:55 8..1	gap2	ATCEA4 S10486 , ATCEA4 C32738	100, 88	ATL8C8 349:55 8..18	0.84					

138552	ATU000 492	ATL8C1 0918:7 38...38 61	gap2	1 ATCEA4 S2706, ATCEA4 S1472, ATCEA4 S34379	99, 92 96, 92	ATL8C1 0918:7 38...38 12	0.84	g40564 37	100	1151	3.1e- 81	(AC005 990) Strong simila rity to PFAM PF1000 69 Eukary otic protei n kinase domain [Arabi dopsis thalia na]
138553	ATU000 493	ATL8C4 7476:1 675...3 455	gap2	ATCEA4 C77561 _1	100	ATL8C4 7476:1 675...3 126	0.84					
138554	ATU000 494	ATL8S3 0595:5 80...69	gap2	ATCEA4 S3152	100	ATL8S3 0595:5 62...69	0.84					
138555	ATU000 495	ATL8C3 6217:3 707...6 430	gap2	ATCEA4 C32013 _1, ATCEA4 S35199 , ATCEA4 C5579_1, ATCEA4 C5579_2, ATCEA4 S30717	99, 96, 92, 89, 85	ATL8C3 6217:4 222...5 966	0.84	g16526 01, g40069 10	100, 76	192, 133	2.3e- 14, 7.9e- 13	(D9090 6) hypoth etical protei n [Synec hocyst is sp.]; (Z9970 8) putati ve protei n [Arabi

138556	ATU000 496	ATL8C1 7772:1 ..550	gap2	ATCEA4 S2381	100	ATL8C1 7772:6 2..550	0.84									dopsis thalia na]
138557	ATU000 497	ATL8C1 2738:1 183..5 1	gap2	ATCEA4 S10754	99	ATL8C1 2738:1 140..2 96	0.84	g42205 31	100	787	1.9e- 56	(AL035 356) hypoth etical protei n [Arabi dopsis thalia na]				
138558	ATU000 498	ATL8C1 0117:2 552..1 436	gap2	ATCEA4 S30584 , ATCEA4 S30594	100, 97	ATL8C1 0117:2 469..1 436	0.84									
138559	ATU000 499	ATL8C1 0987:2 06..36 01	gap2	ATCEA4 C70754 1, ATCEA4 C88630 1, ATCEA4 S13326 , ATCEA4 S26697	99, 99, 98, 82	ATL8C1 0987:2 15..35 13	0.84	g45811 50	100	851	1.3e- 70	(AC006 919) hypoth etical protei n [Arabi dopsis thalia na]				
138560	ATU000 500	ATL8C3 2083:7 74..46	gap2	ATCEA4 S2263	100	ATL8C3 2083:7 74..46	0.84									
138561	ATU000 501	ATL8C2 7211:4 81..1	gap2	ATCEA4 C47393 _1	100	ATL8C2 7211:4 81..13 0	0.84									
138562	ATU000 502	ATL8C9 990:13 51..25 88	gap2	ATCEA4 S1657, ATCEA4 C19759 1	100, 98	ATL8C9 990:14 73..25 88	0.84									

138563	ATU000 503	ATL8C5 496:42 80..1	gap2	ATCEA4 S1767, ATCEA4 S885, ATCEA4 S2680, ATCEA4 S31425	100, 98, 94	ATL8C5 496:42 80..18 8	0.83						
138564	ATU000 504	ATL8C6 045:13 31..18	gap2	ATCEA4 C25499 1, ATCEA4 C10909 1, ATCEA4 S11388	100, 99, 98	ATL8C6 045:13 29..18	0.83						
138565	ATU000 505	ATL8C9 745:34 9..845	gap2	ATCEA4 S25997	100	ATL8C9 745:70 6..845	0.83						
138566	ATU000 506	ATL8C4 4838:1 10..14 62	gap2	ATCEA4 C44130 1 _	99	ATL8C4 4838:1 51..14 62	0.83	g22450 87	100	999	2.6e- 98	(Z9734 3) hypoth etical protein [Arabi dopsis thalia nal]	
138567	ATU000 507	ATL8C1 2208:3 396..1 113	gap2	ATCEA4 S1964	100	ATL8C1 2208:3 396..1 298	0.83						
138568	ATU000 508	ATL8C1 5179:3 50..14 09	gap2	ATCEA4 C5593 1 _	99	ATL8C1 5179:3 50..11 38	0.83	g35137 44	100	220	8.7e- 13	(AF080 118) contai ns simila rity to Medica go trunca tula	

138577	ATU000 517		314..4 118	gap2	ATCEA4 C48650 1, ATCEA4 C48650 4, ATCEA4 S8096, ATCEA4 S6911, ATCEA4 S6617	88, 85, 84, 83	386..3 873	0.82	g34026 93	100	1789	3.7e- 160	(AC004 697) unknown protein [Arabi dopsis thalia na]
138578	ATU000 518		ATL8C4 837:42 96..32	gap2	ATCEA4 C20893 1	99	ATL8C4 837:42 96..32	0.82	g12239 22	100	726		(U4944 5) Vigna radiat a vicili n peptid ohydro lase [Vigna radiat al]
138579	ATU000 519		ATL8C1 5329:2 338..1	gap2	ATCEA4 C14609 1, ATCEA4 C19656 1, ATCEA4 C14609 2, ATCEA4	99, 98, 96, 95, 83	ATL8C1 5329:2 338..1 37	0.82	g44689 86	100	1002	4.7e- 103	(AL035 605) putati ve protei n [Arabi dopsis thalia na]

138580	ATU000 520	ATL8C4 7486:7 470...3 657	gap2	S13578 , ATCEA4 S19192	99, 97, 97, 95, 86	ATL8C4 7486:7 110...3 657	0.82	948352 36, 921321 86	100, 67	788, 261	8.3e- 80, 8.4e- 18	(AL049 862) putati ve protei n [Arabi dopsis thalia na]; hypoth etical protei n YPL096 w - yeast (Sacch aromyc es cerevi siae) [Sacch aromyc es cerevi siae]
138581	ATU000 521	ATL8C2 5754:6 02...85 8	gap2	ATCEA4 C29685 1	100	ATL8C2 5754:6 78...83 8	0.81					
138582	ATU000 522	ATL8S1 1095:8 2...385	gap2	ATCEA4 S2542	100	ATL8S1 1095:8 2...385	0.81					
138583	ATU000 523	ATL8C1 3229:1 450...3 75	gap2	ATCEA4 C70323 1, ATCEA4 C87513 1, ATCEA4	100, 98, 86	ATL8C1 3229:1 166...7 78	0.81					

138584	ATU000 524	ATL8C1 0898:1 42..11 12	gap2	C564_1 ATCEA4 C74222 _1	99	ATL8C1 0898:2 52..98 4	0.81	944544 60	100	542	5.4e- 44	(AC006 234) unknown protein [Arabi dopsis thalia na]
138585	ATU000 525	ATL8C2 7396:1 28..27 22	gap2	ATCEA4 S15629	99	ATL8C2 7396:1 28..26 43	0.81	931766 73	100	539		(AC003 671) Simila r to serine /threo nine kinase gb Y12 531 from Brassi ca olerac ea. [Arabi dopsis thalia na]
138586	ATU000 526	ATL8S1 6647:1 07..33 8	gap2	ATCEA4 S15186	100	ATL8S1 6647:1 07..25 3	0.81					
138587	ATU000 527	ATL8C1 8746:3 28..1	gap2	ATCEA4 S22612 , ATCEA4 S13274	100, 99	ATL8C1 8746:2 26..71	0.81					
138588	ATU000 528	ATL8C2 1193:1 ..555	gap2	ATCEA4 C5069 _1	100	ATL8C2 1193:1 4..555	0.81					
138589	ATU000 529	ATL8C3 3224:1	gap2	ATCEA4 S1708	100	ATL8C3 3224:9	0.81					

		290					317											ved phosdu cin- like hypoth etical protei n [Schiz osacch aromyc es pombe]
138595	ATU000 535	ATL8C2 6614:1 419..3 75	gap2	ATCEA4 S2815	99		ATL8C2 6614:1 256..4 52	0.80	g30245 28	100	963	1.2e- 97					RAS- RELATE D PROTEI N RAB2BV [Beta vulgar is]	
138596	ATU000 536	ATL8C5 374:49 1..216 7	gap2	ATCEA4 S935	100		ATL8C5 374:62 4..216 7	0.80										
138597	ATU000 537	ATL8C4 7320:1 243..1	gap2	ATCEA4 C6010_ 1, ATCEA4 C8975_ 1	100, 99		ATL8C4 7320:1 146..1 99	0.80										
138598	ATU000 538	ATL8C4 7936:1 374..1	gap2	ATCEA4 C856_ 1, ATCEA4 S5114, ATCEA4 S34989	100, 100, 91		ATL8C4 7936:1 373..2 98	0.80										
138599	ATU000 539	ATL8C4 3051:1 647..3 043	gap2	ATCEA4 S14022 , ATCEA4 S31772	99, 89		ATL8C4 3051:1 713..2 762	0.79	g24438 76, g32648 28	100, 100	301, 305	1.9e- 33, 1.2e- 32					(AC002 294) Hypoth etical protei	

138600	ATU000 540	ATL8C1 7405:1 236..4 7	gap2	ATCEA4 C30186 2, ATCEA4 C20598 1, ATCEA4 C30186 1	100, 95, 92	ATL8C1 7405:8 76..20 5	0.79									n [Arabi dopsis thalia na]; (AF072 404) cotton fiber expres sed protei n 1 [Gossy pium hirsut um]
138601	ATU000 541	ATL8C1 4795:1 ..2151	gap2	ATCEA4 C19158 2, ATCEA4 C10983 9 1, ATCEA4 S11794 , ATCEA4 C19158 1	100, 93, 90, 85	ATL8C1 4795:5 3..215 1	0.79									
138602	ATU000 542	ATL8C2 2262:9 26..21 4	gap2	ATCEA4 C20109 1, ATCEA4 S18376	100, 85	ATL8C2 2262:8 62..21 4	0.79									
138603	ATU000 543	ATL8C3 9239:5	gap2	ATCEA4 C10094	99, 95, 90	ATL8C3 9239:5	0.79	g25296 63	100	1178	2.6e- 104	(AC002 535)				

138604	ATU000 544	08..18 03		2_1, ATCEA4 S33367 , ATCEA4 S32419		91..17 66											putative lysophospholipase [Arabis dopsis thaliana]
	ATU000 544	ATL8C1 0782:1 ..873	gap2	ATCEA4 C14473 1	100	ATL8C1 0782:6 1..873	0.79										
138605	ATU000 545	ATL8C1 6020:1 773..6 176	gap2	ATCEA4 C757_1 , ATCEA4 S32471 , ATCEA4 S28511	99, 94 96, 94	ATL8C1 6020:1 773..6 073	0.79	917306 00	100	373	4.1e- 28						HYPOTHETICAL 35.3 KD PROTEIN IN FTSL 5'REGION (ORF) [Bacillus subtilis]
138606	ATU000 546	ATL8C9 603:11 5..139 0	gap2	ATCEA4 C21293 _1	100	ATL8C9 603:11 5..138 4	0.79										
138607	ATU000 547	ATL8C1 4176:1 111..1	gap2	ATCEA4 C20163 1, ATCEA4 S33243	100, 84	ATL8C1 4176:1 111..1 92	0.78										
138608	ATU000 548	ATL8C3 6216:1 63..17 99	gap2	ATCEA4 S34297 , ATCEA4 C18937 _1	99, 97	ATL8C3 6216:3 49..16 83	0.78	945390 00	100	706	6.2e- 35						(AL049 481) putative protein [Arabis dopsis thaliana]

138609	ATU000 549	ATL8C1 2849:7 39..19 0	gap2	ATCEA4 C22620 _1	100	ATL8C1 2849:7 06..19 0	0.78						na]
138610	ATU000 550	ATL8C3 1243:2 48..14 26	gap2	ATCEA4 S26254 , ATCEA4 S2334	100, 90	ATL8C3 1243:2 48..12 56	0.78						
138611	ATU000 551	ATL8C4 5091:1 ..380	gap2	ATCEA4 C12992 1	100	ATL8C4 5091:3 2..380	0.78						
138612	ATU000 552	ATL8C4 7883:7 91..1	gap2	ATCEA4 C1850_3, ATCEA4 S36368 , ATCEA4 S25958 , ATCEA4 C1850_1	100, 98, 92, 83	ATL8C4 7883:5 45..29	0.78						
138613	ATU000 553	ATL8C5 957:39 10..25	gap2	ATCEA4 S3858, ATCEA4 S922, ATCEA4 C7010_1, ATCEA4 S15128 , ATCEA4 C2222_1	99, 98, 97, 87, 86	ATL8C5 957:35 45..25	0.78	g28282 95	100	1141			(AL021 687) putati ve protei n [Arabi dopsis thalia na]
138614	ATU000 554	ATL8C1 7802:2 866..1	gap2	ATCEA4 S3078, ATCEA4 S6684	100, 99	ATL8C1 7802:2 866..2 0	0.78						
138615	ATU000 555	ATL8C7 315:11	gap2	ATCEA4 S36228	99, 95,	ATL8C7 315:11	0.78	g33347 56	100	677	1.5e- 16		(Y1667 2)

		46..49 61		, ATCEA4 C17283 1, ATCEA4 S19334 , ATCEA4 S19271 , ATCEA4 S14226	87, 84, 82	46..49 61						putati ve argini ne/ser ine- rich splici ng factor [Medic ago sativa j
138616	ATU000 556	ATL8C5 796:27 08..29 3	gap2	ATCEA4 C11594 61, ATCEA4 S4590, ATCEA4 S29005	100, 98, 97	ATL8C5 796:27 08..42 7	0.78					
138617	ATU000 557	ATL8C6 337:26 1..1	gap2	ATCEA4 C17003 1	100	ATL8C6 337:26 1..136	0.78					
138618	ATU000 558	ATL8C1 3287:2 775..4 764	gap2	ATCEA4 S2313	100	ATL8C1 3287:2 775..4 764	0.78					
138619	ATU000 559	ATL8C3 1612:4 78..21 6	gap2	ATCEA4 S3343	100	ATL8C3 1612:4 13..21 6	0.77					
138620	ATU000 560	ATL8C2 4849:1 ..1273	gap2	ATCEA4 C2964 1	100	ATL8C2 4849:5 16..12 73	0.77					
138621	ATU000 561	ATL8C1 8659:2 0..556	gap2	ATCEA4 S10543	100	ATL8C1 8659:2 62..36 0	0.77					
138622	ATU000 562	ATL8C1 1054:1 ..722	gap2	ATCEA4 C325_1 , ATCEA4 S12903	100, 93	ATL8C1 1054:6 7..597	0.77					

138623	ATU000 563	ATL8C6 681:78 3..108	gap2	ATCEA4 S32249 , ATCEA4 C4410_1, ATCEA4 C4410_2	100, 98, 89	ATL8C6 681:78 3..108	0.77					
138624	ATU000 564	ATL8C4 3526:3 66..43 27	gap2	ATCEA4 C3286_1, ATCEA4 S2206, ATCEA4 S10790	99, 99, 92	ATL8C4 3526:1 422..3 470	0.77	g39293 68	100	589	PRE- MRNA SPLICI NG FACTOR SF2 (SR1 PROTEI N) [Arabi dopsis thalia na]	
138625	ATU000 565	ATL8C1 7480:2 683..5 62	gap2	ATCEA4 S13239 , ATCEA4 C89327 1, ATCEA4 C12189 9 1, ATCEA4 C1976_5	100, 99, 92 98, 92	ATL8C1 7480:2 683..9 96	0.77					
138626	ATU000 566	ATL8C4 534:30 50..13 8	gap2	ATCEA4 C29707 1, ATCEA4 S11489	99, 89	ATL8C4 534:24 02..13 9	0.77	g12204 53	100	1495	(M7932 8) alpha- amylase [Solan um tubero sum]	
138627	ATU000 567	ATL8C3 6065:1	gap2	ATCEA4 S27215	100, 98	ATL8C3 6065:1	0.77					

					C3458_1											pollen surface protein [Arabidopsis thaliana]
138633	ATU000 573	ATL8C9 642:20 47..10 88	gap2	ATCEA4 S29512 , ATCEA4 S26366	100, 99	ATL8C9 642:20 43..12 35	0.77									
138634	ATU000 574	ATL8C4 2028:2 416..3 22	gap2	ATCEA4 C5036_1	100	ATL8C4 2028:2 416..3 22	0.77									
138635	ATU000 575	ATL8C4 091:1. .1645	gap2	ATCEA4 C19672 _1, ATCEA4 S19029	99, 84	ATL8C4 091:12 1..150 9	0.76	g41153 79	100	810	1.3e- 68	(AC005 967) putative carbon yl. reductase [Arabidopsis thaliana]				
138636	ATU000 576	ATL8C4 5592:2 5..264 0	gap2	ATCEA4 S13988 , ATCEA4 S472, ATCEA4 S30724	99, 87 96, 87	ATL8C4 5592:2 83..26 31	0.76	g22447 49	100	1446	2.6e- 140	(Z9733 5) hydroxymethyl transferase [Arabidopsis thaliana]				
138637	ATU000 577	ATL8C4 337:10 4..951	gap2	ATCEA4 C31411 _1	100	ATL8C4 337:19 3..951	0.76									
138638	ATU000	ATL8C3	gap2	ATCEA4	100	ATL8C3	0.76									

578	0236:6 54..11 9		S32183		0236:6 02..11 9							
138639	ATU000 579	gap2	ATCEA4 C6235_1	100	ATL8C6 748:48 6..18	0.76						
138640	ATU000 580	gap2	ATCEA4 C266_1 , ATCEA4 S1010, ATCEA4 S34969 , ATCEA4 S26188	100, 94, 84, 84	ATL8C4 9757:9 93..19	0.76						
138641	ATU000 581	gap2	ATCEA4 C9670_1	100	ATL8C2 2331:5 7..172 6	0.76						
138642	ATU000 582	gap2	ATCEA4 S1971	100	ATL8C3 2871:8 72..14 21	0.76						
138643	ATU000 583	gap2	ATCEA4 C4383_1, ATCEA4 C5478_1	99, 98	ATL8C2 2351:3 562..1 754	0.76	928299 13	100	1274	6.6e- 131	(AC002 291) putati ve carbox yphosp honoen olpyru vate mutase [Arabi dopsis thalia na]	
138644	ATU000 584	gap2	ATCEA4 S12646 , ATCEA4 C6799_1	100, 97	ATL8C4 5431:1 36..52 4	0.76						

					S18414 , ATCEA4 C27837 _1												ASSOCIATED PROTEIN C [Pennisetum ciliare]
138655	ATU000 595	ATL8C3 737:22 02..38 53	gap2	ATCEA4 S830	100	ATL8C3 737:22 02..38 53	0.74										
138656	ATU000 596	ATL8C1 6645:4 708..2 008	gap2	ATCEA4 C19249 _1, ATCEA4 S31945 , ATCEA4 S32409	100, 92, 91	ATL8C1 6645:4 523..2 167	0.74										
138657	ATU000 597	ATL8C3 0131:4 52..15 72	gap2	ATCEA4 S1470	99	ATL8C3 0131:6 18..15 72	0.74	g13701 52	100	690	4.1e- 71	(27395 4) RAB11F [Lotus japonicus]					
138658	ATU000 598	ATL8C4 3853:8 37..15 90	gap2	ATCEA4 S32600 , ATCEA4 C1380_1, ATCEA4 S27811 , ATCEA4 S20815	100, 99, 96, 92	ATL8C4 3853:9 79..14 10	0.74										
138659	ATU000 599	ATL8C4 9194:1 361..1 06	gap2	ATCEA4 S706, ATCEA4 C9119_1	100, 99	ATL8C4 9194:1 325..1 06	0.74										
138660	ATU000 600	ATL8C4 9139:3	gap2	ATCEA4 C13123	100	ATL8C4 9139:3	0.74										

1386668	607	869:22 50..1		S13714 , ATCEA4 S884, ATCEA4 C6134_2, ATCEA4 S35248 , ATCEA4 C6134_1	99, 97, 88, 86	869:21 56..31 6						
	ATU000 608	ATL8C4 1195:3 77..23 3	gap2	ATCEA4 C7110_1	100	ATL8C4 1195:3 59..23 3	0.73					
1386669	ATU000 609	ATL8C2 4673:3 30..18 80	gap2	ATCEA4 S1849	99	ATL8C2 4673:4 01..18 80	0.73	935	100	942637 96	1.4e- 71	(AC006 068) hypoth etical protein [Arabi dopsis thalia na]
1386670	ATU000 610	ATL8C3 1761:3 87..32 2	gap2	ATCEA4 S17988	100	ATL8C3 1761:3 87..34 3	0.73					
1386671	ATU000 611	ATL8C1 4897:1 32..43 3	gap2	ATCEA4 S10886	100	ATL8C1 4897:1 32..28 9	0.73					
1386672	ATU000 612	ATL8C2 0929:1 97..43 98	gap2	ATCEA4 S6221, ATCEA4 S11777	100, 97	ATL8C2 0929:1 97..43 98	0.73					
1386673	ATU000 613	ATL8C2 4498:3 99..94	gap2	ATCEA4 C6816_1	100	ATL8C2 4498:3 79..94	0.73					
1386674	ATU000 614	ATL8C3 935:1.	gap2	ATCEA4 C9369	100	ATL8C3 935:53	0.73					

138675	ATU000 615	.148 ATL8C2 4864:1 ..2797	gap2	1 ATCEA4 C4258_1, ATCEA4 S27848 , ATCEA4 C14874 1, ATCEA4 C29802 1, ATCEA4 C14874 3, ATCEA4 S103	99, 94, 94, 92, 91, 88	..148 ATL8C2 4864:5 8..185 7	0.73	g24941 44	100	1701	1.4e- 135	(AC002 329) predic ted leucin e-rich protei n [Arabi dopsis thalia na]
138676	ATU000 616	ATL8C3 6088:1 609..2 96	gap2	ATCEA4 C96940 1, ATCEA4 C11171 1	100, 99	ATL8C3 6088:1 609..7 34	0.72					
138677	ATU000 617	ATL8C1 6150:6 76..37 91	gap2	ATCEA4 S3137, ATCEA4 S36123	100, 95	ATL8C1 6150:6 76..37 91	0.72					
138678	ATU000 618	ATL8C5 609:57 ..679	gap2	ATCEA4 S30281	100	ATL8C5 609:57 ..679	0.72					
138679	ATU000 619	ATL8C1 9836:4 12..46 43	gap2	ATCEA4 S4488, ATCEA4 C9224_1, ATCEA4 C5697_2	99, 94, 84	ATL8C1 9836:4 12..46 43	0.72	g48352 26	100	668	1.0e- 31	(AL049 862) putati ve protei n [Arabi dopsis thalia na]
138680	ATU000 620	ATL8C4 5615:1 580..2	gap2	ATCEA4 C48602 1	100	ATL8C4 5615:1 902..1	0.72					

138685	ATU000 625	ATL8C2 4711:1 ..1852	gap2	ATCEA4 C32495 1, ATCEA4 C20811 1, ATCEA4 S26617	99, 94 98, 94	ATL8C2 4711:8 8..169 8	0.72	g23472 08, g72886 8	100, 74	482, 548	2.7e- 44, 2.7e- 52	(AC002 338) APG protei n isolog [Arabi dopsis thalia nal; ANTER- SPECIF IC PROLIN E-RICH PROTEI N APG (PROTE IN CEX) [Brass ica napus]
138686	ATU000 626	ATL8C4 426:74 5..1	gap2	ATCEA4 C1934 1, ATCEA4 S14340 , ATCEA4 S8045, ATCEA4 S31280 , ATCEA4 S8182, ATCEA4 S24816	100, 99, 93, 88, 86, 84	ATL8C4 426:70 6..168	0.72					
138687	ATU000 627	ATL8C1 2716:2 82..16 38	gap2	ATCEA4 S36263	100	ATL8C1 2716:2 82..16 36	0.72					
138688	ATU000 628	ATL8C2 4364:5 93..28	gap2	ATCEA4 S618, ATCEA4	99, 98, 98	ATL8C2 4364:6 08..24	0.72	g42637 14, g30335	100, 100	373, 388	7.5e- 19, 3.7e-	(AC006 223) putati

138690	ATU000 630	ATL8C3 412:1. .3601	gap2	ATCEA4 C4272- 2, ATCEA4 S26903 , ATCEA4 C27087 3, ATCEA4 C27087 1, ATCEA4 S31735	99, 99, 97, 95, 87	ATL8C3 412:39 3..103 2, ATL8C3 412:33 91..17 00	0.72, 0.73	g22136 26, g32692 88, g44940 08	100, 100, 45	282, 566, 201	5.0e- 17, 8.0e- 42, 1.4e- 14	for by C. elegan s cDNA yk257d 4.3; coded for by C. elegan s cDNA yk303f 4.5; coded for by C. elegan s cDNA yk257d 4.5;.. . []
												(AC000 103) F21J9. 18 [Arabi dopsis thalia nal]; (AL030 978) putati ve protei n [Arabi dopsis thalia nal]; (AL034 559) predic ted using hexExo

		06				06						ve n kinase [Arabi dopsis thalia na]
138692	ATU000 632	ATL8C3 7689:3 56..10 04	gap2	ATCEA4 S11316 , ATCEA4 S10995	100, 96	ATL8C3 7689:6 63..10 04	0.71					
138693	ATU000 633	ATL8C4 6297:9 19..17 50	gap2	ATCEA4 S29795	100	ATL8C4 6297:9 19..11 20	0.71					
138694	ATU000 634	ATL8C1 3727:1 42..15 80	gap2	ATCEA4 S31842 , ATCEA4 C80570 1	100, 93	ATL8C1 3727:1 42..14 27	0.71					
138695	ATU000 635	ATL8C2 6911:2 163..1 065	gap2	ATCEA4 C32097 1, ATCEA4 S30620	100, 82	ATL8C2 6911:2 163..1 604	0.71					
138696	ATU000 636	ATL8C3 2679:4 340..9 189	gap2	ATCEA4 S833, ATCEA4 S392, ATCEA4 S33497 , ATCEA4 S29570	100, 99, 97, 93	ATL8C3 2679:4 340..9 189	0.70					
138697	ATU000 637	ATL8C1 6105:4 7..641	gap2	ATCEA4 C21781 1	100	ATL8C1 6105:4 7..513	0.70					
138698	ATU000 638	ATL8C1 5796:1 869..5 87	gap2	ATCEA4 C33629 2, ATCEA4	100, 99, 97	ATL8C1 5796:1 685..7 65	0.70					

138699	ATU000 639	ATL8C1 0092:3 19..1	gap2	ATCEA4 S12687	100, 99	ATL8C1 0092:3 19..47	0.70	g36680 80	100	1438	7.4e- 98	(AC004 667) unknown protein [Arabi dopsis thalia na]
138700	ATU000 640	ATL8C1 619:21 45..1	gap2	ATCEA4 S14065 , ATCEA4 C88829 1, ATCEA4 C13651 1, ATCEA4 S18237	99, 99, 98, 96	ATL8C1 619:19 58..19 3	0.70					
138701	ATU000 641	ATL8C4 0601:1 33..14 45	gap2	ATCEA4 S4774	100	ATL8C4 0601:1 33..11 25	0.69					
138702	ATU000 642	ATL8C4 1824:1 03..56 1	gap2	ATCEA4 S1619	100	ATL8C4 1824:1 45..39 9	0.69					
138703	ATU000 643	ATL8C1 7928:2 60..12 49	gap2	ATCEA4 C21418 1, ATCEA4 S34578	100, 92	ATL8C1 7928:2 94..99 4	0.69					
138704	ATU000 644	ATL8C8 45:564 ..2998	gap2	ATCEA4 S12068	99	ATL8C8 45:576 ..2939	0.69	g44172 87, g49144 63	100, 89	668, 632	1.5e- 64, 1.7e- 56	(AC007 019) unknown protein [Arabi dopsis thalia na];

138705	ATU000 645	ATL8C1 7920:1 371..2 152	gap2	ATCEA4 S3350	100	ATL8C1 7920:1 573..2 152	0.69						(AL050 400) putati ve protei n [Arabi dopsis thalia na]
138706	ATU000 646	ATL8C4 4702:1 314..1	gap2	ATCEA4 C24695 1, ATCEA4 S32534	100, 90	ATL8C4 4702:1 273..6 8	0.69						
138707	ATU000 647	ATL8C3 6946:1 ..1641	gap2	ATCEA4 C5391_ 2, ATCEA4 C5391_ 1, ATCEA4 C28643 2, ATCEA4 C28643 1, ATCEA4 C7449_ 2	100, 97, 96, 93, 82	ATL8C3 6946:8 2..146 6	0.69						
138708	ATU000 648	ATL8C4 7587:1 ..3139	gap2	ATCEA4 S432, ATCEA4 C19720 1, ATCEA4 S33082 , ATCEA4 S1167, ATCEA4	99, 98, 93, 91, 89	ATL8C4 7587:9 27..29 23	0.69	g27608 39	100	1323	2.1e- 136	(AC003 105) putati ve recept or kinase [Arabi dopsis thalia na]	

138716	ATU000 656	ATL8C1 9203:7 128..5 5	gap2	ATCEA4 C7150_ 1, ATCEA4 C86015 _1	99, 94	ATL8C1 9203:6 930..5 5	0.67	g47311 11, g12038 32	100, 100	1597, 1462	3.2e- 154, 4.0e- 140	subunit [Homo sapien s]
138717	ATU000 657	ATL8C2 6084:2 21..16 78	gap2	ATCEA4 C11922 _1, ATCEA4 C5497_ 1	99, 98	ATL8C2 6084:2 23..15 88	0.67	g39281 50	100	1126	3.1e- 112	(AJ131 049) hypoth etical protein [Cicer arietini num]
138718	ATU000 658	ATL8C2 7969:7 40..15 5	gap2	ATCEA4 C655_ 1	100	ATL8C2 7969:6 99..15 5	0.67					
138719	ATU000 659	ATL8C4 8425:3 2..197 4	gap2	ATCEA4 S1053	100	ATL8C4 8425:3 2..197 4	0.67					

		773..2 3		ATCEA4 C4567_1		773..2 3		0.62	930241 35, 945672 79	100, 97	745, 1483	1.9e- 55, 6.6e- 165	hypothetical protein [Arabidopsis thaliana]
138750	ATU000 690	ATL8C1 6954:1 ..4299	gap2	ATCEA4 S36147 , ATCEA4 S1288	99, 99	ATL8C1 6954:6 50..42 96	0.62						PUTATIVE SEPTUM SITE-DETERMINING PROTEIN MIND [Chlorella vulgaris]; (AC006841) putative serine/threonine protein kinase [Arabidopsis thaliana]
138751	ATU000 691	ATL8C2 9284:1 066..1 27	gap2	ATCEA4 S1159, ATCEA4 S12613 , ATCEA4 C11704 1	100, 98, 95	ATL8C2 9284:8 02..12 7	0.62						
138752	ATU000 692	ATL8C2 2066:3 6..173	gap2	ATCEA4 C16832 1,	100, 92	ATL8C2 2066:3 6..168	0.62						

	7		ATCEA4 S33200		8							
138753	ATU000 693	gap2	ATL8C1 5859:4 34..26 45	gap2	ATL8C1 5859:4 34..26 13	100, 97, 89	ATL8C1 5859:4 34..26 13	0.62				
138754	ATU000 694	gap2	ATL8C1 1290:3 117..2 99	gap2	ATL8C1 1290:3 115..2 99	99	ATL8C1 1290:3 115..2 99	0.61	944690 24	100	3485	0.0 (AL035 602) putati ve protei n [Arabi dopsis thalia na]
138755	ATU000 695	gap2	ATL8C3 7488:8 7..118 4	gap2	ATL8C3 7488:8 7..118 4	100	ATL8C3 7488:8 7..118 4	0.61				
138756	ATU000 696	gap2	ATL8C3 7572:5 005..3 849	gap2	ATL8C3 7572:4 947..4 061	99, 93, 91	ATL8C3 7572:4 947..4 061	0.61	932818 67	100	165	1.4e- 12 (AL031 004) putati ve protei n [Arabi dopsis thalia na]
138757	ATU000 697	gap2	ATL8S2 0626:1 ..524	gap2	ATL8S2 0626:3 55..50 6	100, 82	ATL8S2 0626:3 55..50 6	0.61				
138758	ATU000 698	gap2	ATL8C1 2431:1 ..444	gap2	ATL8C1 2431:1 13..44 0	100, 94	ATL8C1 2431:1 13..44 0	0.61				

138759	ATU000 699	ATL8C3 8146:3 61..28 80	gap2	ATCEA4 C49233 1, ATCEA4 C430_1	99, 87	ATL8C3 8146:2 603..2 209	0.61	g25831 28, g30368 14	100, 39	472, 80	7.3e- 40, 0.0095	(AC002 387) hypoth etical protei n [Arabi dopsis thalia na]; (AL022 373) hypoth etical protei n [Arabi dopsis thalia na]
138760	ATU000 700	ATL8C1 1404:1 883..5 430	gap2	ATCEA4 C10834 1, ATCEA4 C19941 1, ATCEA4 S12151	99, 97, 94	ATL8C1 1404:1 914..5 430	0.61	g44552 87, g40380 34	100, 99	301, 335	4.7e- 14, 5.2e- 24	(AL035 527) putati ve protei n [Arabi dopsis thalia na]; (AC005 936) unknow n protei n [Arabi dopsis thalia na]
138761	ATU000 701	ATL8C1 7040:2 537..8 09	gap2	ATCEA4 S10310 , ATCEA4	100, 91, 89	ATL8C1 7040:2 537..8 09	0.60					

138762	ATU000 702	ATL8C1 4541:8 66..54 4	gap2		C855_1 , ATCEA4 S15745	100, 96	ATL8C1 4541:7 76..58 3	0.60							
138763	ATU000 703	ATL8C1 3007:1 36..66 4	gap2		ATCEA4 C5830_1, ATCEA4 C32973_1	100, 98	ATL8C1 3007:1 36..31 8	0.60							
138764	ATU000 704	ATL8C2 4380:3 31..1	gap2		ATCEA4 C67029_1 S3866	100	ATL8C2 4380:3 31..27 1	0.60							
138765	ATU000 705	ATL8C4 5589:4 449..1 39	gap2		ATCEA4 S12104 , ATCEA4 S13170	100, 93	ATL8C4 5589:4 260..1 39	0.60							
138766	ATU000 706	ATL8C3 1156:2 62..10 38	gap2		ATCEA4 S4082	100	ATL8C3 1156:8 35..10 38	0.60							
138767	ATU000 707	ATL8C3 2015:1 ..1160	gap2		ATCEA4 C9156_1, ATCEA4 C10244_1_1	100, 93	ATL8C3 2015:2 6..892	0.59							
138768	ATU000 708	ATL8C5 843:34 32..20 4	gap2		ATCEA4 S3777	99	ATL8C5 843:34 32..20 4	0.59	g43888 26	100	720				(AC006 528) hypoth etical protei n [Arabi dopsis thalia na]

138779	ATU000 719	ATL8C1 6333:9 96...54 75	gap2	ATCEA4 S29889 , ATCEA4 C34674 1, ATCEA4 S30583 , ATCEA4 C29889 1, ATCEA4 S4773	99, 98, 96, 93, 84	ATL8C1 6333:9 96...53 39	0.58	g22528 41	100	2963	4.2e- 240	thalia nal (AF013 293) No defini tion line found [Arabi dopsis thalia nal]
138780	ATU000 720	ATL8C1 3330:5 25...24 91	gap2	ATCEA4 C18745 1, ATCEA4 S5349	100, 100	ATL8C1 3330:5 25...24 91	0.58					
138781	ATU000 721	ATL8C4 9598:2 638...1 32	gap2	ATCEA4 S1242, ATCEA4 C14863 5 1, ATCEA4 S26757	99, 87, 82	ATL8C4 9598:2 638...1 32	0.57	g29206 66, g16518 67	100, 99	671, 206	2.8e- 60, 3.4e- 20	(AF048 978) 2, 4-D induci ble glutata hione S- transf erase [Glyci ne max]; (D9090 0) hypoth etical protei n [Synec hocyst is sp.]
138782	ATU000	ATL8C2	gap2	ATCEA4	100	ATL8C2	0.57					

138783	722	0208:4 646..5 689	gap2	S3338		0208:5 689..4 646	0.57, 0.48	g23471 88, 944671 34	100, 31	2140, 105	1.1e- 196, 8.6e- 10	(AC002 338) \\ laccas e isolog [Arabi dopsis thalia na]; (AL035 540) protei n kinase like protei n [Arabi dopsis thalia na]
138784	ATU000 723	ATL8C4 9902:3 041..7 173	gap2	ATCEA4 S6054	99	ATL8C4 9902:3 439..4 999, ATL8C4 9902:5 346..6 956	0.57					
138785	ATU000 724	ATL8C1 3736:2 74..88 6	gap2	ATCEA4 C13486 6_1	100	ATL8C1 3736:2 74..74 8	0.57					
138786	ATU000 725	ATL8C1 3486:4 45..19 86	gap2	ATCEA4 C999_1	100	ATL8C1 3486:6 54..19 12	0.56					
138787	ATU000 726	ATL8C3 1918:2 448..1 041	gap2	ATCEA4 S36166 , ATCEA4 S31095 , ATCEA4 S33175	99, 89, 88	ATL8C3 1918:2 442..1 262	0.56	g21045 36	100	1050	2.4e- 110	(AF001 308) predic ted glycos yl transf erase [Arabi dopsis thalia na]

138792	ATU000 732	ATL8C3 3387:2 296..5 616	gap2	ATCEA4 C2790_1, ATCEA4 C90147_1, ATCEA4 S34635, ATCEA4 C54462_2	99, 91, 83, 82	ATL8C3 3387:5 546..2 296	0.56	g28326 96, g44552 03	100, 73	681, 673	1.2e- 65, 2.8e- 67	(AL021 713) putati ve protei n [Arabi dopsis thalia na]; (AL035 440) putati ve protei n [Arabi dopsis thalia na]
138793	ATU000 733	ATL8C7 936:85 0..399 5	gap2	ATCEA4 S14015, ATCEA4 S2629	100, 98	ATL8C7 936:10 07..37 76	0.55					
138794	ATU000 734	ATL8C3 7200:1 187..2 529	gap2	ATCEA4 S417	100	ATL8C3 7200:1 187..2 529	0.55					
138795	ATU000 735	ATL8C4 4976:2 69..73 5	gap2	ATCEA4 S26404	100	ATL8C4 4976:2 69..40 8	0.55					
138796	ATU000 736	ATL8C1 0829:8 3..500 0	gap2	ATCEA4 C47741_1	99	ATL8C1 0829:8 3..245 4, ATL8C1 0829:3 556..4 623	0.55, 0.71	g27393 73	100	1019	8.5e- 101	(AC002 505) putati ve flavon ol 3- o- glucos yltran sferas e [Arabi

		99...61 29					42...60 57		g30245 05			1.2e- 84	putative protein [Arabidopsis thaliana]; RAS-RELATED PROTEIN RAB11D [Nicotiana tabacum]
138807	ATU000 747	ATL8C1 7070:1 38...50 20	gap2	ATCEA4 C13520 81, ATCEA4 C60312 1, ATCEA4 S19892 , ATCEA4 C58267 1, ATCEA4 S11148 , ATCEA4 C3143 1, ATCEA4 S8964, ATCEA4 C21396 1, ATCEA4 S5374	99, 99, 99, 97, 95, 93, 91, 89, 85	ATL8C1 7070:1 38...45 43	0.53	g11990 5, g30368 07	100, 100	1373, 2004	1.8e- 111, 5.5e- 197	FERRED OXIN-- NADP REDUCT ASE, LEAF ISOZYM E PRECUR SOR (FNR) [Arachis hypogaea]; (AL022373) putative protein [Arabidopsis thaliana]	
138808	ATU000 748	ATL8C3 9634:7	gap2	ATCEA4 S5212	100	ATL8C3 9634:7	0.53						

138815	ATU000 755	ATL8C2 0836:1 147..1 01	gap2	ATCEA4 C6765 1, ATCEA4 S4658, ATCEA4 C21613 1	100, 98, 93	76..99 ATL8C2 0836:1 093..1 63	0.53	932692 95	100	2396	1.5e- 221	(AL030 978) putati ve protei n [Arabi dopsis thalia na]
138816	ATU000 756	ATL8C2 5188:8 79..33 80	gap2	ATCEA4 S30442	99	ATL8C2 5188:8 79..32 33	0.53					
138817	ATU000 757	ATL8S8 559:87 ..521	gap2	ATCEA4 S23811	100	ATL8S8 559:87 ..272	0.53					
138818	ATU000 758	ATL8C2 3832:1 355..3 06	gap2	ATCEA4 S1258, ATCEA4 S337	100, 99	ATL8C2 3832:1 210..3 06	0.53					
138819	ATU000 759	ATL8C2 4120:1 402..6 71	gap2	ATCEA4 S36225	100	ATL8C2 4120:1 236..6 71	0.52					
138820	ATU000 760	ATL8C4 438:85 ..2015	gap2	ATCEA4 C48227 1, ATCEA4 S8398	100, 96	ATL8C4 438:85 ..2015	0.52					
138821	ATU000 761	ATL8C1 2326:1 84..92 2	gap2	ATCEA4 S25967	100	ATL8C1 2326:1 84..56 8	0.52					
138822	ATU000 762	ATL8C4 8092:8 36..1	gap2	ATCEA4 S33449 , ATCEA4 S7818	100, 100	ATL8C4 8092:8 36..11 2	0.52					

138823	ATU000 763	ATL8C3 4959:3 91..41 65	gap2	ATCEA4 S2447, ATCEA4 S29958 , ATCEA4 S31201 , ATCEA4 C15312 1	100, 97, 91 92, 91	ATL8C3 4959:3 91..41 65	0.52					
138824	ATU000 764	ATL8C2 588:56 5..11	gap2	ATCEA4 C82248 1	100	ATL8C2 588:36 4..11	0.51					
138825	ATU000 765	ATL8S2 6919:1 ..486	gap2	ATCEA4 S13859 , ATCEA4 S10742	100, 94	ATL8S2 6919:8 3..486	0.51					
138826	ATU000 766	ATL8C9 204:21 2..418 5	gap2	ATCEA4 C6425_ 1, ATCEA4 S13022 , ATCEA4 C34127 1, ATCEA4 S17831	100, 99, 84 94, 84	ATL8C9 204:21 2..396 4	0.51					
138827	ATU000 767	ATL8C1 589:29 67..1	gap2	ATCEA4 C6770_ 3, ATCEA4 C4345_ 1, ATCEA4 C6770_ 1	99, 97, 83	ATL8C1 589:26 33..17 5	0.51	g44067 56	100	1270	8.7e- 125	(AC006 836) putati ve integr al membra ne protei n A3 [Arabi dopsis thalia na]

138828	ATU000 768	ATL8C4 9351:1 84..86	gap2	ATCEA4 S10672	100	ATL8C4 9351:1 84..77 8	0.51					
138829	ATU000 769	ATL8C1 8464:8 38..10 59	gap2	ATCEA4 C894_1	100	ATL8C1 8464:9 64..10 59	0.51					
138830	ATU000 770	ATL8C3 9884:1 ..597	gap2	ATCEA4 C361_1	100	ATL8C3 9884:6 5..582	0.50					
138831	ATU000 771	ATL8C2 3019:4 7..215 4	gap2	ATCEA4 C32447 _1	99	ATL8C2 3019:3 49..18 21	0.50	g40493 41, g44557 84	100, 58	216, 56	1.2e- 21, 0.0002 5	(AL034 567) putati ve protei n [Arabi dopsis thalia nal; (AL035 536) phosph ate- phosph oenolp yruvat e transl ocator precu rsor. [Schiz osacch aromyc es pombe]
138832	ATU000 772	ATL8C1 3536:1 609..4	gap2	ATCEA4 S1032, ATCEA4 S8325	100, 98	ATL8C1 3536:1 609..1 84	0.50					
138833	ATU000 773	ATL8C9 95:116	gap2	ATCEA4 S29521	99	ATL8C9 95:120	0.50	g28327 06	100	784	6.2e- 82	(AL021 713)

138842	781	6617:1 648..1 82	gap2	S3386, ATCEA4 S27593 , ATCEA4 C18208 1	98, 88	6617:1 243..1 82	0.48	g22448 55	100	2493	7.9e- 150	(Z9733 7) hypoth etical protei n [Arabi dopsis thalia na]
138843	ATU000 782	ATL8C1 3165:4 080..4 00	gap2	ATCEA4 C34332 1, ATCEA4 C34332 2	99, 98	ATL8C1 3165:4 080..7 03	0.48					
138844	ATU000 783	ATL8C1 866:91 8..97	gap2	ATCEA4 S1499	100	ATL8C1 866:91 8..97	0.47					
138845	ATU000 784	ATL8C2 4046:1 095..9 3	gap2	ATCEA4 S29650 , ATCEA4 S2417	100, 96	ATL8C2 4046:1 095..9 3	0.47					
138846	ATU000 785	ATL8C6 138:50 4..1	gap2	ATCEA4 S1300, ATCEA4 S3115	100, 94	ATL8C6 138:40 0..74	0.46					
138847	ATU000 786	ATL8C8 851:87 1..36	gap2	ATCEA4 S6755, ATCEA4 C96498 1, ATCEA4 S31848	100, 99, 90	ATL8C8 851:67 4..509	0.45					
138848	ATU000 787	ATL8C2 209:77 5..113 8	gap2	ATCEA4 C4360- 1	100	ATL8C2 209:83 2..102 0	0.45					
138849	ATU000 788	ATL8C2 5698:1 75..56	gap2	ATCEA4 S36372	100	ATL8C2 5698:1 75..56	0.45					
138849	ATU000	ATL8C3	gap2	ATCEA4	100,	ATL8C3	0.45					

[illegible]

138862	ATU000 802	ATL8C4 1283:4 51..10 1	gap2	ATCEA4 C18923 1	100	ATL8C4 1283:4 03..10 1	0.42						
138863	ATU000 803	ATL8C3 7056:2 22..66 3	gap2	ATCEA4 S14028	100	ATL8C3 7056:2 42..66 3	0.42						
138864	ATU000 804	ATL8C1 1227:7 74..38 9	gap2	ATCEA4 S943	100	ATL8C1 1227:6 34..38 9	0.42						
138865	ATU000 805	ATL8C3 2491:9 7..399	gap2	ATCEA4 C21477 1, ATCEA4 C21477 4	100, 96	ATL8C3 2491:3 32..23 2	0.42						
138866	ATU000 806	ATL8C2 0613:4 48..1	gap2	ATCEA4 S1875	100	ATL8C2 0613:4 31..13 4	0.42						
138867	ATU000 807	ATL8C2 860:35 7..419 7	gap2	ATCEA4 S1220, ATCEA4 C7997 1, ATCEA4 C23648 1	99, 90, 84	ATL8C2 860:38 5..397 4	0.42	g39285 43	100	1982	6.9e- 193	(AB016 819) UDP- glucos e glucos yltran sferas e [Arabi dopsis thalia na]	
138868	ATU000 808	ATL8C1 8794:4 744..1 367	gap2	ATCEA4 S29543 , ATCEA4 C35531 1, ATCEA4 S25985	99, 94, 85, 85	ATL8C1 8794:4 693..2 279	0.41	g33096 20	100	2290	3.3e- 225	(AF074 916) resist ance to Pseudo monas syring ae	

138869	ATU000 809	ATL8C1 0327:9 446..1	gap2	ATCEA4 S12710	99, 97, 96, 96, 86	ATL8C1 0327:4 70..86 42	0.41	g54184 9, g45586 63, g37460 69	100, 35 48, 35	978, 58, 1126		prote n 5 [Arabi dopsis thalia nal]
				ATCEA4 C4058_6, ATCEA4 C4058_8, ATCEA4 C4058_10, ATCEA4 C4058_7, ATCEA4 S13104								anthra nilate syntha se (EC 4.1.3. 27) beta chain - Arabid opsis thalia na [Arabi dopsis thalia nal]; (AC007 063) unknow n protei n [Arabi dopsis thalia nal]; (AC005 311) putati ve revers e transc riptas e [Arabi dopsis thalia

138870	ATU000 810	ATL8S2 2367:6 05..19 5	gap2	ATCEA4 S13947	100	ATL8S2 2367:5 67..19 5	0.41							na]
138871	ATU000 811	ATL8C1 558:10 58..21 66	gap2	ATCEA4 S1742	100	ATL8C1 558:11 02..21 66	0.41							
138872	ATU000 812	ATL8C8 956:1. .393	gap2	ATCEA4 S27989 , ATCEA4 C828 7	100, 92	ATL8C8 956:50 ..302	0.41							
138873	ATU000 813	ATL8C3 8312:7 15..18 2	gap2	ATCEA4 S2805	100	ATL8C3 8312:5 29..18 2	0.40							
138874	ATU000 814	ATL8C4 5123:1 ..432	gap2	ATCEA4 S3025	100	ATL8C4 5123:2 65..43 2	0.40							
138875	ATU000 815	ATL8C4 091:16 97..13 80	gap2	ATCEA4 S310	100									
138876	ATU000 816	ATL8C9 894:38 6..496	gap2	ATCEA4 C4969 _ 2, ATCEA4 S486, ATCEA4 C4969 _ 1	100, 98, 90									
138877	ATU000 817	ATL8C2 864:29 7..848	gap2	ATCEA4 S1908, 100, ATCEA4 S27951 , ATCEA4 S27956	100, 100, 88									
138878	ATU000 818	ATL8C2 1270:1 067..2	gap2	ATCEA4 C8224 _ 1	99			g32985 39	100	1817	3.1e- 181	(AC004 681) NPK1-		

138987	ATU000 927	ATL8C2 1523:8 10..66	gap2	C38 1 ATCEA4 C12015 0_1	99				g25296 59	100	530	7.0e- 46	(AC002 535) putati ve pectin estera se [Arabi dopsis thalia na]
138988	ATU000 928	ATL8C1 6711:1 ..191	gap2	ATCEA4 C89331 1	100								
138989	ATU000 929	ATL8C5 0212:5 86..94	gap2	ATCEA4 S13716 , ATCEA4 C10997 1	100, 99								
138990	ATU000 930	ATL8C3 4296:7 5..298	gap2	ATCEA4 S1302	100								
138991	ATU000 931	ATL8S1 8209:5 12..23 6	gap2	ATCEA4 C82061 _1	100								
138992	ATU000 932	ATL8C2 6685:1 ..777	gap2	ATCEA4 C10278 9 1, ATCEA4 C17117 1	100, 96								
138993	ATU000 933	ATL8C4 566:17 8..1	gap2	ATCEA4 S28267	100								
138994	ATU000 934	ATL8C1 9123:2 139..1 865	gap2	ATCEA4 S32937	100								
138995	ATU000 935	ATL8C1 7094:6 3..475	gap2	ATCEA4 C17028 1	100								

139085	ATU001 025	ATL8C2 1686:3 426..1 755	gap2	ATCEA4 C36606 _1, ATCEA4 S31818 , ATCEA4 C21431 _1	99, 97, 97					g38191 64	100	2344	1.3e- 219	protei n [Arabi dopsis thalia na]
139086	ATU001 026	ATL8C3 738:34 93..13 09	gap2	ATCEA4 S32142 , ATCEA4 S1807	99, 98					g45875 50	100	920	3.4e- 97	(AJ012 318) cytoso lic chaper onin, delta- subuni t [Glyci ne max] (AC006 577) EST gb R64 848 comes from this gene. [Arabi dopsis thalia na]
139087	ATU001 027	ATL8S3 0340:1 ..529	gap2	ATCEA4 S35404 , ATCEA4 C19361 _1	100, 99									
139088	ATU001 028	ATL8C3 74:165 8..281 0	gap2	ATCEA4 C26858 _1	99					g33675 93	100	378	3.7e- 30	(AL031 135) putati ve protei n [Arabi dopsis

139109	ATU001 049	ATL8C3 8341:1 145..1 572	gap2	ATCEA4 C78689 _1	100							gb F15 470, gb Z35 182, gb H76 373, gb Z34 678 an... []; (D1455 0) EDGP precur sor [Daucu s carota]
139110	ATU001 050	ATL8C1 3396:2 181..2 299	gap2	ATCEA4 C20200 _1	100							
139111	ATU001 051	ATL8C1 2019:9 4..1	gap2	ATCEA4 S8198, ATCEA4 C18391 _1	100, 97							
139112	ATU001 052	ATL8C2 2137:5 72..98 5	gap2	ATCEA4 S3888	100							
139113	ATU001 053	ATL8C1 7737:1 778..9 64	gap2	ATCEA4 S5050	100							
139114	ATU001 054	ATL8C3 2821:5 52..90 8	gap2	ATCEA4 C6797_ 2, ATCEA4	100, 98							

[illegible]

139120	ATU001 060	0	gap2	ATCEA4 S12418 ATCEA4 S26596 , ATCEA4 C32187 1, ATCEA4 S3687, ATCEA4 C6337_ 1, ATCEA4 S31787	99, 98, 95, 95, 88				g33193 42	100	966	8.9e- 83	(AF077 407) simila r to mitoch ondria l carrie r protei ns (Pfam: mit_ca rr.hmm , score: 79.74 and 42.50) [Arabi dopsis thalia na]
139121	ATU001 061	ATL8C3 3409:7 17..11 03	gap2	ATCEA4 S3682	100								
139122	ATU001 062	ATL8S2 8090:3 59..72 5	gap2	ATCEA4 C21023 _1	100								
139123	ATU001 063	ATL8C2 7154:8 33..55 4	gap2	ATCEA4 C27310 _1	100								
139124	ATU001 064	ATL8C3 2327:5 91..1	gap2	ATCEA4 S35530 , ATCEA4 S13701	100, 99								
139125	ATU001 065	ATL8C1 1364:4	gap2	ATCEA4 C5609	99, 86				g20886 51,	100, 87	353, 72	4.8e- 45,	(AF002 109)

		25...22 66		1, ATCEA4 C92394 _1						g11715 77			3.0e- 10	hypers ensiti vity- relate d gene 201 isolog [Arabi dopsis thalia nal; (X9534 3) hypers ensiti vity- relate d gene [Nicot iana tabacu m]
139126	ATU001 066	ATL8C4 1554:6 25...35 6	gap2	ATCEA4 S25839	100									
139127	ATU001 067	ATL8C3 6863:9 89...57 6	gap2	ATCEA4 C37706 _1	100									
139128	ATU001 068	ATL8C1 7457:2 115...2 316	gap2	ATCEA4 S8377, ATCEA4 C4457_ 1, ATCEA4 S8378	100, 91, 84									
139129	ATU001 069	ATL8C2 0038:1 285...3 56	gap2	ATCEA4 S7718	99					932928 15	100	228		(AL031 018) hypoth etical protei n [Arabi dopsis

139130	ATU001 070	ATL8S1 4515:1 ..52	gap2	ATCEA4 S2391	100													thalia na]
139131	ATU001 071	ATL8C1 5600:3 75..62 5	gap2	ATCEA4 S11332	100													
139132	ATU001 072	ATL8C1 5626:1 ..322	gap2	ATCEA4 S12873	100													
139133	ATU001 073	ATL8C1 3337:2 38..31 6	gap2	ATCEA4 C25033 _1	100													
139134	ATU001 074	ATL8C3 960:50 2..866	gap2	ATCEA4 S36327	100													
139135	ATU001 075	ATL8C3 7566:4 28..63 6	gap2	ATCEA4 C4323_15, ATCEA4 S11896	100, 85													
139136	ATU001 076	ATL8C3 0590:9 3..331	gap2	ATCEA4 S29844	100													
139137	ATU001 077	ATL8S1 088:1. .160	gap2	ATCEA4 S2705	100													
139138	ATU001 078	ATL8C6 0:1556 ..1073	gap2	ATCEA4 C20780 _1	100													
139139	ATU001 079	ATL8C8 412:12 76..59	gap2	ATCEA4 C25256 _1, ATCEA4 C19866 _1	99, 92													(AC004 392) Simila r to gb U08 285 membra ne- associ ated salt-

139140	ATU001 080	ATL8C3 6895:1 ..133	gap2	ATCEA4 S27134	100								inducible protein from Nicotiana tabacum. ESTs gb T44131 and gb T04378 come from this gene. [Arabidopsis thaliana]
139141	ATU001 081	ATL8C3 1194:9 37..57 4	gap2	ATCEA4 S2531, ATCEA4 S16632	100, 94								
139142	ATU001 082	ATL8C2 2511:4 52..27 0	gap2	ATCEA4 C17883 _1	100								
139143	ATU001 083	ATL8C4 8634:5 76..51 9	gap2	ATCEA4 C19815 _1	100								
139144	ATU001 084	ATL8C3 3840:1 51..18 23	gap2	ATCEA4 S4131	99								(AC007169) hypothetical protein [Arabidopsis thaliana]

139145	ATU001 085	ATL8C8 940:43 6..90	gap2	ATCEA4 S11640	100													dopsis thalia na]; (AC007 070) hypoth etical protei n [Arabi dopsis thalia na]
139146	ATU001 086	ATL8C3 758:66 8..819	gap2	ATCEA4 C411_1	100													
139147	ATU001 087	ATL8C4 6879:6 26..53 1	gap2	ATCEA4 S13247	100													
139148	ATU001 088	ATL8C3 760:1. .316	gap2	ATCEA4 C62449 3	100													
139149	ATU001 089	ATL8C2 4831:8 050..6 981	gap2	ATCEA4 C955_1	99													THAUMA TIN- LIKE PROTEI N PRECUR SOR [Arabi dopsis thalia na]
139150	ATU001 090	ATL8C4 3291:2 599..3 279	gap2	ATCEA4 S16111 , ATCEA4 S27710 , ATCEA4	100, 93, 84													

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[illegible][illegible]

139185	ATU001 125	ATL8C2 274:10 275..7 779	gap2	ATCEA4 S13679 , ATCEA4 C10292 1, ATCEA4 C33093 1, ATCEA4 C14384 9 1, ATCEA4 S35090	99, 99, 99, 94, 89				g25589 38	100	1822	1.9e- 154	(AF024 625) arm repeat contai ning protei n [Brass ica napus]
139186	ATU001 126	ATL8C3 6997:4 37..80 9	gap2	ATCEA4 S13033	100								
139187	ATU001 127	ATL8C2 002:99 0..137 5	gap2	ATCEA4 S11940	100								
139188	ATU001 128	ATL8C4 7186:1 061..1 199	gap2	ATCEA4 C19370 _1	100								
139189	ATU001 129	ATL8S1 3702:3 94..26 0	gap2	ATCEA4 S1604	100								
139190	ATU001 130	ATL8C3 2524:1 289..3 290	gap2	ATCEA4 C8757 _ 1, ATCEA4 C76131 _1	99, 96				g45726 76	100	558	2.9e- 61	(AC006 954) unknow n protei n [Arabi dopsis thalia na]
139191	ATU001 131	ATL8C4 1107:5 23..1	gap2	ATCEA4 C1808 _ 2, ATCEA4	100, 84								

139199	ATU001 139	ATL8S3 246:22 5..60	gap2	S31159	100								thalia na]
139200	ATU001 140	ATL8C1 5856:4 38..14 6	gap2	ATCEA4 C2124_1 ATCEA4 S7721	100								
139201	ATU001 141	ATL8C2 7328:1 08..1	gap2	ATCEA4 S12490	100								
139202	ATU001 142	ATL8C9 332:12 80..14 41	gap2	ATCEA4 C22581 3, ATCEA4 S20963	100, 86								
139203	ATU001 143	ATL8C3 7209:4 32..39 86	gap2	ATCEA4 C31221 1, ATCEA4 S54, ATCEA4 C53097 1, ATCEA4 C73693 _1	99, 96, 84, 84					g31422 89	100	1892	(AC002 411) Strong simila rity to beta- keto- Coa syntha se gb U37 088 from Simmon dsia chinen sis. [Arabi dopsis thalia na]
139204	ATU001 144	ATL8C4 9097:1 199..3 57	gap2	ATCEA4 S33002 , ATCEA4 S28964	100, 98, 93								

Year	Age	Sex	Location	Length (mm)	Weight (g)	Stomach contents	Notes
1961	1	M
1962	2	F
1963	3	M
1964	4	F
1965	5	M
1966	6	F
1967	7	M
1968	8	F
1969	9	M
1970	10	F
1971	11	M
1972	12	F
1973	13	M
1974	14	F
1975	15	M
1976	16	F
1977	17	M
1978	18	F
1979	19	M
1980	20	F

[illegible]

[illegible]

139231	170	7471:1 401..1 831	gap2	C96900 _1	99, 92					g33954 41	100	558	1.8e- 56	(AC004 683) unknow n protei n [Arabi dopsis thalia na]
139232	ATU001 171	ATL8C4 079:23 19..31 30	gap2	ATCEA4 C9352_1, ATCEA4 S17609	100									
139233	ATU001 172	ATL8C1 6236:7 31..95 5	gap2	ATCEA4 C27390 _1	100									
139234	ATU001 173	ATL8C2 0293:3 78..78 9	gap2	ATCEA4 C89283 _1	100									
139235	ATU001 174	ATL8C4 7537:7 58..12 03	gap2	ATCEA4 C14394 _1	100									
139236	ATU001 175	ATL8C2 6279:1 ..207	gap2	ATCEA4 S3447	100									
139237	ATU001 176	ATL8C1 6864:5 36..10 88	gap2	ATCEA4 C2139_1, ATCEA4 C2139_2	100, 98									
139238	ATU001 177	ATL8C2 12:606 ..400	gap2	ATCEA4 S12980	100									
139239	ATU001 178	ATL8S8 590:1. ..94	gap2	ATCEA4 S32762	100									
139240	ATU001 179	ATL8C7 60:125 7..105 7	gap2	ATCEA4 C8150_1	100									

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[illegible][illegible]

139332	ATU001 272	ATL8C4 44:642 3..483 9	gap2	ATCEA4 C13903 1, ATCEA4 S19887 , ATCEA4 S11471	99, 97, 95	ATL8C4 44:634 0..500 7	0.98	g21601 82	99	117	2.4e- 06	S0295 comes from this gene. [Arabi dopsis thalia na]
139333	ATU001 273	ATL8C2 2353:1 947..1	gap2	ATCEA4 C12063 1, ATCEA4 S35265 , ATCEA4 S35112 , ATCEA4 S26421 , ATCEA4 S31466 , ATCEA4 S31164 ,	99, 98, 98, 95, 93, 88, 84, 82	ATL8C2 2353:1 359..5 25	0.97	g16661 73	99	432	2.0e- 25	(Y0910 6) transc riptio n factor [Nicot iana plumba ginifo lia]

139334	ATU001 274	ATL8C3 4262:9 52..20 07	gap2	ATCEA4 S25392 , ATCEA4 S10111	99	ATL8C3 4262:9 73..18 31	0.96	g31229 38	99	188	5.8e- 15	THIORE- DOXIN- LIKE PROTEI N SLR113 9 [Synec hocyst is sp.]
139335	ATU001 275	ATL8C1 6467:2 734..1 170	gap2	ATCEA4 C18359 _1	99	ATL8C1 6467:2 712..1 170	0.95	g30236 26	99	189	3.9e- 15	POLYPE PTIDE DEFORM YLASE (PDF) (FORMY LMETHI ONINE DEFORM YLASE) [Therm otoga mariti ma]
139336	ATU001 276	ATL8C3 6522:1 241..3 621	gap2	ATCEA4 C18182 _1, ATCEA4 C18182 _2	99, 93	ATL8C3 6522:3 013..3 413	0.94	g17082 92, g45104 22	99, 31	211, 85	6.9e- 11, 1.8e- 06	HEAT- RESPON SIVE PROTEI N 12 [Mus muscul us]; (AC006 929) putati ve zinc- finger protei

139341	ATU001 281	ATL8C1 9754:7 1..396 9	gap2	ATCEA4 S137, ATCEA4 S13142	99, 86	ATL8C1 9754:7 1..396 9	0.87	g22749 93, g42622 27	99, 99	349, 277	1.4e- 31, 2.8e- 11	(AJ000 230) unname d protei n produc t [Horde um vulgar el; (AC006 200)
												cm10c2 ; coded for by C. elegan s cDNA yk61d8 .5; coded for by C. elegan s cDNA yk107e 8.5; coded for by C. elegan s cDNA CEESF5 5F; coded for by C. elegan s cDNA yk107e 8.3;.. []

139350	ATU001 290	ATL8C1, 6481:1 ..2052	gap2	ATCEA4 S3264, ATCEA4 S13737 ATCEA4 C24646 1, ATCEA4 S1424	99, 99, 99, 98	ATL8C1 6481:1 73..19 94	0.80	g22449 68, g42622 33	99, 83	188, 376	2.1e- 05, 2.6e- 33	dopsis thalia na] (Z9734 0) unname d protei n produc t [Arabi dopsis thalia na]; (AC006 200) hypoth etical protei n [Arabi dopsis thalia na]
139351	ATU001 291	ATL8C1 1679:2 296..4 945	gap2	ATCEA4 C27519 2, ATCEA4 C18619 1, ATCEA4 C27519 1, ATCEA4 S33709	99, 99, 98, 86	ATL8C1 1679:2 375..4 945	0.80	g21601 82	99	143	9.8e- 10	(AC000 132) ESTs gb ATT S1236, gb T43 334, gb N9701 9, gb A A39520 3 come from this gene. [Arabi dopsis thalia na]
139352	ATU001 292	ATL8C4 7135:3	gap2	ATCEA4 C6781	99, 89	ATL8C4 7135:3	0.80	g12983 9	99	75	0.21	PERIOD CLOCK

		350..1 459		1, ATCEA4 S35903		317..2 884							PROTEIN N (P230) [Acetabularia mediterranea]
139353	ATU001 293	ATL8C1 337:23 63..1	gap2	ATCEA4 C1058_2, ATCEA4 S2884, ATCEA4 S34067	99, 86 99, 86	ATL8C1 337:22 34..21	0.79	g46782 67	99	270	9.6e-27	(AL049 660) putative protein [Arabidopsis thaliana]	
139354	ATU001 294	ATL8C5 374:37 50..28 70	gap2	ATCEA4 C1059_1	99	ATL8C5 374:35 67..30 32	0.78	g26669 3	99	350	6.0e-20	OLEOSIN N [Arabidopsis thaliana]	
139355	ATU001 295	ATL8C1 641:25 59..47 89	gap2	ATCEA4 S2630	99	ATL8C1 641:27 90..47 89	0.76	g10026 6	99	263	2.7e-19	homeotic protein Hox7 - Peruvian tomato [Lycopersicon peruvianum]	
139356	ATU001 296	ATL8C1 886:58 7..1	gap2	ATCEA4 S33952, ATCEA4 C10083 01, ATCEA4	99, 90 95, 90	ATL8C1 886:45 3..173	0.75	g45672 25	99	494	2.8e-40	(AC007 119) unknown protein [Arabidopsis thaliana]	

139357	ATU001 297	ATL8C4 6623:1 820..1 29	gap2	ATCEA4 C6812_1, ATCEA4 C32419_1	99, 87	ATL8C4 6623:1 700..1 36	0.75	g25641 14	99	1269	2.1e- 129	dopsis thalia na] (AF000 372) UDP glucos e:flav onoid 3-o- glucos yltran sferas e [Vitis vinife ra]
139358	ATU001 298	ATL8C3 7130:1 299..1	gap2	ATCEA4 S25793 , ATCEA4 C409_1 , ATCEA4 S13404 , ATCEA4 S8989, ATCEA4 S27268	99, 98, 98, 84, 83	ATL8C3 7130:1 113..3 60	0.74	g41562 43	99	556		(AB012 569) ATHP2 [Arabi dopsis thalia na]
139359	ATU001 299	ATL8C3 2480:4 28..10 39	gap2	ATCEA4 S1335, ATCEA4 S35807	99, 88	ATL8C3 2480:6 86..10 31	0.73	g43096 97	99	482	2.7e- 47	(AC006 266) putati ve DNA- direct ed RNA polyme rase subuni t [Arabi dopsis thalia na]

139360	ATU001 300	ATL8C3 6208:5 9...304 8	gap2	ATCEA4 C8332_ 1, ATCEA4 S2355, ATCEA4 C70699 _1	99, 96 99, 96	ATL8C3 6208:5 9...284 7	0.72	g39151 31, g28275 44	99, 34	279, 478	1.3e- 20, 6.7e- 31	THIORE DOXIN H-TYPE (TRX- H) (PHLOE M SAP 13 KD PROTEI N-1) [Oryza sativa]; (AL021 635) HSP associ ated protei n like [Arabi dopsis thalia nal]
139361	ATU001 301	ATL8C2 6595:1 008..1	gap2	ATCEA4 C6670_ 1, ATCEA4 C6670_ 2, ATCEA4 S10511	99, 87 95, 87	ATL8C2 6595:9 27...61 5	0.68	g24993 18	99	124	1.2e- 11	PUTATI VE NADH- UBIQUI NONE OXIDOR EDUCTA SE 17.3 KD SUBUNI T (COMPL EX I- 17.3KD) (CI- 17.3KD) [Caeno rhabdi tis

139362	ATU001 302	ATL8C2 4048:5 36..22 75	gap2	ATCEA4 S13067	99	ATL8C2 4048:5 36..22 60	0.67	g19033 67	99	188	4.4e- 10	elegant s] (AC000 104) ESTs gb N65 789,gb T0462 8 come from this gene. [Arabi dopsis thalia na]
139363	ATU001 303	ATL8C1 8808:1 487..3 452	gap2	ATCEA4 S121, ATCEA4 C2965_1	99, 93	ATL8C1 8808:1 487..3 452	0.66	g27064 55	99	385	9.9e- 29	(AL021 046) probab le involv ement in transc riptio n initia tion [Schiz osacch aromyc es pombe]
139364	ATU001 304	ATL8C2 2005:8 03..1	gap2	ATCEA4 S30275 , ATCEA4 C50072 _1	99, 96	ATL8C2 2005:7 15..66 8	0.66	g44551 94	99	155	8.1e- 05	(AL035 440) putati ve protei n [Arabi dopsis thalia na]
139365	ATU001 305	ATL8C4 4147:1	gap2	ATCEA4 C1018	99, 83,	ATL8C4 4147:1	0.65	g16686 7	99	653	2.0e- 44	(J0521 6)

		..2667		1, ATCEA4 C934_1 , ATCEA4 C27863 1, ATCEA4 S24405 , ATCEA4 C934_3	82, 82, 82	61..24 30							riboso mal protei n S11 (proba ble start codon at bp 67) [Arabi dopsis thalia na]
139366	ATU001 306	ATL8C9 692:11 52..26 57	gap2	ATCEA4 S29524 , ATCEA4 C19901 1, ATCEA4 S29489	99, 98, 97	ATL8C9 692:12 94..26 57	0.64	g30213 44	99	309	3.5e- 28	(AJ004 959) hypoth etical protei n [Cicer arieti num]	
139367	ATU001 307	ATL8C1 0923:1 ..4439	gap2	ATCEA4 C44881 1, ATCEA4 C12056 2, ATCEA4 C12056 5	99, 96, 93	ATL8C1 0923:1 31..41 52	0.64	g30370 45	99	103	1.6e- 05	(AF052 621) hypoth etical protei n COX4AL [Mus muscul us]	
139368	ATU001 308	ATL8C4 2543:1 ..969	gap2	ATCEA4 S11962 , ATCEA4 S13504 , ATCEA4 C1382_1, ATCEA4 S13152	99, 85, 83, 82, 82	ATL8C4 2543:1 16..60 7	0.63	g14084 73	99	598	9.2e- 59	(U4893 9) actin depoly merizi ng factor 2 [Arabi dopsis thalia na]	

139369	ATU001 309	ATL8C3 3724:4 854..3 766	gap2	ATCEA4 S29816 ATCEA4 S2944, ATCEA4 S33994	99, 95	ATL8C3 3724:4 854..3 860	0.63	g42635 19	99	444	2.8e- 37	(AC004 044) small nuclea r ribopr oteins Sm-D1 [Arabi dopsis thalia na]
139370	ATU001 310	ATL8C1 364:12 9..242 0	gap2	ATCEA4 S2595, ATCEA4 C12311 81, ATCEA4 S32464	99, 98, 88	ATL8C1 364:12 9..242 0	0.61	g41057 90, g17106 26	99, 54	100, 155	5.3e- 06, 4.6e- 10	(AF049 926) PGP219 [Petun ia x hybrid al]; HETERO GENE S NUCLEA R RIBONU CLEOPR OTEIN A3 HOMOLO G 2 (HNRNP A3(B)) [Xenop us laevis]
139371	ATU001 311	ATL8C1 2660:1 601..5 379	gap2	ATCEA4 S3416, ATCEA4 C26193 1, ATCEA4 S2917	99, 97, 97	ATL8C1 2660:1 601..5 138	0.58	g44328 61	99	126	3.4e- 07	(AC006 300) hypoth etical protei n [Arabi

139372	ATU001 312	ATL8C4 5656:5 033..8 20	gap2	ATCEA4 S13312 , ATCEA4 C5794_1, ATCEA4 S5765, ATCEA4 S26906 , ATCEA4 S34546	99, 98, 97, 90, 88	ATL8C4 5656:4 879..3 409, ATL8C4 5656:1 146..8 90	0.57, 0.94	g29839 97, g48352 41, g17070 07	99, 99, 71	250, 260, 584	3.1e- 16, 3.6e- 17, 1.9e- 67	dopsis thalia na] (AE000 749) hypoth etical protei n [Aquif ex aeolic us]; (AL049 862) hypoth etical protei n [Arabi dopsis thalia na]; (U7872 1) hypoth etical protei n [Arabi dopsis thalia na]
139373	ATU001 313	ATL8C6 623:48 5..165 2	gap2	ATCEA4 C62700 2, ATCEA4 C62700 1, ATCEA4 S31794	99, 97, 92	ATL8C6 623:53 8..165 2	0.55	g33954 27	99	176	3.3e- 14	(AC004 683) unknow n protei n [Arabi dopsis thalia na]
139374	ATU001 314	ATL8C3 8019:9	gap2	ATCEA4 C32422	99	ATL8C3 8019:1	0.53	g13576 7	99	78	6.3e- 07	THIORE DOXIN

139375	ATU001 315	51..16 33	gap2	ATCEA4 S1994	99	ATL8C5 12:164 9..764	0.48	g38611 89	99	298	9.4e- 21	[Gallus gallus] (AJ235 272) 50S RIBOSO MAL PROTEI N L14 (rplN) [Ricke ttsia prowaz ekii]
139376	ATU001 316	ATL8C1 5557:7 8..106 4	gap2	ATCEA4 C50872 _1, ATCEA4 S9868	99, 82	ATL8C1 5557:1 57..10 64	0.48	g37460 61	99	127	3.4e- 10	(AC005 311) unknown n protei n [Arabi dopsis thalia na]
139377	ATU001 317	ATL8C4 7589:2 437..1 88	gap2	ATCEA4 C18669 _1	99	ATL8C4 7589:1 745..1 90	0.45	g22752 17	99	187	5.1e- 08	(AC002 337) chloro plast protei n CP12 isolog [Arabi dopsis thalia na]
139378	ATU001 318	ATL8C1 1543:6 8..915	gap2	ATCEA4 S27456	99	ATL8C1 1543:1 92..91 5	0.44	g45672 08	99	194	3.2e- 14	(AC007 168) unknown n protei n [Arabi dopsis

139379	ATU001 319	ATL8C3 8559:1 616..1	gap2	ATCEA4 C19295 1, ATCEA4 S19871	99, 97	ATL8C3 8559:1 542..1 13	0.40	g11292 5	99	133	1.0e- 10	thalia na] 41-2 PROTEI N ANTIGE N PRECUR SOR [Plasm odium falcip arum]
139380	ATU001 320	ATL8C2 2442:6 73..76	gap2	ATCEA4 C13179 51, ATCEA4 C11940 4_1	99, 93			g99771	99	752	3.9e- 60	ubiqui tin 81-aa extens ion protei n 1 - Arabid opsis thalia na [Arabi dopsis thalia na] (AC006 220) putati ve glycin e rich protei n [Arabi dopsis thalia na]
139381	ATU001 321	ATL8C4 4763:1 475..1 075	gap2	ATCEA4 C25088 3_	99			g45811 70	99	563	0.19	(AC006 220) putati ve glycin e rich protei n [Arabi dopsis thalia na]
139382	ATU001 322	ATL8C5 400:1. .1413	gap2	ATCEA4 C13630 2, ATCEA4 C13630	99, 91			g29831 95	99	139	1.3e- 12	(AE000 695) hypoth etical protei

139383	ATU001 323	ATL8C2 0206:4 962..4 281	gap2	ATCEA4 C21578 2, ATCEA4 S20780	99, 83					g25831 10	99	173	1.2e- 08	n [Aquif ex aeolic us] (AC002 387) unknow n protei n [Arabi dopsis thalia na]
139384	ATU001 324	ATL8C3 1899:9 60..25 8	gap2	ATCEA4 C28268 _1	99					g10648 87	99	151	8.3e- 06	(X9295 5) pollen coat protei n [Brass ica olerac ea]
139385	ATU001 325	ATL8C4 6713:1 995..2 478	gap2	ATCEA4 S3331	99					g41057 94	99	438	2.0e- 41	(AF049 928) PGP224 [Petun ia x hybrid a]
139386	ATU001 326	ATL8C1 6841:1 ..1139	gap2	ATCEA4 S4375, ATCEA4 S5372	99, 95					g36876 88	99	450	1.3e- 43	(AF057 027) respon se regula tor protei n [Brass ica napus]
139387	ATU001	ATL8C4	gap2	ATCEA4	99, 98					g17233	99	248	5.0e-	HYPOTH

327	0304:4 26..13 09		S18438 , ATCEA4 C19936 _1						39				09	ETICAL 19.2 KD PROTEI N YCF36 (ORF16 5) [Porph yra purpur eal]
139388	ATU001 328	ATL8C4 7655:1 388..5 49	gap2	ATCEA4 C10164 2_1	99				g24980 69	99	215	4.9e- 22	NUCLEO SIDE DIPHOS PHATE KINASE (NDK) (NDP KINASE) [Pseud omonas aerugi nosa]	
139389	ATU001 329	ATL8C1 1390:4 89..1	gap2	ATCEA4 C62656 _1	99				g17085 77	99	324	5.1e- 28	TRYPSI N INHIBI TOR 2 PRECUR SOR (MTI- 2) [Sinap is alba]	
139390	ATU001 330	ATL8C2 7359:8 3..701	gap2	ATCEA4 C5343_1	99				g34027 00	99	330		(AC004 261) unknow n protei n [Arabi dopsis thalia	

139391	ATU001 331	ATL8C4 7629:1 101...2 85	gap2	ATCEA4 C7159_1	99	ATL8C4 7629:8 47...28 5	1.00	g17551 62	98	804	2.7e- 81	(U7519 2) germin -like protei n [Arabi dopsis thalia na]
139392	ATU001 332	ATL8C2 7001:7 10...1	gap2	ATCEA4 C25627_1, ATCEA4 C483_1	99, 93			g28268 82	99	238	5.5e- 21	(AJ223 634) transc riptio n factor IIA small subuni t [Arabi dopsis thalia na]
139393	ATU001 333	ATL8C1 6576:1 ..1346	gap2	ATCEA4 S436, ATCEA4 C30854_1, ATCEA4 S246	99, 99, 97			g22890 05	99	264	1.9e- 23	(AC002 335) hypoth etical protei n [Arabi dopsis thalia na]
139394	ATU001 334	ATL8C2 7540:1 048...4 55	gap2	ATCEA4 C18799_1	99			g37859 87	99	270		(AC005 560) hypoth etical protei n [Arabi dopsis thalia na]

139395	ATU001 335	ATL8C3 1034:2 330..2 816	gap2	ATCEA4 C716_4 , ATCEA4 S35414	99, 85				g24078 02	99	653	2.4e- 40	(Y1257 6) histone H2B [Arabi dopsis thaliana]
139396	ATU001 336	ATL8C3 4898:1 66..88 2	gap2	ATCEA4 S7264, ATCEA4 S9958	99, 84				g73046 3	99	221	1.3e- 21	60S RIBOSOMAL PROTEIN N L37B (YL37) (RP47) [Saccharomyces cerevisiae]
139397	ATU001 337	ATL8C2 8847:2 2..157 9	gap2	ATCEA4 S30929 , ATCEA4 S3586, ATCEA4 C6071_1	99, 94 98, 94	ATL8C2 8847:1 06..15 62			g22450 66	98	632	4.9e- 70	(Z9734 2) Beta-Amylase [Arabi dopsis thaliana]
139398	ATU001 338	ATL8C3 4562:2 276..1 00	gap2	ATCEA4 C12277 5_1	99	ATL8C3 4562:2 276..1 00			g11725 97	98	145	1.3e- 09	WOUND-INDUCED BASIC PROTEIN [Phaseolus vulgaris]
139399	ATU001 339	ATL8C1 4810:1 ..377	gap2	ATCEA4 S3800	99	ATL8C1 4810:2 60..33 8			g13346 05	98	113	2.9e- 05	(X0167 6) unidentified reading

139400	ATU001 340	ATL8C8 808:1. .1458	gap2	ATCEA4 C19205 _1	99	ATL8C8 808:33 5..123 1	0.84	g48369 01	98	457	1.1e- 36	frame ORF 59 [Pisum sativu m] (AC007 369) Unknown protein [Arabi dopsis thalia na]
139401	ATU001 341	ATL8C2 012:73 2..1	gap2	ATCEA4 C31024 _1	99	ATL8C2 012:73 2..21	0.83	g48504 07	98	133	1.5e- 05	(AC007 357) EST gb T21 221 comes from this gene. [Arabi dopsis thalia na]
139402	ATU001 342	ATL8C4 1653:1 ..572	gap2	ATCEA4 C9773 _1, ATCEA4 S26499	99, 88			g46807 13	98	499	5.2e- 49	(AF132 971) CGI-37 protein [Homo sapien s]
139403	ATU001 343	ATL8S1 6878:1 47..48 5	gap2	ATCEA4 S36258 , ATCEA4 C69_1	99, 98			g28038 4	98	191	5.7e- 07	hypoth etical protein (Athb- 2 5' region) - Arabid

139404	ATU001 344	ATL8C1 4759:4 50..1	gap2	ATCEA4 C3999_1, ATCEA4 S32264	99, 96					g13290 1	98	320	1.0e- 26	CHLORO PLAST 50S RIBOSO MAL PROTEI N L33 [Nicot iana tabacu m]	opsis thalia na [Arabi dopsis thalia na]
139405	ATU001 345	ATL8C4 8897:9 90..1	gap2	ATCEA4 S1522	99	ATL8C4 8897:7 90..65	0.98			g42204 70	97	184	2.1e- 08	(AC006 069) hypoth etical protei n [Arabi dopsis thalia na]	
139406	ATU001 346	ATL8C4 9755:1 ..4104	gap2	ATCEA4 C23374 1, ATCEA4 C26316 _1	99, 98	ATL8C4 9755:1 34..41 04	0.91			g14958 04	97	1943	3.9e- 214	(X9640 6) 13- lipoxy genase [Solan um tubero sum]	
139407	ATU001 347	ATL8C1 7345:1 ..2775	gap2	ATCEA4 C29332 1, ATCEA4 C2089_7	99, 93	ATL8C1 7345:5 2..276 1	0.86			g42204 74	97	1792	8.2e- 165	(AC006 069) putati ve myosin heavy chain [Arabi dopsis na]	

139408	ATU001 348	ATL8C2 7114:7 77..24 22	gap2	ATCEA4 C23977 1, ATCEA4 S4083	99, 97	ATL8C2 7114:7 86..23 35	0.83	g34213 82	97	408	7.2e- 37	thalia na] (AF081 214) caffei c acid- 3-O- methyl transf erase [Capsi cum chinen se]
139409	ATU001 349	ATL8C1 3052:4 60..32 95	gap2	ATCEA4 C4493 1, ATCEA4 C27739 1, ATCEA4 S24222	99, 98, 85	ATL8C1 3052:6 44..31 00	0.82	g45859 77	97	435	3.5e- 43	(AC005 287) Unknown protein [Arabi dopsis thalia na]
139410	ATU001 350	ATL8C3 340:37 80..15 29	gap2	ATCEA4 S846, ATCEA4 S34009	99, 92	ATL8C3 340:36 96..19 32	0.81	g37382 98	97	958	6.5e- 76	(AC005 309) unknown protein [Arabi dopsis thalia na]
139411	ATU001 351	ATL8C2 2817:1 61..22 08	gap2	ATCEA4 S39, ATCEA4 C71715 1	99, 87	ATL8C2 2817:4 04..21 65	0.70	g37383 15	97	316	2.9e- 18	(AC005 170) unknown protein [Arabi dopsis thalia na]

139412	ATU001 352	ATL8C2 1397:4 36..21 30	gap2	ATCEA4 C57357 _1	99	ATL8C2 1397:4 36..21 30	0.59	g26606 73	97	1283	7.0e- 129	(AC002 342) unknown protein [Arabidopsis thaliana]
139413	ATU001 353	ATL8C9 45:742 ..1	gap2	ATCEA4 C3677_1, ATCEA4 C3967_1	99, 90			g13468 31	97	151	1.3e- 09	PHOTOSY- STEM I REACTI- ON CENTRE SUBUNIT VIII (PSI-I) [Glycine max]
139414	ATU001 354	ATL8C3 6352:1 476..1	gap2	ATCEA4 S4931	99			g25831 28	97	516	1.9e- 51	(AC002 387) hypothetical protein [Arabidopsis thaliana]
139415	ATU001 355	ATL8C2 56:142 0..294	gap2	ATCEA4 C1353_1	99	ATL8C2 56:136 9..335	0.99	g13455 92	96	948	2.8e- 99	14-3- 3-LIKE PROTEIN N GFL4 EPSILON [Arabidopsis thaliana]
139416	ATU001 356	ATL8C4 6490:1	gap2	ATCEA4 S14477	99, 98	ATL8C4 6490:1	0.90	g24999 89	96	197	2.3e- 15	PEPTIDYL- YL-

			602..1		, ATCEA4 C31884 _1			602..5 8								TRNA HYDROL ASE (PTH) [Synec hocyst is sp.]
139417	ATU001 357		ATL8C1 6262:4 166..1 275	gap2	ATCEA4 S15413 , ATCEA4 C8674_1, ATCEA4 S29210 , ATCEA4 S33882	99, 98, 96, 90		ATL8C1 6262:4 049..1 884	0.94	g28874 99	95	119	3.4e- 09			(AC004 143) R29893 _1 [Homo sapien s]
139418	ATU001 358		ATL8C6 229:1. .1777	gap2	ATCEA4 S13069	99		ATL8C6 229:52 8..151 9	0.73	g28292 75	95	832	5.0e- 73			(AF044 265) nucleo side diphos phate kinase 3 [Arabi dopsis thalia na]
139419	ATU001 359		ATL8C1 2217:1 ..2165	gap2	ATCEA4 S2663, ATCEA4 S2943	99, 96		ATL8C1 2217:4 20..21 65	0.70	g22450 04	95	1384	4.2e- 134			(Z9734 1) simila rity to membra ne transp ort protei n [Arabi dopsis thalia

139420	ATU001 360	ATL8C3 5419:1 594..1	gap2	ATCEA4 S26426 , ATCEA4 C1884_1, ATCEA4 C1884_2	99, 97, 85	ATL8C3 5419:1 317..1 84	0.70	g24974 86	95	809	3.5e- 75	na] URIDYL ATE KINASE (UK) (URIDI NE MONOPH OSPHAT E KINASE) (UMP KINASE) [Arabi dopsis thalia na]
139421	ATU001 361	ATL8C4 5462:3 291..1	gap2	ATCEA4 S2853, ATCEA4 C11623 1_1, ATCEA4 S33140	99, 97, 88	ATL8C4 5462:3 132..1 61	0.58	g34200 54	95	2245	6.7e- 250	(AC004 680) unknown protein [Arabi dopsis thalia na]
139422	ATU001 362	ATL8C3 4277:2 995..1 677	gap2	ATCEA4 C21453 _1	99	ATL8C3 4277:2 525..1 677)	0.92	g17084 20	94	984	6.2e- 89	ISOFLA VONE REDUCT ASE HOMOLO G P3 [Arabi dopsis thalia na]
139423	ATU001 363	ATL8C8 390:43 83..32 0	gap2	ATCEA4 C2122_1, ATCEA4 S15630 , ATCEA4	99, 98, 95, 95, 89	ATL8C8 390:41 48..81 2	0.91	g44159 34	94	1084	3.7e- 75	(AC006 418) putati ve auxin respon se

139424	ATU001 364	ATL8C2 1964:3 819..1 099	gap2	C2122_2, ATCEA4 S465, ATCEA4 S34831 ATCEA4 S1593, ATCEA4 C26864 _1	99, 96	ATL8C2 1964:3 228..1 099	0.77	g45875 54	94	1046	3.5e- 113	factor 1 [Arabi dopsis thalia na]
139425	ATU001 365	ATL8C1 2813:1 719..1	gap2	ATCEA4 C12196 3, ATCEA4 S26810 , ATCEA4 C12196 1,	99, 98, 94, 93, 93	ATL8C1 2813:1 550..2 89	0.75	g38941 71	94	737	1.1e- 55	(AC005 312) putati ve glutat hione s- transf erase

139426	ATU001 366	ATL8C2 2585:1 414..1	gap2	ATCEA4 C11599 41, ATCEA4 S34160	99, 99 84, 82	ATL8C2 2585:1 060..1 30	0.74	g10868 33	94	230	1.2e- 19	[Arabi dopsis thalia na]
				ATCEA4 C17320 1, ATCEA4 S4194, ATCEA4 S8885								(U4126 4) coded for by C. elegan s cDNA CEESN2 6F; coded for by C. elegan s cDNA CEES18 9F; simila r to 60S acidic riboso mal protei n Po (L10) [Caeno rhabdi tis elegan s]
139427	ATU001 367	ATL8C1 1687:1 410..1	gap2	ATCEA4 C42123 1, ATCEA4 S913	99, 99	ATL8C1 1687:1 385..6 33	0.69	g38596 96	94	189	2.1e- 27	[AL033 497) unknow n hypoth etical protei n [Candi da]

139428	ATU001 368	ATL8C1 2981:2 799..1 576	gap2	ATCEA4 S4989	99	ATL8C1 2981:2 741..1 894	0.67	g44552 02	94	1638	1.9e- 165	albicans (AL035 440) putative APG protein [Arabi dopsis thaliana na]
139429	ATU001 369	ATL8C1 1542:1 898..5 0	gap2	ATCEA4 C50753 _1	99	ATL8C1 1542:1 882..3 41	0.44	g10013 09	94	233	1.2e- 18	(D6400 6) aspartate aminotransferase [Synec hocystis sp.]
139430	ATU001 370	ATL8C2 4665:1 951..7 3	gap2	ATCEA4 C9972_1	99	ATL8C2 4665:1 951..8 4	0.86	g22449 45	93	582	2.0e- 49	(Z9733 9) similar to HYPOTHETICAL MYELOID CELL LINE PROTEIN 6 (FRAGMENT) [Arabi dopsis thaliana na]
139431	ATU001 371	ATL8C3 8263:3 74..20 67	gap2	ATCEA4 C1378_2, ATCEA4 C1378	99, 92, 95, 92	ATL8C3 8263:1 124..2 007	0.86	g21296 04	93	736	1.3e- 70	GFP-binding protein 1 -

139432	ATU001 372	ATL8C2 3863:7 38...23 76	gap2	ATCEA4 S1413	99	ATL8C2 3863:9 22...23 15	0.64	g28326 77	93	227	2.7e- 21	Arabidopsis thaliana [Arabidopsis thaliana] (AL021712) hypothetical protein [Arabidopsis thaliana] (Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana] (AC005278) Similar to gb U85207 snRNP core protein
139433	ATU001 373	ATL8C4 3538:1 ..1558	gap2	ATCEA4 C6831_2, ATCEA4 C6831_4, ATCEA4 S35708	99, 97, 91	ATL8C4 3538:5 6..1558	0.60	g22449 93	93	486		
139434	ATU001 374	ATL8C4 435:1. .1113	gap2	ATCEA4 C29148_1	99	ATL8C4 435:45 ..963	0.46	g38505 71	93	492	9.1e- 41	

139435	ATU001 375	ATL8C3 1782:1 ..3119	gap2	ATCEA4 S3295, ATCEA4 S31608 , ATCEA4 S13104 , ATCEA4 S31607	99, 99, 93, 90				g45593 81, g26186 96	93, 39	1302, 71	3.3e- 140, 0.046	homolog Sm- X5 from Mus muscul us. EST : gb AA6 12141 comes from this gene. [Arabi dopsis thalia na]
139436	ATU001 376	ATL8C1 3270:1 ..1362	gap2	ATCEA4 C21917 2, ATCEA4 S30162 , ATCEA4	99, 94 96, 94				g22448 86	93	1345	5.3e- 140	(Z9733 8) strong simila rity to UTP-

139440	ATU001 380	ATL8C4 6240:3 456..3 98	gap2	ATCEA4 C6914_2, ATCEA4 S22449, ATCEA4 C6914_1	99, 99, 93	ATL8C4 6240:3 456..3 98	0.90	g26422 17	91	110	4.6e- 07	thalia na] (AF030 387) NOI protei n [Oryza sativa]
139441	ATU001 381	ATL8C1 2709:1 ..2206	gap2	ATCEA4 S10301	99	ATL8C1 2709:4 45..22 06	0.69	g45824 88	91	2226	1.5e- 201	(AL021 768) putati ve protei n [Arabi dopsis thalia na]
139442	ATU001 382	ATL8C3 2620:3 405..1	gap2	ATCEA4 S224, ATCEA4 C3553_1, ATCEA4 C69976_1	99, 94, 84	ATL8C3 2620:2 491..3 11	0.69	g31690 59	91	1357	3.5e- 117	(AL023 704) weak simila rity to B.subt ilis spore outgro wth f actor B [Schiz osacch aromyc es pombel]
139443	ATU001 383	ATL8C8 729:35 37..1	gap2	ATCEA4 S29863, ATCEA4 S23393	99, 91	ATL8C8 729:23 27..19 6	0.61	g44688 04, g22449 28	91, 81	1001, 625	1.3e- 91, 9.6e- 62	(AL035 601) putati ve protei n

139444	ATU001 384	ATL8C3 2489:1 ..1146	gap2	ATCEA4 S26727 , ATCEA4 C10338 _1	99, 87					g31526 06	91	556	3.7e- 50	(AC004 482) putati ve ring zinc finger protei n [Arabi dopsis thalia na]
139445	ATU001 385	ATL8C4 8276:1 285..1 90	gap2	ATCEA4 S13937 , ATCEA4 C2854_1, ATCEA4 S25445 , ATCEA4 C2854_2	99, 97, 93, 93	ATL8C4 8276:1 211..3 71	0.91			g45392 92	90	541	2.9e- 38	(AL049 480) putati ve riboso mal protei n S10 [Arabi dopsis thalia na]
139446	ATU001 386	ATL8C1 885:10 65..1	gap2	ATCEA4 S1226, ATCEA4 C99376 _1, ATCEA4	99, 85 92, 85	ATL8C1 885:94 5..21	0.85			g45875 47	90	205	2.3e- 26	(AC006 577) Contai ns simila rity

139447	ATU001 387	ATL8C2 8002:8 46..1	gap2	ATCEA4 S12992 , ATCEA4 C25755 _1	99, 97	ATL8C2 8002:6 00..49 3	0.58	g38057 60	90	366	1.2e- 26	to DNA- bindin g protei n Gt-2 gb X68 261 from Oryza sativa [Arabi dopsis thalia na]
139448	ATU001 388	ATL8C1 0058:9 14..14 64	gap2	ATCEA4 C7237 _1	99			g24648 58	90	110		(Z9970 7) putati ve protei n [Arabi dopsis thalia na]
139449	ATU001 389	ATL8C1 4519:1 ..1242	gap2	ATCEA4 C2242 _1, ATCEA4 C69015 _1, ATCEA4 S8042	99, 82 96, 82			g14028 5	90	425	1.0e- 40	HYPOTH ETICAL 19 KD PROTEI N (ORF 168) [Nicot iana tabacu

139450	ATU001 390	ATL8C4 6193:1 ..389	gap2	ATCEA4 S14690	99						g30969 45	90	102	7.5e- 08	m] (AL023 094) putati ve auxin- regula ted protei n [Arabi dopsis thalia na]
139451	ATU001 391	ATL8C1 88:571 3..387 3	gap2	ATCEA4 S3425	99	ATL8C1 88:568 8..387 3	0.90			g63972 2	89	1488			(L2748 4) calciu m- depend ent protei n kinase [Zea mays]
139452	ATU001 392	ATL8C5 748:17 ..2915	gap2	ATCEA4 C11718 0 1, ATCEA4 C26548 1, ATCEA4 S12358 , ATCEA4 S12938 , ATCEA4 S30487	99, 98, 92, 90, 84	ATL8C5 748:17 ..1212 , ATL8C5 748:15 25..28 22	0.89, 0.61			g44067 59	89	730			(AC006 836) hypoth etical protei n [Arabi dopsis thalia na]
139453	ATU001 393	ATL8C1 3455:1 1275.. 5622	gap2	ATCEA4 C1063 37,- ATCEA4 C37173 1	99, 93	ATL8C1 3455:1 0161.. 5622	0.81			g45060 13, g30636 91	89, 74	322, 1254	4.1e- 18, 9.5e- 129		protei n phosph atase 1, regula

139454	ATU001 394	ATL8C1 3110:2 006..7 028	gap2	ATCEA4 S398, ATCEA4 S6844, ATCEA4 S6226, ATCEA4 S959	99, 98, 97, 92	ATL8C1 3110:2 006..6 982	0.79	g37021 21	89	2330	8.4e- 226	tory subuni t 7 [Homo sapien sl]; (AL022 537) putati ve protei n [Arabi dopsis thalia na]
139455	ATU001 395	ATL8C3 6784:1 ..1984	gap2	ATCEA4 C6031- 1	99	ATL8C3 6784:5 36..91 8	0.79	g45672 51	89	791	1.9e- 76	(AJ011 681) retino blasto ma- relate d protei n [Cheno podium rubrum]
139456	ATU001 396	ATL8C1 8075:5 524..2 645	gap2	ATCEA4 C20602 1, ATCEA4 C98103 2,	99, 98, 85, 85	ATL8C1 8075:5 371..2 645	0.77	g27391 68	89	730	3.9e- 57	(AF032 386) aldose -1- epimer ase-

139457	ATU001 397	ATL8C4 7898:1 ..1603	gap2	ATCEA4 S13277 , ATCEA4 S23356	99, 98, 97	ATL8C4 7898:3 40..15 95	0.75	g36436 11	89	872	2.2e- 83	like protei n [Nicot iana tabacu m] (AC005 395) putati ve casein kinase [Arabi dopsis thalia na]
139458	ATU001 398	ATL8C5 0119:1 ..3780	gap2	ATCEA4 C4552_ 1, ATCEA4 C57820 2, ATCEA4 C57820 _1	99, 98, 96	ATL8C5 0119:8 7..378 0	0.53	g32876 91, g34149 30	89, 33	771, 100	2.6e- 51, 1.2e- 07	(AC003 979) Contai ns simila rity to RING zinc finger protei n gb X95 455 from Gallus gallus . [Arabi dopsis thalia na]; (AF076 599) FutA [Dicty osteli um]

139459	ATU001 399	ATL8C2 9925:2 467..6 8	gap2	ATCEA4 S2457, ATCEA4 S29278 , ATCEA4 C23643 1	99, 93, 91	ATL8C2 9925:2 467..6 8	0.53	g14917 12	89	164	2.3e- 13	(X9996 1) unknown [Homo sapien s]
139460	ATU001 400	ATL8C8 465:22 64..1	gap2	ATCEA4 S11344	99	ATL8C8 465:22 64..99	0.44	g27608 39, g25860 81	89, 39	724, 343	3.5e- 71, 9.7e- 28	(AC003 105) putati ve recept or kinase [Arabi dopsis thalia na]; (U7272 5) recept or kinase -like protei n [Oryza longis tamina ta]
139461	ATU001 401	ATL8C2 0673:1 ..1923	gap2	ATCEA4 C5210 - 2, ATCEA4 C5210 - 1, ATCEA4 S18277 , ATCEA4 S25371	99, 99, 96, 87			g46783 49	89	2254	2.0e- 227	(AL049 659) putati ve protei n [Arabi dopsis thalia na]
139462	ATU001	ATL8C4	gap2	ATCEA4	99,			g25296	89	1529	8.5e-	(AC002

402	8845:1 ..2157		C1739_ 1, ATCEA4 S14666 , ATCEA4 S35279	99, 86				81		123	535) putati ve MYB- relate d transc riptio n factor (prote in P) [Arabi dopsis thalia nal]
139463	ATU001 403	gap2	ATCEA4 S26873 , ATCEA4 C74593 1, ATCEA4 S32971 , ATCEA4 S35756 , ATCEA4 C48941 1, ATCEA4 S28447	99, 98, 95, 95, 87, 85	ATL8C1 5931:4 7..235 8	0.98	g17233 47, g16520 57	88, 87	758, 836	2.5e- 55, 3.3e- 64	HYPOTH ETICAL 64.2 KD PROTEI N YCF45 (ORF56 5) [Porph yra purpur eal; (D9090 2) hypoth etical protei n [Synec hocyst is sp.]
139464	ATU001 404	gap2	ATCEA4 S4644	99	ATL8C3 8658:4 71..11 11	0.89	g45859 24	88	696	1.0e- 63	(AC007 211) hypoth etical protei n

139469	ATU001 409	ATL8C3 3870:1 95..61 72	gap2	ATCEA4 C14561 1, ATCEA4 S16175 , ATCEA4 C32840 1, ATCEA4 S2480	99, 92, 90, 87	ATL8C3 3870:2 475..6 126	0.50	g13634 92, g19316 50	88, 42	2391, 363	outer envelo pe membra ne protei n OEP75 precur sor - garden pea [Pisum sativu m]; (U9597 3) diseas e resist ance protei n RPM1 isolog [Arabi dopsis thalia na]
139470	ATU001 410	ATL8C3 8971:1 595..1	gap2	ATCEA4 C6294 1, ATCEA4 S6438	99, 97			g30333 86	88	276	2.5e- 26 (AC004 238) RING3- like protei n [Arabi dopsis thalia na]
139471	ATU001 411	ATL8C3 1792:8 33..1	gap2	ATCEA4 S5529	99			g31842 85	88	357	7.9e- 19 (AC004 136) hypoth etical protei n

139472	ATU001 412	ATL8C1 1862:1 748..1	gap2	ATCEA4 S401	99					g45899 66	88	927	1.1e- 89	[Arabi dopsis thalia na]
139473	ATU001 413	ATL8C2 7331:1 ..1519	gap2	ATCEA4 S36233 , ATCEA4 C271_2 , ATCEA4 S35014 , ATCEA4 C271_1	99, 99, 94, 87	ATL8C2 7331:5 4..758	0.94			g28152 52	87	572		[X7138 1) ubiqui tin carrie r protei n [Arabi dopsis thalia na]
139474	ATU001 414	ATL8C3 7937:9 29..1	gap2	ATCEA4 S13866	99	ATL8C3 7937:9 28..40	0.94			g32506 92	87	825	6.3e- 64	[AL024 486) putati ve protei n [Arabi dopsis thalia na]
139475	ATU001 415	ATL8C3 6722:1 ..1403	gap2	ATCEA4 C35088 _1, ATCEA4 C52584 _1, ATCEA4 S32892	99, 97, 84	ATL8C3 6722:3 90..12 18	0.90			g41851 43	87	656	1.4e- 57	[AC005 724) putati ve signal recogn ition partic le

139476	ATU001 416	ATL8C2 1733:2 082..1	gap2	ATCEA4 C91392 1, ATCEA4 S35252 , ATCEA4 C10270 1	99, 91, 90	ATL8C2 1733:1 973..1 37	0.83	944540 26	87	979	9.3e- 76	(AL035 394) phosph atase like protei n [Arabi dopsis thalia na]
139477	ATU001 417	ATL8C4 7230:1 410..3 38	gap2	ATCEA4 C13014 1	99	ATL8C4 7230:1 294..4 54	0.71	946436 7	87	922	3.3e- 89	POLYGA LACTUR ONASE INHIBI TOR PRECUR SOR (POLYG ALACTU RONASE - INHIBI TING PROTEI N) [Pyrus commun is]
139478	ATU001 418	ATL8C1 2980:6 223..1	gap2	ATCEA4 C32641 1, ATCEA4 C19645 1, ATCEA4	99, 98, 98, 97, 97, 96, 94	ATL8C1 2980:5 893..1 03	0.64	973182 1, g30235 22	87, 64	95, 949	0.0001 2, 4.0e- 76	HYPOTH ETICAL 36.1 KD PROTEI N IN RNR3-

139479	ATU001 419	ATL8C1 0945:4 690..7 59	gap2	ATCEA4 S13395	99	ATL8C1 0945:4 690..1 584	0.60	g28092 46	87	1517	4.1e- 121	ARC15 INTERG ENIC REGION [Sacch aromyc es cerevi siae]; COATOM ER BETA' SUBUNI T (BETA' -COAT PROTEI N) (BETA' -COP) (P102) [Rattu s norveg icus]
139480	ATU001 420	ATL8C2 6610:2 894..5 92	gap2	ATCEA4 C8609 1	99			g45394 52	87	1689	3.6e- 182	(AC002 560) F2401. 15 [Arabi dopsis thalia na] (AL049 500) putati ve phosph oribos ylanth ranila te transf erase [Arabi

139481	ATU001 421	ATL8C3 7223:4 207..1 046	gap2	ATCEA4 C2830_1, ATCEA4 S27322 , ATCEA4 S13867 , ATCEA4 S35450	99, 94, 82 84, 82	ATL8C3 7223:4 140..1 186	0.87	g19290 56	86	1517	(Y1209 0) putati ve 3,4- dihydr oxy-2- butano ne kinase [Lycop ersico n escule ntum]
139482	ATU001 422	ATL8C1 2679:5 590..7 37	gap2	ATCEA4 C10590 91, ATCEA4 C31036 1, ATCEA4 S2228	99, 98, 97	ATL8C1 2679:4 822..9 75	0.85	g46269 2	86	229	2.0e- 10 NEDD1 PROTEI N []
139483	ATU001 423	ATL8C4 223:1. .1923	gap2	ATCEA4 S12124	99	ATL8C4 223:45 ..1923	0.82	g26739 07	86	628	1.3e- 71 (AC002 561) hypoth etical protei n [Arabi dopsis thalia na]
139484	ATU001 424	ATL8C4 8782:4 562..1	gap2	ATCEA4 C14908 _1	99	ATL8C4 8782:4 562..9 6	0.69	g27022 67	86	1992	6.8e- 208 (AC003 033) hypoth etical protei n [Arabi dopsis thalia na]

139485	ATU001 425	ATL8S2 7218:3 06..1	gap2	ATCEA4 C49207 _1	99					g44553 32	86	137	2.1e- 06	na] (AL035 525) putati ve protei n [Arabi dopsis thalia na]
139486	ATU001 426	ATL8C1 9916:1 ..1340	gap2	ATCEA4 S14364 , ATCEA4 S3158, ATCEA4 C27853 _1	99, 98, 98	ATL8C1 9916:3 84..13 31	1.00			g31352 52	85	957	2.4e- 78	(AC003 058) hypoth etical protei n [Arabi dopsis thalia na]
139487	ATU001 427	ATL8C4 9564:3 73..11 17	gap2	ATCEA4 C1002_1, ATCEA4 S11796 , ATCEA4 S11728 , ATCEA4 S11819	99, 87, 87, 86					g15926 77	86	851	3.5e- 53	(X9191 2) LEA76 homolo gue type2 [Arabi dopsis thalia na]
139488	ATU001 428	ATL8C7 527:16 95..1	gap2	ATCEA4 S164	99	ATL8C7 527:16 41..30	0.97			g45593 80	85	2238	3.2e- 238	(AC006 526) putati ve auxin- respon sive GH3 protei n [Arabi dopsis thalia na]

139489	ATU001 429	ATL8C2 1766:9 066..5 843	gap2	ATCEA4 C4226_2, ATCEA4 C33219 2, ATCEA4 S24840 , ATCEA4 C74007 1, ATCEA4 S32004 , ATCEA4 C4226_1, ATCEA4 S9385, ATCEA4 S21297	99, 99, 96, 94, 91, 88, 86, 83	ATL8C2 1766:8 985..6 109	0.97	g39246 15	85	709	6.3e- 56	na] (AF069 442) hypoth etical protein [Arabi dopsis thalia na]
139490	ATU001 430	ATL8C2 5177:1 678..1	gap2	ATCEA4 S36279	99	ATL8C2 5177:7 79..77	0.95	g13518 99	85	778	6.6e- 70	FLORAL HOMEOT IC PROTEI N AGL6 [Arabi dopsis thalia na]
139491	ATU001 431	ATL8C3 6942:6 103..6 17	gap2	ATCEA4 S12015 , ATCEA4 C7116_2, ATCEA4 S6759, ATCEA4 S35286	99, 98, 96, 85	ATL8C3 6942:4 898..6 17	0.89	g45835 44	85	1266	3.6e- 109	(Z9563 7) acyl- CoA:1- acylgly cerol -3- phosph ate acyltr ansfer ase [Brass

139492	ATU001 432	ATL8C1 6250:3 68...32 00	gap2	ATCEA4 C16357 1, ATCEA4 S1618, ATCEA4 S29635 , ATCEA4 C15428 1	99, 98, 93, 87	ATL8C1 6250:1 353...3 200	0.58	g30886 46	85	999	1.1e- 107	ica napus] (AF056 493) pectin methyl esterase [Pisum sativum]
139493	ATU001 433	ATL8C1 4589:1 052...1	gap2	ATCEA4 C13754 1, ATCEA4 S13914	99, 93	ATL8C1 4589:9 27...36	0.51	g45726 75	85	840	3.2e- 50	(AC006 954) unknown protein [Arabis dopsis thaliana]
139494	ATU001 434	ATL8C2 2709:1 ...2927	gap2	ATCEA4 C4126_ 1, ATCEA4 C64053 1_ 1	99, 98	ATL8C2 2709:4 07...28 45	0.93	g22752 01, g43371 76	84, 63	550, 170	8.7e- 48, 1.6e- 12	(AC002 337) unknown protein [Arabis dopsis thaliana] ; (AC006 416) T31J12 .4 [Arabis dopsis thaliana] na]
139495	ATU001 435	ATL8C1 3312:1 231...1 88	gap2	ATCEA4 S16008 , ATCEA4	99, 91	ATL8C1 3312:1 080...3 06	0.84	g35496 59	84	262	1.2e- 23	(AL031 394) putative

139496	ATU001 436	ATL8C2 5545:9 48..97	gap2	ATCEA4 C4622_1	99	ATL8C2 5545:8 26..97	0.81	g26186 95	84	566	3.9e- 57	protein [Arabidopsis thaliana]
139497	ATU001 437	ATL8C3 0721:1 519..3 815	gap2	ATCEA4 C39749_1	99	ATL8C3 0721:1 948..3 737	0.75	g33416 97	84	639	1.1e- 48	protein [Arabidopsis thaliana]
139498	ATU001 438	ATL8C2 329:33 00..85 0	gap2	ATCEA4 S34248 , ATCEA4 C8377_1	99, 94	ATL8C2 329:31 40..11 57	0.73	g92757 5	84	856	2.5e- 72	protein [U1292 6) alpha galact osidas e [Glyci ne max]
139499	ATU001 439	ATL8C2 818:21 39..11 48	gap2	ATCEA4 C93628_1	99	ATL8C2 818:18 27..12 29	0.71	g40564 41	84	830	9.1e- 85	protein [AC005 990) Simila r to OBP32p ep protein gb U37 698

139500	ATU001 440	ATL8C1 4471:3 577..1	gap2	ATCEA4 C30734 _1	99	ATL8C1 4471:3 272..4 99	0.64	g11709 17, g22931 46	84, 80	207, 292	1.4e- 21, 2.5e- 27	from Arabid opsis thaliana. [Arabidopsis thaliana]
												2- SUCCIN YL-6- HYDROX Y-2,4- CYCLOH EXADIE NE-1- CARBOX YLATE SYNTHA SE (SHCH SYNTHA SE) / 2- OXOGLU TARATE DECARB OXYLAS E (ALPHA - KETOGL UTARAT E DECARB OXYLAS E) (KDC) [Haemo philus influe nzae Rd]; (AF008

139501	ATU001 441	ATL8C1 3042:3 936..1	gap2	ATCEA4 S6423, ATCEA4 C22791 _1	99, 97	ATL8C1 3042:3 936..6 5	0.41	g24983 29	84	3799	0.0	220) SHCHC syntha se [Bacil lus subtil is]
139502	ATU001 442	ATL8C4 5165:1 123..1	gap2	ATCEA4 C35353 _1, ATCEA4 S13848	99, 98	ATL8C4 5165:9 91..21 0	0.40	g32985 36	84	1739	4.5e- 167	PATTE N FORMAT ION PROTEI N EMB30 [Arabi dopsis thalia na]
139503	ATU001 443	ATL8C4 4514:1 ..3116	gap2	ATCEA4 C21004 _1, ATCEA4 S3234, ATCEA4 S1410	99, 97 98, 97			g42048 49	84	1214	6.7e- 112	(U5587 5) protei n kinase [Arabi dopsis thalia na]
139504	ATU001 444	ATL8C3 3096:1 ..893	gap2	ATCEA4 S933	99			g73031 8, g15523 26	84, 84	319, 331	2.7e- 18, 2.1e- 18	POTENT HEAT- STABLE PROTEI N PHOSPH ATASE

139506	ATU001 446	ATL8C1 684:74 4..364 7	gap2	ATCEA4 S30261 , ATCEA4 S30277	99, 95	ATL8C1 684:74 4..294 1	0.89	g10768 21	83	263	4.0e- 23	phosphoglycerate kinase [Pyrococcus horikoshii]
139507	ATU001 447	ATL8C9 86:14. .1039	gap2	ATCEA4 S284	99	ATL8C9 86:14. .861	0.88	g43771 80	83	470	2.7e- 51	(AE001667) Phosphoglycerate Mutase [Chlamydia pneumoniae]
139508	ATU001 448	ATL8C2 4712:3 350..1	gap2	ATCEA4 C19668 1, ATCEA4 C43218 1, ATCEA4 C39810 1, ATCEA4 C10275 0_1	99, 96, 95, 95	ATL8C2 4712:3 009..9 7	0.81	g58514 7, g48875 63	83, 69	266, 727	7.5e- 27, 1.2e- 44	FLUG PROTEIN [Emerella nidulans]; (AJ133118) nodulin 6 [Medicago truncatula]

139509	ATU001 449	ATL8C1 1811:8 53..30 03	gap2	ATCEA4 S1529	99	ATL8C1 1811:8 53..29 56	0.79	g44540 51	83	779	1.2e- 64	tula] (AL035 394) putati ve polyga lactur onase [Arabi dopsis thalia na]
139510	ATU001 450	ATL8C3 5358:7 02..56 22	gap2	ATCEA4 S23, ATCEA4 C51693 1, ATCEA4 S10477 , ATCEA4 S5627, ATCEA4 S4630	99, 92, 90, 88, 86	ATL8C3 5358:7 02..45 43	0.74	g31221 17	83	668	5.7e- 57	CELL DIVISI ON PROTEI N FTSH HOMOLO G [Bacil lus firmus]
139511	ATU001 451	ATL8C1 7091:1 ..3393	gap2	ATCEA4 C26125 1	99	ATL8C1 7091:2 63..33 53	0.73	g22752 06, g22752 08	83, 53	931, 807	3.4e- 96, 5.9e- 70	(AC002 337) pectin estera se isolog [Arabi dopsis thalia na]; (AC002 337) hypoth etical protei n [Arabi dopsis thalia na]
139512	ATU001	ATL8C1	gap2	ATCEA4	99, 97	ATL8C1	0.69	g45843	83	460	1.6e-	(AC006

139513	452	6985:1 825..1 26	S30298 , ATCEA4 C34960 _1	99, 99	ATL8C2 2223:2 637..9 6	0.56	929247 77	83	2887	8.6e- 275	420) putati ve PttA- like transp oson protei n [Arabi dopsis thalia na]
139514	ATU001 454	ATL8C4 586:77 0..185 1	ATCEA4 C627_2	99	ATL8C4 586:77 3..175 8	0.56	954901 0	83	1723	8.2e- 174	(AC002 334) putati ve recept or protei n kinase [Arabi dopsis thalia na]
											EUKARY OTIC PEPTID E CHAIN RELEASE E FACTOR SUBUNI T 1 (ERF1) (OMNIP OTENT SUPPRE SSOR PROTEI N 1 HOMOLO G)

139515	ATU001 455	ATL8C5 352:18 88..1	gap2	ATCEA4 C11606 7_1	99	ATL8C5 352:18 88..13	0.55	g12235 79	83	874	5.3e- 76	(X9648 1) CDNA10 1 [Arabi dopsis thalia na]
139516	ATU001 456	ATL8C4 1503:4 28..11 30	gap2	ATCEA4 C25051 1, ATCEA4 C4355_1	99, 82	ATL8C4 1503:8 90..10 06	0.42	g17078 68	83	224	1.0e- 18	(Y0963 6) 40S riboso mal subuni t protei n S21 [Zea mays]
139517	ATU001 457	ATL8C3 8068:1 123..1	gap2	ATCEA4 S26884 , ATCEA4 S33208 , ATCEA4 C11704 8 1	99, 90 90, 90			g47419 23	83	173	1.5e- 11	(AF130 849) PIT1 [Arabi dopsis thalia na]
139518	ATU001 458	ATL8C7 646:21 25..1	gap2	ATCEA4 C77519 1, ATCEA4 S7786	99, 90			g45593 95	83	2360	2.8e- 238	(AC006 526) putati ve cyclic nucleo tide- regula ted ion channe

139523	ATU001 463	ATL8C3 2719:1 912...3 563	gap2	ATCEA4 C76547 1, ATCEA4 C12306 1	99, 85				g41159 33	82	539	1.0e- 44	(AF118 223) contai ns simila rity to human RNA polyme rase II comple x compon ent SRB7 (GB:U5 2960) [Arabi dopsis thalia na]
139524	ATU001 464	ATL8C3 7433:5 86...21 43	gap2	ATCEA4 C36277 1	99	ATL8C3 7433:6 61...20 83	0.96	g33675 15	81	1493	(AC004 392) Simila r to glucos e-6- phosph ate/ph osphat e- transl ocator (GPT) gb AF0 20814 from Pisum sativu m. [Arabi dopsis thalia		

139525	ATU001 465	ATL8C4 8898:1 020..2 340	gap2	ATCEA4 C35127 1, ATCEA4 S13810 , ATCEA4 C4039- 1	99, 98, 86	ATL8C4 8898:1 155..2 308	0.84	g45103 83	81	1585	1.5e- 142	(AC007 017) unknown protein [Arabi dopsis thalia na]
139526	ATU001 466	ATL8C4 3160:1 ..904	gap2	ATCEA4 S8318, ATCEA4 C4172- 1, ATCEA4 S32829 , ATCEA4 S7763, ATCEA4 C4172- 2	99, 97, 95, 93, 85	ATL8C4 3160:2 02..82 7	0.74	g22752 10	81	740	4.8e- 80	(AC002 337) peptid yl- prolyl cis- trans isomer ase isolog [Arabi dopsis thalia na]
139527	ATU001 467	ATL8C5 02:403 5..610 7	gap2	ATCEA4 S13201	99	ATL8C5 02:453 1..597 2	0.64	g33675 68	81	911	3.6e- 96	(AL031 135) protein kinase - like protein [Arabi dopsis thalia na]
139528	ATU001 468	ATL8C2 0272:1 ..2143	gap2	ATCEA4 S34999 , ATCEA4 S26401	99, 85	ATL8C2 0272:5 8..176 7	0.55	g29829 47	81	86	0.0001 2	(AE000 679) riboso mal protein S15 [Aquif ex

139529	ATU001 469	ATL8C1 1812:1 ..1435	gap2	ATCEA4 C23250 _1	99	ATL8C1 1812:3 84..12 43	0.53	g29823 11	81	480	9.1e- 36	aeolic us] (AF051 240) probab le ubiqui tin- conjug ating enzyme E2 [Picea marian al]
139530	ATU001 470	ATL8C1 2001:2 70..32 44	gap2	ATCEA4 S13708 , ATCEA4 S1946	99, 99			g28299 10	81	2005	1.9e- 195	(AC002 291) Unknown n protei n, contai ns regula tor of chromo some conden sation motifs [Arabi dopsis thalia na]
139531	ATU001 471	ATL8C1 8023:2 20..31 03	gap2	ATCEA4 C18294 2, ATCEA4 S34498 , ATCEA4 C33956 _1	99, 91 93, 91	ATL8C1 8023:2 20..29 56	0.90	g11622 9	80	1554	1.7e- 138	MITOCH ONDRIA L CHAPER ONIN HSP60 PRECUR SOR [Arabi dopsis thalia

139532	ATU001 472	ATL8C3 7664:1 ..1392	gap2	ATCEA4 C37364 _1	99	ATL8C3 7664:6 8..139 2	0.62	g31525 83	80	523	3.8e- 43	na] (AC002 986) Contai ns simila rity to inhibi tor of apopto sis protei n gblU45 881 from D. melano gaster . [Arabi dopsis thalia na]
139533	ATU001 473	ATL8C4 3272:8 9..156 1	gap2	ATCEA4 C13056 1, ATCEA4 C4869 _1	99, 98	ATL8C4 3272:8 9..156 1	0.60	g33293 68	80	1847	6.0e- 163	(AF031 244) noduli n-like protei n [Arabi dopsis thalia na]
139534	ATU001 474	ATL8S1 6352:1 ..565	gap2	ATCEA4 C43273 _1	99	ATL8S1 6352:2 77..35 8	0.45	g29470 67	80	380	2.3e- 38	(AC002 521) hypoth etical protei n [Arabi dopsis thalia na]

139535	ATU001 475	ATL8C4 7836:6 1..199 5	gap2	ATCEA4 S1483	99	ATL8C4 7836:6 1..195 3	0.94	g26186 99	79	495	1.2e- 52	(AC002 510) unknown protein [Arabi dopsis thalia na]
139536	ATU001 476	ATL8C3 6650:2 532..9 34	gap2	ATCEA4 S8250, ATCEA4 C32420 1, ATCEA4 C30888 1, ATCEA4 S7277, ATCEA4 S19500	99, 96, 95, 90, 85	ATL8C3 6650:2 462..1 228	0.88	g31766 76	79	786	6.5e- 58	(AC003 671) Simila r to carbon ic anhydr ase gb L19 255 from Nicoti ana tabacu m. ESTs gb AA5 97643, gb T45 390, gb T43 963 and gb AA5 97734 come from this gene. [Arabi dopsis thalia na]
139537	ATU001 477	ATL8C4 4593:1	gap2	ATCEA4 S688,	99, 95,	ATL8C4 4593:1	0.87	g48368 90	79	416	3.7e- 54	(AC007 369)

139538	ATU001 478	ATL8C3 0602:1 ..4048	gap2	ATCEA4 S3286, ATCEA4 S13885 , ATCEA4 S2940	95, 90	61..36 90	0.80	g24926 07, g11344 9	79, 51	346, 376	2.8e- 15, 3.1e- 32	Unknown protein [Arabidopsis thaliana]
139539	ATU001 479	ATL8C4 2627:2 401..3 26	gap2	ATCEA4 C17891 1, ATCEA4 S16631 , ATCEA4 S33111	99, 93, 91, 90	ATL8C4 2627:1 920..6 21	0.79	g38941 93	79	476	3.9e- 38	(AC005 662) putative strict osidine synthase

139540	ATU001 480	ATL8C3 7168:1 ..5380	gap2	ATCEA4 S35857	99, 97	ATL8C3 7168:5 4..535 0	0.78	g13303 43, g46783 06	79, 51	255, 1027	[Arabi dopsis thalia na]
139541	ATU001 481	ATL8C2 9486:1 ..1269	gap2	ATCEA4 S10876	99	ATL8C2 9486:8 7..110 5	0.73	g48952 05	79	1227	(U5875 5) C34D4. 12 gene produc t [Caeno rhabdi tis elegan sl]; (AL049 655) kinesi n-like protei n [Arabi dopsis thalia na]
139542	ATU001 482	ATL8C2 6067:8 83..1	gap2	ATCEA4 C76069 1, ATCEA4 S15726	99, 92, 90	ATL8C2 6067:8 00..56 2	0.67	g32838 93	79	416	(AC007 661) putati ve alcohol dehydr ogenase [Arabi dopsis thalia na]
										3.6e- 36	(AF070 626) unknow n [Homo sapien s]

139543	ATU001 483	ATL8C1 264:42 99..87 2	gap2	ATCEA4 C83522 1	99, 98, 91, 87, 84	ATL8C1 264:42 53..10 03	0.67	g40380 66	79	557	1.7e- 33	(AC005 897) hypoth etical protei n [Arabi dopsis thalia na]
139544	ATU001 484	ATL8C2 9243:8 2..595	gap2	ATCEA4 S26803 , ATCEA4 C10783 2, ATCEA4 S26804	99, 97, 93			g35496 63	79	381	1.7e- 33	(AL031 394) putati ve protei n [Arabi dopsis thalia na]
139545	ATU001 485	ATL8C3 9923:1 336..2 13	gap2	ATCEA4 C57983 1	99			g40493 48	79	249	2.1e- 24	(AL034 567) putati ve protei n [Arabi dopsis thalia na]
139546	ATU001 486	ATL8C1 9622:2 249..4 10	gap2	ATCEA4 S27026 , ATCEA4 C494_1 , ATCEA4 S35062	99, 99, 93	ATL8C1 9622:2 139..6 61	0.86	g32818 46	78	2383	5.5e- 194	(AJ006 404) late elonga ted hypoco tyl [Arabi dopsis thalia na]

139547	ATU001 487	ATL8C1 2609:9 6..289 5	gap2	ATCEA4 C19733 1, ATCEA4 S12012 , ATCEA4 S12016	99, 95, 90	ATL8C1 2609:2 85..22 59	0.81	g40975 43	78	98	0.0002 8	(U6490 4) ATFP1 [Arabi dopsis thalia na]
139548	ATU001 488	ATL8C5 0138:1 319..1	gap2	ATCEA4 C12212 1, ATCEA4 S3324	99, 95	ATL8C5 0138:1 295..1 1	0.80	g48503 69	78	1615	4.1e- 166	(AB027 151) threon ine syntha se [Arabi dopsis thalia na]
139549	ATU001 489	ATL8C4 5216:2 31..48 62	gap2	ATCEA4 S26171 , ATCEA4 S10890 , ATCEA4 S27946 , ATCEA4 S2261	99, 97, 96, 95	ATL8C4 5216:2 31..47 57	0.77	g23426 90	78	838	3.7e- 63	(AC000 106) Simila r to Homo copine I (gb U8 3246). [Arabi dopsis thalia na]
139550	ATU001 490	ATL8C2 6249:1 ..2077	gap2	ATCEA4 C31970 1, ATCEA4 C33757 1	99, 98	ATL8C2 6249:5 25..18 77	0.74	g44688 10	78	1631	4.2e- 126	(AL035 601) putati ve protei n [Arabi dopsis thalia na]
139551	ATU001 491	ATL8C1 3104:3 072..6 953	gap2	ATCEA4 C39598 1, ATCEA4	99, 96 97, 96	ATL8C1 3104:3 136..6 953	0.68	g11283 7	78	591	4.7e- 76	NAD(P) H DEPEND ENT

139552	ATU001 492	ATL8C3 6653:1 22...38 38	gap2	ATCEA4 C8403 1, ATCEA4 S6381, ATCEA4 C12329 7 1	99, 97, 96	ATL8C3 6653:1 22...35 55	0.64	g38196 97	78	1789	1.0e- 162	6'- DEOXYC HALCON E SYNTHA SE [Glyci ne max] (AJ009 608) BnMAP4 K alpha1 [Brass ica napus]
139553	ATU001 493	ATL8C3 5068:4 167..2 297	gap2	ATCEA4 C10588 0 1, ATCEA4 C30873 _1	99, 93	ATL8C3 5068:4 162..2 554	0.98	g11694 21	77	916	1.9e- 95	DEVELO PMENTA LLY REGULA TED GTP- BINDIN G PROTEI N DRG (XDRG) [Xenop us laevis]
139554	ATU001 494	ATL8C3 7479:1 993..9 10	gap2	ATCEA4 C79449 1, ATCEA4 C31356 _1	99, 98	ATL8C3 7479:1 945..1 212	0.97	g45875 47	77	229	2.3e- 19	(AC006 577) Contai ns simila rity to DNA- bindin g protei n Gt-2 gb X68

139555	ATU001 495	ATL8C2 0649:1 276..4 493	gap2	ATCEA4 C30292 1, ATCEA4 S34271	99, 98	ATL8C2 0649:1 505..3 665	0.80	g11686 54	77	839	9.0e- 63	BETA- GALACT OSIDAS E PRECUR SOR (LACTA SE) [Aspar agus offici nalis]	261 from Oryza sativa [Arabi dopsis thalia na]
139556	ATU001 496	ATL8C4 6237:1 688..1	gap2	ATCEA4 S8207, ATCEA4 S1864, ATCEA4 C10247 9 1, ATCEA4 S34774	99, 98, 96, 92	ATL8C4 6237:1 378..7 9	0.80	g43357 73	77	215	6.7e- 25	(AC006 284) unknow n protei n [Arabi dopsis thalia na]	
139557	ATU001 497	ATL8C1 7765:5 396..1	gap2	ATCEA4 S1935, ATCEA4 C13341 1, ATCEA4 C17835 1, ATCEA4 S22356	99, 98, 90, 84	ATL8C1 7765:5 199..1 355	0.74	g33602 91, g41153 73	77, 55	490, 117	2.4e- 62, 6.7e- 06	(AF023 165) leucin e-rich repeat transm embran e protei n kinase 2 [Zea mays];	

139558	ATU001 498	ATL8C3 475:10 3..599	gap2	ATCEA4 C32656 _1	99	ATL8C3 475:17 9..551	0.73	g34618 28	77	324	2.8e- 32	(AC005 967) recept or- like protei n kinase [Arabi dopsis thalia na]
139559	ATU001 499	ATL8C2 083:40 45..1	gap2	ATCEA4 S1457, ATCEA4 C17154 _1	99, 89	ATL8C2 083:39 08..56	0.72	g48951 83	77	2513	6.7e- 235	(AC007 661) hypoth etical protei n [Arabi dopsis thalia na]
139560	ATU001 500	ATL8C2 8348:8 43..1	gap2	ATCEA4 S36231 , ATCEA4 S33557 , ATCEA4 C256_1 , ATCEA4 S27789	99, 98, 97, 92	ATL8C2 8348:7 50..13 2	0.71	g39536 01	77	508	3.0e- 58	(AB008 489) respon se regula tor 6 [Arabi dopsis thalia na]
139561	ATU001 501	ATL8C8 617:26	gap2	ATCEA4 C4755	99, 97, 86	ATL8C8 617:21	0.99	g48357 83	76	1050	3.6e- 92	(AC007 296)

		70..1			1, ATCEA4 C12114 51, ATCEA4 S25244		13..10 1							Strong similarity to []
139562	ATU001 502	ATL8C4 1961:5 10..45 57	gap2	ATCEA4 S6369	99		ATL8C4 1961:5 10..45 57	0.90	g38735 50, g23427 31	76, 54	81, 254	0.98, 1.7e- 17	(AL033 534) serine -rich protein [Schiz osacch aromyc es pombe] ;(AC002 341) hypoth etical protein [Arabi dopsis thalia na]	
139563	ATU001 503	ATL8C2 2015:4 64..20 79	gap2	ATCEA4 C23946 1, ATCEA4 C22198 1	99, 97		ATL8C2 2015:4 64..16 54	0.82	g48836 18	76	591	3.5e- 44	(AC006 922) hypoth etical protein [Arabi dopsis thalia na]	
139564	ATU001 504	ATL8C1 7360:5 700..5 0	gap2	ATCEA4 C30861 1	99		ATL8C1 7360:3 360..5 0, ATL8C1 7360:5 700..4	0.81, 0.97	g19463 55, g30634 61	76, 59	789, 560	1.7e- 81, 1.6e- 54	(U9321 5) maize transp oson MuDR mudrA	

		11		ATCEA4 S34745 , ATCEA4 C18663 _1		55										ns similarity to protein- tyrosine phosphatase 2 gb L15 420 from Dictyostelium discoideum. EST gb N38 718 comes from this g [Arabidopsis thaliana]
139569	ATU001 509	ATL8C4 9323:8 466..7 149	gap2	ATCEA4 C50423 _1, ATCEA4 C22076 _1	99, 88			g22890 02	76	372	7.7e- 32	(AC002 335) unknown protein [Arabidopsis thaliana]				
139570	ATU001 510	ATL8C1 7113:1 ..1032	gap2	ATCEA4 C754_1	99	ATL8C1 7113:4 32..86 1	0.93	g11408 6	75	709	1.1e- 71	RAS- RELATE D PROTEI N ARA- 2				

139571	ATU001 511	ATL8C9 168:76 2..230 6	gap2	ATCEA4 C62729 1, ATCEA4 C8905_1, ATCEA4 S30238 , ATCEA4 S32373	99, 97, 89, 89	ATL8C9 168:81 8..221 5	0.90	g31840 98	75	675	[Arabi dopsis thalia na]
139572	ATU001 512	ATL8C4 9325:1 ..1691	gap2	ATCEA4 C14673 2, ATCEA4 S28641 , ATCEA4 S2467	99, 98, 91	ATL8C4 9325:6 78..15 83	0.86	g11720 48	75	63	0.0019 <

139574	ATU001 514	ATL8C2 7741:1 ..2932	gap2	ATCEA4 S1433	99	ATL8C2 7741:1 39..23 33	0.71	g40637 51, g45586 65, g40383 52	75, 68, 67	525, 319, 443	na]	
											(AC005 851) putati ve. white protei n [Arabi dopsis thalia na]; (AC007 063) putati ve white protei n [Arabi dopsis thalia na]; (AF098 951) breast cancer resist ance protei n [Homo sapien s]	
139575	ATU001 515	ATL8C1 9246:2 269..1	gap2	ATCEA4 S19872 , ATCEA4 S31326	99, 91	ATL8C1 9246:2 269..6 6	0.68	g13516 12	75	231	1.9e- 21	HYPOTH ETICAL OXIDOR EDUCTA SE C23D3. 11 IN CHROMO SOME I []
139576	ATU001	ATL8C2	gap2	ATCEA4	99, 86	ATL8C2	0.40	g48862	75	1104	7.5e-	(AL050

	516	6600:1 ..676		C34989 1, ATCEA4 S11115		6600:5 3..566		81				102	300) putati ve protei n [Arabi dopsis thalia na]
139577	ATU001 517	ATL8C4 7725:2 588..1	gap2	ATCEA4 C3525_2, ATCEA4 C3525_1, ATCEA4 C3525_3, ATCEA4 S34401	99, 99, 96, 94	ATL8C4 7725:2 550..2 96	0.93	g23427 22	74	136	8.9e-07	(AC002 341) unknown protein [Arabi dopsis thalia na]	
139578	ATU001 518	ATL8C5 360:49 3..312 8	gap2	ATCEA4 S1954, ATCEA4 S7885	99, 90	ATL8C5 360:13 48..29 62	0.89	g48357 71	74	621	3.4e-51	(AC007 202) Simila r to []	
139579	ATU001 519	ATL8C3 2145:1 084..1	gap2	ATCEA4 S34892, ATCEA4 S13031	99, 97	ATL8C3 2145:1 084..1 10	0.89	g30333 86	74	212	5.0e-23	(AC004 238) RING3- like protein [Arabi dopsis thalia na]	
139580	ATU001 520	ATL8C2 8577:5 00..36 08	gap2	ATCEA4 C32711 1, ATCEA4 C9962_1, ATCEA4 S4251	99, 98, 89	ATL8C2 8577:6 24..35 88	0.86	g15757 76	74	445	1.8e-31	(U7085 9) cation ic amino acid transp orter [Mus muscul	

139581	ATU001 521	ATL8C3 7471:4 526..1 542	gap2	ATCEA4 C48883 1, ATCEA4 S32158 , ATCEA4 S4632, ATCEA4 S32159	99, 99, 99, 95	ATL8C3 7471:4 261..1 542	0.86	g22451 31	74	473	us] (Z9734 4) hypoth etical protei n [Arabi dopsis thalia na]
139582	ATU001 522	ATL8C5 676:63 ..1868	gap2	ATCEA4 C74068 1, ATCEA4 C74068 3, ATCEA4 S32357	99, 95, 93	ATL8C5 676:63 ..1693	0.85	g73183 4	74	136	HYPOTH ETICAL 41.9 KD PROTEI N IN SDS3- THS1 INTERG ENIC REGION [Sacch aromyc es cerevi siae]
139583	ATU001 523	ATL8C1 3455:9 638..1 4110	gap2	ATCEA4 S1043	99	ATL8C1 3455:1 0769.. 13987	0.77	g45067 75	74	1826	UNKNOWN N [Homo sapien s]
139584	ATU001 524	ATL8C2 8220:7 86..1	gap2	ATCEA4 C11026 1 _	99	ATL8C2 8220:6 74..20 6	0.77	g49144 17	74	405	(AL050 352) putati ve protei n [Arabi dopsis thalia na]
139585	ATU001 525	ATL8C4 8105:1	gap2	ATCEA4 S7736,	99, 92	ATL8C4 8105:1	0.71	g12796 40	74	523	(X9220 4) NAM

		533..8 3		ATCEA4 C54574 _1		350..8 3								[Petunia x hybrid al]
139586	ATU001 526	ATL8C9 185:37 9..1	gap2	ATCEA4 C8936_1	99	ATL8C9 185:30 5..75	0.56	g44689 91	74	166				(AL035605) ribosomal-like protein [Arabidopsis thaliana]
139587	ATU001 527	ATL8C2 4559:1 706..1	gap2	ATCEA4 C20065_1	99	ATL8C2 4559:1 706..1 64	0.90	g17306 73	73	165	2.1e-15			HYPOTHETICAL 48.1 KD PROTEIN IN SEC12-SSK2 INTERGENIC REGION [Saccharomyces cerevisiae]
139588	ATU001 528	ATL8C2 4107:7 74..20 60	gap2	ATCEA4 C8682_1, ATCEA4 S875	99, 98	ATL8C2 4107:8 33..19 90	0.81	g41917 91	73	666	8.9e-70			(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]

139589	ATU001 529	ATL8C2 5655:1 433..1	gap2	ATCEA4 S7740, ATCEA4 S7383	99, 93	ATL8C2 5655:1 433..3	0.74	g29831 78	73	153	3.1e- 12	na] (AE000 694) hypoth etical protei n [Aquif ex aeolic us]
139590	ATU001 530	ATL8C4 2164:1 ..989	gap2	ATCEA4 C15710 1, ATCEA4 C11707 6_1, ATCEA4 S33049	99, 97, 91	ATL8C4 2164:4 ..780	0.55	g27603 21	73	679	2.0e- 77	(AC002 130) F1N21. 6 [Arabi dopsis thalia na]
139591	ATU001 531	ATL8C4 1514:1 227..1	gap2	ATCEA4 S3520, ATCEA4 C36130 _1	99, 96			g32876 91	73	178	1.5e- 14	(AC003 979) Contai ns simila rity to RING zinc finger protei n gb X95 455 from Gallus gallus . [Arabi dopsis thalia na]
139592	ATU001 532	ATL8C3 1383:1 219..1	gap2	ATCEA4 C7334_2, ATCEA4	99, 98, 93, 88,			g25292 29	73	1421	5.8e- 148	(AB007 907) 6- phosph

139593	ATU001 533	ATL8S2 7535:1 25..54 5	gap2	S31604 , ATCEA4 S31603 , ATCEA4 S34073 , ATCEA4 C46318 1, ATCEA4 C7334 1	87, 82					73	519	3.6e- 45	(AC003 027) Hypoth etical protei n [Arabi dopsis thalia na]	ogluco nate dehydr ogenas e [Glyci ne max]
139594	ATU001 534	ATL8C1 143:1. .2064	gap2	ATCEA4 C12396 1, ATCEA4 S11093 , ATCEA4 C21315 1, ATCEA4 S11095	99, 94, 93, 82					73	2272	2.3e- 174	(Z9734 4) trehal ose-6- phosph ate syntha se homolo g [Arabi dopsis thalia na]	(Z9734 4) trehal ose-6- phosph ate syntha se homolo g [Arabi dopsis thalia na]
139595	ATU001 535	ATL8C2 8022:1 ..751	gap2	ATCEA4 C29350 1, ATCEA4 S11079	99, 95					73	532	6.1e- 35	(AL049 524) putati ve protei n [Arabi	(AL049 524) putati ve protei n [Arabi

139596	ATU001 536	ATL8C3 232:53 18..31 21	gap2	ATCEA4 S6201, ATCEA4 C2009_1	99, 85	ATL8C3 232:51 88..31 77	0.96	g22577 43	72	1465	1.3e- 123	dopsis thalia na]
139597	ATU001 537	ATL8C3 2339:3 002..9 3	gap2	ATCEA4 S30099 , ATCEA4 C10550 7.1, ATCEA4 C30170 1, ATCEA4 C70136 2, ATCEA4 S24777	99, 98, 97, 94, 89	ATL8C3 2339:2 706..1 30	0.96	g28044 09	72	101	0.98	(AF043 692) No defini tion line found [Caeno rhabdi tis elegan s]
139598	ATU001 538	ATL8C4 1748:1 626..1	gap2	ATCEA4 C52790 1_	99	ATL8C4 1748:1 587..5 5	0.95	g47339 81	72	1164	6.8e- 119	(AC007 268) putati ve serine carbox ypepti dase [Arabi dopsis thalia na]
139599	ATU001 539	ATL8C6 819:19 12..1	gap2	ATCEA4 C25028 1	99	ATL8C6 819:18 98..30	0.89	g31229 52	72	348	4.2e- 38	TIPD PROTEI N

139600	ATU001 540	ATL8C1 4744:6 340..1 66	gap2	ATCEA4 C8194_1, ATCEA4 S35006, ATCEA4 S32950, ATCEA4 C8194_2, ATCEA4 S34990, ATCEA4 S31938, ATCEA4 S25002, ATCEA4 S6067	99, 96, 93, 92, 91, 88, 83, 82	ATL8C1 4744:6 298..5 22	0.69	g41707 3	72	6739	0.0	[Dicty osteli um discoi deum] GLUTAM ATE SYNTHA SE (NADH) PRECUR SOR (NADH- GOGAT) [Medic ago sativa]
139601	ATU001 541	ATL8C2 4696:7 68..48 55	gap2	ATCEA4 S1588, ATCEA4 C23820 1, ATCEA4 S9719, ATCEA4 S34595	99, 98, 88, 84	ATL8C2 4696:7 68..48 55	0.66	g16518 28	72	747	9.1e- 64	(D9090 0) dihydr olipoa mide dehydr ogenas e [Synec hocyst is sp.]
139602	ATU001 542	ATL8C4 0889:1 259..1 47	gap2	ATCEA4 S27172	99	ATL8C4 0889:1 146..1 47	0.66	g22528 49	72	815	3.5e- 97	(AF013 294) contai ns simila

139603	ATU001 543	ATL8C3 5346:6 188..1	gap2	ATCEA4 C937_2 , ATCEA4 S19242 , ATCEA4 S15127 , ATCEA4 S33614 , ATCEA4 S25760 , ATCEA4 S25761	99, 95, 93, 88, 83, 83	ATL8C3 5346:5 926..1 17	0.65	g24941 29	72	1318	1.4e- 106	(AC002 376) T1G11. 3 [Arabi dopsis thalia na]
139604	ATU001 544	ATL8C4 0141:1 ..1230	gap2	ATCEA4 C3320_ 1, ATCEA4 C10155 _1	99, 98			g15321 69	72	361	9.9e- 36	(U6381 5) simila r to a E. coli hypoth etical protei n F402 encode d by GenBan k Access ion Number S47768 [Arabi dopsis

139605	ATU001 545	ATL8C4 5612:2 114..1	gap2	ATCEA4 S28149 , ATCEA4 S31522 , ATCEA4 C423_1 , ATCEA4 S28387 , ATCEA4 S7464, ATCEA4 C423_4 , ATCEA4 S2387	99, 99, 95, 90, 85, 83, 82				g39285 43	72	1706	1.4e- 169	thalina na] (AB016 819) UDP- glucos e glucos yltran sferas e [Arabi dopsis thalina]
139606	ATU001 546	ATL8C3 6907:1 643..1	gap2	ATCEA4 S13487 , ATCEA4 S33430	99, 96	ATL8C3 6907:1 413..4 2	0.99		g45875 18	71	1222	2.9e- 139	(AC007 060) Strong simila rity to F19I3. 8 []
139607	ATU001 547	ATL8C3 4847:1 196..1	gap2	ATCEA4 S2951, ATCEA4 C13465 5_1	99, 95	ATL8C3 4847:1 196..2 77	0.97		g44690 19	71	1124	2.3e- 114	(AL035 602) putati ve protei n [Arabi dopsis thalina]
139608	ATU001 548	ATL8C3 9684:1 ..800	gap2	ATCEA4 C3297_1, ATCEA4 S14102	99, 99, 97, 87	ATL8C3 9684:5 88..20 5	0.85		g32288 4	71	143	9.8e- 09	pollen - prefer ential protei n -

139609	ATU001 549	ATL8C4 8310:4 650..1	gap2	ATCEA4 S25550 , ATCEA4 S30912	99, 97, 96, 94, 92, 92, 85	ATL8C4 8310:4 647..8 7	0.84	g45887 58, g15728 19, g15321 35	71, 54 64, 54	38, 431, 530	0.93, 1.1e- 34, 3.3e- 38	(AF115 476) rac- like GTP bindin g protei n [Physc omitre lla patens l; (U7085 5) simila r to the RAS gene family [Caeno rhabdi tis elegan s]; (U4944 2) chloro plast mRNA- bindin g protei n CSP41 precu sor
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139610	ATU001 550	ATL8C3 5536:1 ..453	gap2	ATCEA4 C14250 _1	99	ATL8C3 5536:7 5..453	0.80	g32490 98	71	273	2.7e- 14	[Spina cia olerac ea] (AC003 114) ESTs gb T04 610, gb N38 459, gb T45 174, gb R30 481 and gb N64 971 come from this gene. [Arabi dopsis thalia na]
139611	ATU001 551	ATL8C2 2957:1 023..2 716	gap2	ATCEA4 C36433 _1, ATCEA4 S3834, ATCEA4 C8042_ _1	99, 98, 93	ATL8C2 2957:1 103..2 626	0.64	g29824 37	71	1340	2.0e- 136	(AL022 224) terpen e cyclas e like protei n [Arabi dopsis thalia na]
139612	ATU001 552	ATL8C3 8203:8 5..122 7	gap2	ATCEA4 S15269 , ATCEA4 C752_1	99, 94	ATL8C3 8203:5 61..35 3	0.64	g13840 44	71	623	7.1e- 59	(D2112 5) APETAL A3 [Arabi dopsis thalia na]

139613	ATU001 553	ATL8C5 378:47 63..13 91	gap2	ATCEA4 S13969 , ATCEA4 C8297_1, ATCEA4 S13948 , ATCEA4 S13784 , ATCEA4 S31273	99, 98, 94, 87 89, 87	ATL8C5 378:41 10..13 91	0.63	g26421 58	71	424	1.5e- 30	na] (AC003 000) hypoth etical protei n [Arabi dopsis thalia na]
139614	ATU001 554	ATL8C4 5714:1 093..1	gap2	ATCEA4 S2636, ATCEA4 C23652 _1	99, 89	ATL8C4 5714:9 41..38	0.55	g22528 55	71	1431	5.2e- 108	(AF013 294) simila r to the myc family of helix- loop- helix transc riptio n factor s [Arabi dopsis thalia na]
139615	ATU001 555	ATL8C1 4493:1 129..6 3	gap2	ATCEA4 C35945 _1, ATCEA4 C57085 _1	99, 83			g13340 5	71	587	8.9e- 58	DNA- DIRECT ED RNA POLYME RASE ALPHA CHAIN [Pisum sativu m]

139616	ATU001 556	ATL8C3 5285:4 512..4 92	gap2	ATCEA4 S1444 , ATCEA4 C33632 1, ATCEA4 S33746 , ATCEA4 C13472 1, ATCEA4 S34826 , ATCEA4 S8017, ATCEA4 S7571	99, 98, 93, 93, 93, 83, 83, 83	ATL8C3 5285:4 420..1 414	0.91	g42622 39	70	471	4.8e- 44	(AC006 200) putati ve membra ne transp orter [Arabi dopsis thalia na]
139617	ATU001 557	ATL8C4 2043:1 ..1434	gap2	ATCEA4 S12092 , ATCEA4 C46799 1	99, 89	ATL8C4 2043:6 25..14 34	0.77	g47340 07	70	698	8.1e- 41	(AC007 178) hypoth etical protei n [Arabi dopsis thalia na]
139618	ATU001 558	ATL8C3 2922:1 ..2582	gap2	ATCEA4 S12683 , ATCEA4 C68537 1, ATCEA4 C7804 1	99, 98, 97	ATL8C3 2922:5 45..21 91	0.74	g19316 40	70	1273	1.5e- 89	(U9597 3) Serine carbox ypepti dase isolog [Arabi dopsis thalia na]
139619	ATU001 559	ATL8C3 6964:1 794..2 846	gap2	ATCEA4 C46438 1, ATCEA4 S33791	99, 90	ATL8C3 6964:1 817..2 698	0.71	g15243 70	70	338	7.1e- 23	(X9249 1) TOM20 [Solan um]

139620	ATU001 560	ATL8C3 7452:1 574..1	gap2	ATCEA4 S3473, ATCEA4 S16390	99, 88	ATL8C3 7452:1 541..1 88	0.70	g45050 29	70	646		tubero sum]
139621	ATU001 561	ATL8C3 0130:2 208..1	gap2	ATCEA4 S2984, ATCEA4 S34941 , ATCEA4 C12669 0_1	99, 86 89, 86	ATL8C3 0130:2 205..3 6	0.68	g33866 06	70	829	6.9e- 72	leukot riene A4 hydrol ase [Homo, sapien s]
139622	ATU001 562	ATL8C1 8050:1 921..1	gap2	ATCEA4 C5829_2, ATCEA4 C45952 1, ATCEA4 C64072 _1	99, 90 96, 90	ATL8C1 8050:1 846..8 9	0.56	g45875 13	70	1252	8.1e- 120	(AC007 060) Contai ns eukary otic protei n kinase domain PF1000 69. [Arabi dopsis thalia na]
139623	ATU001 563	ATL8C2 4767:4 9..353 3	gap2	ATCEA4 C31153 1, ATCEA4 S34488	99, 94	ATL8C2 4767:4 9..352 2	0.49	g45444 50	70	842	3.1e- 96	(AC006 592) hypoth etical protei n [Arabi dopsis

139624	ATU001 564	ATL8C4 5465:1 310..2 992	gap2	ATCEA4 S6742, ATCEA4 C20065 _1	99, 84	ATL8C4 5465:1 337..2 773	0.96	g34514 63	69	204	5.8e- 16	thalia na] (AL031 349) hypoth etical protei n [Schiz osacch aromyc es pombe]
139625	ATU001 565	ATL8C3 2544:2 220..1	gap2	ATCEA4 S11397 , ATCEA4 C11911 _1, ATCEA4 S34025	99, 97, 89	ATL8C3 2544:2 123..2 8	0.90	g92742 8	69	1233	3.7e- 110	(X8673 3) fis1 [Linum usitat issimu m]
139626	ATU001 566	ATL8C1 3291:1 992..3 78	gap2	ATCEA4 S748, ATCEA4 S11247	99, 98	ATL8C1 3291:1 876..3 78	0.67	g39804 07, g31932 90	69, 65	471, 708	4.6e- 42, 1.2e- 80	(AC004 561) putati ve recept or- like protei n kinase [Arabi dopsis thalia na]; (AF069 298) contai ns simila rity to a protei n kinase

139627	ATU001 567	ATL8C3 6177:1 522..1	gap2	ATCEA4 C32862 _1	99	ATL8C3 6177:1 476..2 25	0.63	g11954 65	69	58	0.9999	(U2467 7) ras- relate d protei n RAB- 4 [Trypa nosoma brucei rhodes iense]
												domain (Pfam: pkinas e.hmm, score: 165.48) , to legume lectin s beta domain (Pfam: lectin legB. hmm, score: 125.64) and legume lectin s alpha domain (Pfam: lectin legA. hmm, score: 16.72) [Arabi do... []]

139628	ATU001 568	ATL8C2 4731:2 744..1 6	gap2	ATCEA4 C7450_2, ATCEA4 S13995, ATCEA4 S30464	99, 92 97, 92	ATL8C2 4731:2 732..7 1	0.59	g45314 45	69	1063	1.8e- 94	(AC006 224) unknown protein [Arabi dopsis thalia na]
139629	ATU001 569	ATL8C4 5349:8 92..1	gap2	ATCEA4 S835, ATCEA4 C12725 0_1	99, 94			g37383 09	69	1208	4.9e- 121	(AC005 309) unknown protein [Arabi dopsis thalia na]
139630	ATU001 570	ATL8C1 0550:1 94..85 2	gap2	ATCEA4 S4666, ATCEA4 C5516_1, ATCEA4 S11517	99, 83 98, 83	ATL8C1 0550:2 54..61 4	0.94	g33186 17	68	648		(AB016 066) mitoch ondria 1 phosph ate transp orter [Arabi dopsis thalia na]
139631	ATU001 571	ATL8C1 5999:1 ..1144	gap2	ATCEA4 S30666	99	ATL8C1 5999:2 2..114 4	0.92	g42205 27	68	542	1.5e- 44	(AL035 356) putati ve protein [Arabi dopsis thalia na]
139632	ATU001 572	ATL8C4 975:1.	gap2	ATCEA4 S13884	99, 96 99, 96	ATL8C4 975:95	0.91	g23154 63	68	337	2.3e- 24	(AF016 449)

139634	ATU001 574	ATL8C7 93:1.. 2714	gap2	ATCEA4 C31626 1, ATCEA4 S6017	99, 96	ATL8C7 93:88. .2561	0.84	954418 4	68	1227	5.7e- 108	dopsis thalia na]
139635	ATU001 575	ATL8C7 567:60 17..35 1	gap2	ATCEA4 C4003_ 1, ATCEA4 S12131 , ATCEA4 C6744_ 1	99, 99, 99	ATL8C7 567:60 17..35 1	0.80	944068 09	68	454	2.2e- 98	(AC006 201) unknow n protei n [Arabi dopsis thalia na]
139636	ATU001 576	ATL8C2 8324:1 50..10 83	gap2	ATCEA4 C12363 _1	99	ATL8C2 8324:3 06..10 75	0.76	942205 27	68	563	1.3e- 37	(AL035 356) putati ve protei n [Arabi dopsis thalia na]

139637	ATU001 577	ATL8C3 3907:2 691...3 813	gap2	ATCEA4 C8313 - 1, ATCEA4 C18474 1, ATCEA4 S1902, ATCEA4 S26243	99, 97, 96, 85	ATL8C3 3907:2 879...3 779	0.75	g38920 54	68	1366	(AC002 330) putati ve glycos yltran sferas e [Arabi dopsis thalia na]
139638	ATU001 578	ATL8C6 059:87 4..1	gap2	ATCEA4 S4606	99	ATL8C6 059:83 5...355	0.75	g44540 50	68	264	(AL035 394) putati ve protei n [Arabi dopsis thalia na]
139639	ATU001 579	ATL8C4 5164:1 ..4127	gap2	ATCEA4 S12172 , ATCEA4 S5094, ATCEA4 S7561	99, 98, 88	ATL8C4 5164:3 34...38 55	0.69	g45593 33, g15101 35	68, 54	686, 402	(AC007 087) unknown n protei n [Arabi dopsis thalia na]; (D8657 4) iron- sulfur subuni t of succin ate dehydr ogenase [Plasm odium

139640	ATU001 580	ATL8C3 9013:7 71..22	gap2	ATCEA4 C12101 3_1	99	ATL8C3 9013:7 55..16 1	0.48	g45858 77	68	263	2.8e- 33	falcip arum] (AC005 850) Hypoth etical protei n [Arabi dopsis thalia na]
139641	ATU001 581	ATL8C4 5967:1 ..859	gap2	ATCEA4 S4140	99	ATL8C4 5967:6 1..859	0.44	g39351 54	68	754	1.3e- 71	(AC005 106) T25N20 .18 [Arabi dopsis thalia na]
139642	ATU001 582	ATL8C3 5161:3 195..1	gap2	ATCEA4 C29618 1, ATCEA4 S3392	99, 97			g27603 25	68	795	6.2e- 60	(AC002 130) F1N21. 10 [Arabi dopsis thalia na]
139643	ATU001 583	ATL8C4 8772:5 27..15 95	gap2	ATCEA4 C4441_1, ATCEA4 C4441_2	99, 95			g58482 5	68	427	8.0e- 38	B2 PROTEI N [Daucu s carota]
139644	ATU001 584	ATL8S8 799:51 7..1	gap2	ATCEA4 C15820 1, ATCEA4 S8383, ATCEA4 C15820 2, ATCEA4	99, 98, 97, 87	ATL8S8 799:48 8..357	1.00	g30969 39	67	192	3.6e- 18	(AL023 094) putati ve protei n [Arabi dopsis thalia

139645	ATU001 585	ATL8C3 5023:1 ..1289	gap2	S23294 ATCEA4 C14729 1, ATCEA4 C50238 _1	99, 97					g23179 08	68	352	1.7e- 41	(U8995 9) Unknown protein [Arabi dopsis thalia na]
139646	ATU001 586	ATL8C1 2876:1 ..852	gap2	ATCEA4 S10400 , ATCEA4 C10208 _1	99, 98	ATL8C1 2876:1 02..76 8	0.86			g44540 48	67	1396	9.4e- 143	(AL035 394) putative protein [Arabi dopsis thalia na]
139647	ATU001 587	ATL8C1 6255:3 25..50 00	gap2	ATCEA4 C50228 2, ATCEA4 S8116, ATCEA4 S35483	99, 91 95, 91	ATL8C1 6255:3 25..49 58	0.85			g44553 38	67	1506	5.0e- 140	(AL035 525) putative protein [Arabi dopsis thalia na]
139648	ATU001 588	ATL8C7 257:34 18..1	gap2	ATCEA4 C24529 _1	99	ATL8C7 257:33 37..99	0.77			g37765 59, g43357 64	67, 55	1019, 642	3.3e- 105, 6.2e- 57	(AC005 388) Strong similarity to gene F14J9. 26 [Arabi dopsis thalia na]; (AC006

139649	ATU001 589	ATL8C4 977:1. .2139	gap2	ATCEA4 C2103_ 1, ATCEA4 S21404	99, 87	ATL8C4 977:14 6..191 9	0.75	g22453 78	67	1884	1.9e- 144	284) putati ve WRKY DNA- bindin g protei n [Arabi dopsis thalia na]
139650	ATU001 590	ATL8C4 4527:1 ..3697	gap2	ATCEA4 C98195 1, ATCEA4 C5681_ 1	99, 98	ATL8C4 4527:1 45..36 97	0.70	g40564 65	67	594	2.1e- 136	(AC005 990) F508.4 0 [Arabi dopsis thalia na]
139651	ATU001 591	ATL8C2 2025:1 ..1800	gap2	ATCEA4 S1418, ATCEA4 C29741 _1	99, 89	ATL8C2 2025:5 2..177 6	0.41	g22621 05	67	1020	2.0e- 109	(AC002 343) unknow n protei n [Arabi dopsis thalia na]
139652	ATU001 592	ATL8C3 7032:1 84..12	gap2	ATCEA4 C8779_ 1,	99, 97, 97, 97			g42205 18	67	337		(AL035 356) hypoth

139653	ATU001 593	40	ATCEA4 S29609 , ATCEA4 S15597	99						g32928 28	67	1263	2.4e- 97	etical protei n [Arabi dopsis thalia na]
			gap2	ATL8C1 4058:1 26..10 84	ATCEA4 C50956 _1									(AL031 018) hypo thetical protei n [Arabi dopsis thalia na]
139654	ATU001 594		gap2	ATL8C3 5238:1 988..1	ATCEA4 S31118	99	ATL8C3 5238:1 742..2 3	0.97		g49143 29, g21601 73	66, 64	728, 259	2.0e- 62, 1.4e- 27	(AC005 489) F14N23 .15 [Arabi dopsis thalia na]; (AC000 132) Simila r to N. tabacu m salt- induci ble protei n (gb U0 8285). [Arabi dopsis thalia na]
139655	ATU001 595		gap2	ATL8C4 819:17	ATCEA4 C5439	99, 95, 94	ATL8C4 819:16	0.97		g44067 80	66	1497	3.5e- 127	(AC006 532)

139656	ATU001 596	25..1	gap2	1, ATCEA4 S9731, ATCEA4 C26384 _1	99, 97	74..37 7	0.91	g32584 35	66	116	2.1e- 07	putative multispanning membrane protein [Arabidopsis thaliana]
		ATL8C3 8098:3 461..1	gap2	ATCEA4 S227, ATCEA4 S30343	99, 97	ATL8C3 8098:3 461..1 99						(AP000 007) 389aa long hypothetical nuclear protein [Pyrococcus horikoshii]
139657	ATU001 597	ATL8C3 64:707 3..768	gap2	ATCEA4 C51920 _1, ATCEA4 C21439 _2, ATCEA4 S34955 , ATCEA4 C21439 _1	99, 97, 97, 96	ATL8C3 64:707 3..768	0.85	g31766 74	66	1098	2.5e- 106	(AC003 671) Containing similarity to Ste20- like kinase homolog from A. thaliana chromosome 4 contig

139658	ATU001 598	ATL8C3 6919:4 042..4 33	gap2	ATCEA4 C81684 1, ATCEA4 C9648_1	99, 98	ATL8C3 6919:4 023..1 205	0.83	g14582 45, g10551 30	66, 56	300, 141	1.7e- 24, 6.1e- 08	gb Z97 336. [Arabi dopsis thalia na] (U6483 4) coded for by C. elegan s cDNA cm17a1 ; coded for by C. elegan s cDNA cm7g1; coded for by C. elegan s cDNA CEMSE2 6F; simila r to methyl transf erases [Caeno rhabdi tis elegan sl]; (U3999 8) coded for by C. elegan s cDNA
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139660	ATU001 600	ATL8C3 7835:1 645..2 646	gap2	ATCEA4 C8510_1	99	ATL8C3 7835:1 726..2 282	0.81	g44544 73	66	559	2.7e- 55	[Arabi dopsis thalia na] (AC006 234) putati ve beta- expans in protei n [Arabi dopsis thalia na]
139661	ATU001 601	ATL8C1 4499:1 805..1	gap2	ATCEA4 C57357_1	99	ATL8C1 4499:1 124..2 6	0.72	g26606 73, g39129 31	66, 33	758, 719	3.4e- 73, 1.8e- 68	(AC002 342) unknow n protei n [Arabi dopsis thalia na]; (AF001 308) putati ve CHP- rich zinc finger protei n simila r to T10M13 .18 [Arabi dopsis thalia na]

139662	ATU001 602	ATL8C3 1339:2 667..1	gap2	ATCEA4 C17881 1, ATCEA4 S7630, ATCEA4 C10429 7_1	99, 96 98, 96	ATL8C3 1339:2 614..9 6	0.72	g21911 52	66	2807	1.4e- 276	(AF007 269) A IG00 2N01.3 1 gene produc t [Arabi dopsis thalia na]
139663	ATU001 603	ATL8C9 290:28 43..1	gap2	ATCEA4 C7633_1	99	ATL8C9 290:28 43..41	0.72	g45593 85	66	1341		(AC006 526) putati ve cyclic nucleo tide- regula ted ion channe l protei n [Arabi dopsis thalia na]
139664	ATU001 604	ATL8C1 7183:1 ..1431	gap2	ATCEA4 C29076 1, ATCEA4 S35651	99, 92	ATL8C1 7183:1 10..13 82	0.68	g45196 71	66	292	3.2e- 23	(AB017 693) transf actor [Nicot iana tabacu m]
139665	ATU001 605	ATL8C4 5109:1 590..1 78	gap2	ATCEA4 S26907 , ATCEA4 C11755 2_1	99, 99	ATL8C4 5109:1 547..2 78	0.55	g45126 51	66	678	3.7e- 58	(AC007 048) putati ve tyrosi ne transa minase

139666	ATU001 606	ATL8C1 3642:1 ..2199	gap2	ATCEA4 C26784 _1	99	ATL8C1 3642:1 612..6 2	0.49	g38735 50	66	141	0.95	[Arabi dopsis thalia na] (AL033 534) serine -rich protei n [Schiz osacch aromyc es pombe]
139667	ATU001 607	ATL8C2 320:1. ..2007	gap2	ATCEA4 C10962 _1	99			g38222 25	66	188	1.9e- 19	(AF079 183) RING- H2 finger protei n RHGla [Arabi dopsis thalia na]
139668	ATU001 608	ATL8C2 7113:1 ..262	gap2	ATCEA4 C16928 _1	99			g30627 91	66	254	4.1e- 21	(AB010 433) Lipid transf er protei n [Brass ica rapa]
139669	ATU001 609	ATL8C1 0890:2 455..1	gap2	ATCEA4 S10986	99	ATL8C1 0890:2 426..7 72	0.78	g37575 16	65	1961	1.0e- 191	(AC005 167) putati ve TMV resist ance protei n

139670	ATU001 610	ATL8C4 5149:9 55..1	gap2	ATCEA4 C1078_1, ATCEA4 S29214	99, 87	ATL8C4 5149:8 77..10	0.76	g16203 71	65	923	1.8e- 99	[Arabi dopsis thalia na] (Y0878 2) peroxi dase ATP23a [Arabi dopsis thalia na]
139671	ATU001 611	ATL8C1 4449:1 ..7469	gap2	ATCEA4 S24105 , ATCEA4 C58256 1, ATCEA4 C74285 1, ATCEA4 C15842 1, ATCEA4 C18641 1	99, 98, 98, 98, 87	ATL8C1 4449:2 69..74 69	0.76	g44553 68	65	1643	1.2e- 160	(AL035 524) pectin estera se like protei n [Arabi dopsis thalia na]
139672	ATU001 612	ATL8C3 4335:1 ..1452	gap2	ATCEA4 S6323, ATCEA4 C10090 4 1, ATCEA4 S32790	99, 95, 87	ATL8C3 4335:1 42..14 29	0.68	g46782 62	65	1332	6.2e- 127	(AL049 657) argini nosucc inate syntha se- like protei n [Arabi dopsis thalia na]
139673	ATU001 613	ATL8C3 6899:9 29..1	gap2	ATCEA4 C17735 1	99	ATL8C3 6899:7 65..10	0.63	g34137 04	65	340	1.3e- 34	(AC004 747) hypoth

								4									etical protei n [Arabi dopsis thalia na]
139674	ATU001 614	ATL8C3 0514:4 042..3 369	gap2	ATCEA4 C30251 _1_	99					65	760	2.3e- 51	(AC006 951) putati ve MAP kinase phosph atase [Arabi dopsis thalia na]				
139675	ATU001 615	ATL8C9 45:687 ..1672	gap2	ATCEA4 C2242_1, ATCEA4 C69015 _1, ATCEA4 C36029 _1, ATCEA4 S5292	99, 95, 92, 90					65	152	1.5e- 10	hypoth etical protei n 77 - common tobacc o chloro plast [Nicot iana tabacu m]				
139676	ATU001 616	ATL8S9 796:56 1..1	gap2	ATCEA4 S13915	99					65	436	3.8e- 46	(AC004 482) cold acclim ation protei n WCOR41 3-like [Arabi dopsis thalia na]				
139677	ATU001	ATL8C1	gap2	ATCEA4	99					64	1022	1.6e-	(Z7164				

	617	1712:1 ..1940	gap2	S312		1712:9 6..183 8	57				92	0) DnaJ homolog [Pisum sativum]
139678	ATU001 618	ATL8C3 5661:2 186..1	gap2	ATCEA4 S950	99	ATL8C3 5661:1 942..3 19	0.87	g36435 98	64	620	7.8e- 52	(AC005 395) putative poly(A)) polymerase [Arabidopsis thaliana]
139679	ATU001 619	ATL8C2 0209:1 403..1	gap2	ATCEA4 C584_1 , ATCEA4 S29010 , ATCEA4 C586_1 , ATCEA4 S32560	99, 85, 85, 83	ATL8C2 0209:1 303..1 15	0.81	g22810 95	64	809	2.3e- 88	(AC002 333) cysteine synthase, cpACS1 [Arabidopsis thaliana]
139680	ATU001 620	ATL8C4 582:47 83..33 46	gap2	ATCEA4 S26897 , ATCEA4 C10192 1, ATCEA4 S28992	99, 93, 88	ATL8C4 582:47 82..34 45	0.74	g31717 31	64	107	0.0001 3	(AJ006 406) AgPET8 [Eremothecium gossypii]
139681	ATU001 621	ATL8C3 319:20 47..1	gap2	ATCEA4 C9393_3, ATCEA4 S4760	99, 96	ATL8C3 319:14 64..93	0.72	g28277 06	64	193	1.4e- 14	(AL021 684) predicted protein [Arabidopsis]

139682	ATU001 622	ATL8C4 9068:1 568..5 44	gap2	ATCEA4 C25588 1, ATCEA4 C35446 _1	99, 85	ATL8C4 9068:1 507..5 44	0.68	g45052 35	64	273	2.7e- 27	dopsis thalia na]
139683	ATU001 623	ATL8C1 6466:4 276..1	gap2	ATCEA4 S2386, ATCEA4 C19048 _1, ATCEA4 S6213, ATCEA4 C62542 _1	99, 97, 96, 92	ATL8C1 6466:4 215..6 04	0.58	g22449 29	64	345	5.8e- 25	(Z9733 9) unname d protei n produc t [Arabi dopsis thalia na]
139684	ATU001 624	ATL8C2 863:29 90..16 54	gap2	ATCEA4 S1324	99	ATL8C2 863:27 25..16 54	0.54	g33373 62	64	254	4.1e- 07	(AC004 481) unknow n protei n [Arabi dopsis thalia na]
139685	ATU001 625	ATL8C3 9093:1 ..562	gap2	ATCEA4 C43314 _1	99			g48039 33	64	315	8.9e- 29	(AC006 264) putati ve diseas e resist ance respon se protei

139686	ATU001 626	ATL8C2 2069:1 ..814	gap2	ATCEA4 S12636	99					g22450 79	64	442	6.2e- 44	(Z9734 3) hypoth etical protei n [Arabi dopsis thalia na]
139687	ATU001 627	ATL8C1 1639:2 621..1 45	gap2	ATCEA4 S1553	99	ATL8C1 1639:2 514..1 45	0.85	g49143 17	63	745	1.1e- 42			(AG005 489) F14N23 .3 [Arabi dopsis thalia na]
139688	ATU001 628	ATL8C1 1115:1 ..1498	gap2	ATCEA4 C46363 1, ATCEA4 S35001	99, 86	ATL8C1 1115:1 09..12 90	0.84	g28326 61	63	532	4.3e- 33			(AL021 710) pherop horin - like protei n [Arabi dopsis thalia na]
139689	ATU001 629	ATL8C4 9821:2 099..3 01	gap2	ATCEA4 C11707 _1	99	ATL8C4 9821:1 922..3 01	0.80	g32647 78	63	870	3.6e- 83			(AF072 536) H- protei n promot er bindin g factor -1

139693	ATU001 633	ATL8C1 0704:5 23..10 75	gap2	ATCEA4 S28934 , ATCEA4 C16134 4_1	99, 96	ATL8C1 0704:5 25..98 1	0.51	g23426 86	63	763	8.0e- 78	50kD subunit - human [1]; (AC005 724) unknown protein [Arabi dopsis thalia na]
139694	ATU001 634	ATL8C3 0073:3 71..17	gap2	ATCEA4 C14870 1,	99, 94	ATL8C3 0073:5 96..10	0.48	g43357 73	63	174	1.4e- 12	(AC006 284) unknown

139695	ATU001 635	33	gap2	ATCEA4 C52617 _1	99	ATL8C1 6369:1 057..6 86	0.41	g45862 57	63	125	4.7e- 07	n protei n [Arabi dopsis thalia na]
139696	ATU001 636	ATL8C1 6369:1 350..1	gap2	ATCEA4 S26342	99	ATL8C1 6369:1 057..6 86	0.41	g45862 57	63	125	4.7e- 07	(AI049 640) putati ve protei n [Arabi dopsis thalia na]
139697	ATU001 637	ATL8C2 7575:1 201..1	gap2	ATCEA4 C5800 _1	99	ATL8C2 7575:1 201..1		g12002 05	63	370		(X9575 3) DAG [Antir rhinum majus]
139697	ATU001 637	ATL8C3 6699:1 ..1775	gap2	ATCEA4 C12664 _1, ATCEA4 S660	99, 82	ATL8C3 6699:1 ..1775		g31766 87	63	2250	6.2e- 239	(AC003 671) Strong simila rity to trehal ose-6- phosph ate syntha se homolo g from A. thalia na chromo some 4 contig gb Z97 344. ESTs

139698	ATU001 638	ATL8C4 4282:9 9..254 1	gap2	ATCEA4 S1613, ATCEA4 C5271_1, ATCEA4 C92191_1	99, 96, 96, 96	ATL8C4 4282:9 9..228 3	0.79	g14018 5	62	227	8.0e- 17	gb H37 594, gb R65 023, gb H37 578 and gb R64 855 come from this gene. [Arabi dopsis thalia na]
139699	ATU001 639	ATL8C4 8676:1 677..1	gap2	ATCEA4 C32724 1, ATCEA4 S11282	99, 94	ATL8C4 8676:1 649..3 9	0.76	g28326 23	62	619	1.9e- 58	(AL021 711) protei n kinase - like protei n [Arabi dopsis thalia na]
139700	ATU001 640	ATL8C3 0648:1 ..1072	gap2	ATCEA4 C2149_1, ATCEA4 S30723	99, 96	ATL8C3 0648:2 50..72 3	0.75	g23885 71	62	848	2.1e- 90	(AC000 098) Strong simila rity to Arabid

139701	ATU001 641	ATL8C4 1635:7 17..1	gap2	ATCEA4 C34649 1, ATCEA4 S26663	99, 98	ATL8C4 1635:5 43..21 7	0.74	g14189 90	62	90	6.0e- 10	opsis peroxi dase ATPERO X7A (gb X9 8321). [Arabi dopsis thalia na]
139702	ATU001 642	ATL8C2 0491:1 ..1475	gap2	ATCEA4 S287	99	ATL8C2 0491:7 9..142 7	0.73	g22448 68	62	507	1.2e- 52	(Z9733 7) cytoch rome P450 [Arabi dopsis thalia na]
139703	ATU001 643	ATL8C1 0475:6 932..4 519	gap2	ATCEA4 C26353 1, ATCEA4 C25033 1	99, 99	ATL8C1 0475:6 777..4 519	0.72	g13505 08, g22450 11	62, 36	112, 262	(L4774 1) mitoch ondria - locali zed low molecu lar weight heat shock protei n 23.5 [Picea	

139704	ATU001 644	ATL8C5 514:27 52..1	gap2	ATCEA4 C12123 1, ATCEA4 S15267	99, 99	ATL8C5 514:27 52..15 2	0.69	g38819 76	62	330	9.5e- 25	glauca l; (Z9734 1) hypoth etical protei n [Arabi dopsis thalia na]
139705	ATU001 645	ATL8C1 0339:1 245..1	gap2	ATCEA4 C27743 _1	99	ATL8C1 0339:1 187..1 27	0.42	g29795 50	62	1463		(AC003 680) putati ve 7- ethoxy coumar in O- deethyl lase [Arabi dopsis thalia na]
139706	ATU001 646	ATL8C3 7267:1 ..772	gap2	ATCEA4 S29069	99			g32693 01	62	425		(AL030 978) putati ve protei n [Arabi dopsis thalia na]
139707	ATU001	ATL8C4	gap2	ATCEA4	99			g45824	62	444	1.0e-	(AC007

	647	7091:8 30..1		S11395					55			45	071) putative receptor protein kinase [Arabidopsis thaliana]
139708	ATU001 648	ATL8C1 6986:9 92..1	gap2	ATCEA4 C13879 1, ATCEA4 C17438 1_	99, 90				g31526 05	62	852	1.8e- 90	(AC004 482) hypothetical protein [Arabidopsis thaliana]
139709	ATU001 649	ATL8C1 9464:5 07..1	gap2	ATCEA4 C5647_2, ATCEA4 C5647_3	99, 98				g40975 69	62	221	9.2e- 18	(U6491 5) GMFP4 [Glycine max]
139710	ATU001 650	ATL8C9 964:29 3..145 5	gap2	ATCEA4 S7200	99		ATL8C9 964:39 9..143 8	0.97	g28299 03	61	1511	3.8e- 142	(AC002 311) unknown protein [Arabidopsis thaliana]
139711	ATU001 651	ATL8C4 7123:1 ..779	gap2	ATCEA4 C23234 1_	99		ATL8C4 7123:9 8..679	0.97	g45038 17	61	173	5.1e- 05	follicular lymphoma variant transl

139712	ATU001 652	ATL8C6 8:1403 ..1	gap2	ATCEA4 C17124 1, ATCEA4 S2186, ATCEA4 S32711 , ATCEA4 C29965 1	99, 99, 95, 84	ATL8C6 8:1391 ..239	0.95	g43252 82	61	452	6.8e- 55	ocatio n 1 [Homo sapien s]
139713	ATU001 653	ATL8C1 0265:1 ..1586	gap2	ATCEA4 C32642 1, ATCEA4 S16051	99, 97	ATL8C1 0265:1 51..14 73	0.93	g49144 28	61	1350		(AL050 351) putati ve protei n [Arabi dopsis thalia na]
139714	ATU001 654	ATL8C1 6946:2 756..1	gap2	ATCEA4 C26087 1, ATCEA4 S10315	99, 93	ATL8C1 6946:2 744..1 0	0.92	g39132 18	61	1464	4.3e- 109	MAGNES IUM- CHELAT ASE SUBUNI T CHLD PRECUR SOR (MG- PROTOP ORPHYR IN IX CHELAT ASE) (MG- CHELAT ASE SUBUNI T D)

139715	ATU001 655	ATL8C4 6377:2 721..1 487	gap2	ATCEA4 S256, ATCEA4 S36020 , ATCEA4 C3744_1	99, 89 97, 89	ATL8C4 6377:2 719..1 854	0.90	g26187 01	61	414	6.6e- 39	[Pisum sativu m] (AC002 510) hypotheno- etical protein [Arabi dopsis thaliana]
139716	ATU001 656	ATL8C3 4358:1 791..4 258	gap2	ATCEA4 C7983_1, ATCEA4 C4713_1, ATCEA4 C58270_1	99, 96 98, 96	ATL8C3 4358:1 864..4 065	0.90	g44552 50	61	368	4.7e- 25	(AL035 523) putative protein [Arabi dopsis thaliana]
139717	ATU001 657	ATL8C4 5377:1 609..1	gap2	ATCEA4 C11477_1, ATCEA4 S12268	99, 90	ATL8C4 5377:1 608..8 3	0.87	g38781 19	61	579	1.9e- 41	(Z4906 8) similar to GTP-binding protein; cDNA EST EMBL:M 89111 comes from this gene; cDNA EST EMBL:D 27709 comes

139718	ATU001 658	ATL8C2 3135:1 804..3 28	gap2	ATCEA4 S13997 , ATCEA4 S2244, ATCEA4 S14003	99, 97 99, 97	ATL8C2 3135:1 789..3 28	0.84	g30753 90	61	204	1.3e- 10	(AC004 484) protei n kinase ARSK1 [Arabi dopsis thalia na]	from this gene; cDNA EST EMBL:D 27708 comes from this gene; cDNA EST EMBL:D 73788 comes from this gene; cDNA EST
139719	ATU001 659	ATL8C5 0220:1 851..1	gap2	ATCEA4 C11460 1, ATCEA4 S35709 , ATCEA4 S11217 , ATCEA4 C4989 1,	99, 95, 92, 87, 85	ATL8C5 0220:1 196..5 7	0.42	g45824 36	61	1688	6.0e- 174	(AC007 196) unknow n protei n [Arabi dopsis thalia na]	from this gene; cDNA EST EMBL:D 27708 comes from this gene; cDNA EST

139720	ATU001 660	ATL8C5 994:1. .687	gap2	ATCEA4 S7917	99, 89	ATL8C5 994:25 ..624	0.90	g40069 34	60	463	(AJ012 571) glutathione transferase [Arabidopsis thaliana]
139721	ATU001 661	ATL8C2 7651:1 ..1154	gap2	ATCEA4 C70871 1, ATCEA4 C96880 1	99, 98	ATL8C2 7651:1 07..10 64	0.89	g28800 49	60	775	(AC002 340) hypothetical protein [Arabidopsis thaliana]
139722	ATU001 662	ATL8C3 2669:1 ..1484	gap2	ATCEA4 S10299 1, ATCEA4 C35107 1, ATCEA4 C28461 1	99, 85, 83	ATL8C3 2669:6 4..144 9	0.88	g44903 10	60	1380	(AL035 678) somatocyt embryogenesis receptor-like kinase-like protein [Arabidopsis thaliana]
139723	ATU001 663	ATL8C3 1647:1 135..1 662	gap2	ATCEA4 C8818 1, ATCEA4 S8359	99, 88	ATL8C3 1647:1 216..1 585	0.85	g17238 28	60	209	HYPOPHOSPHATASE 30.8 KD PROTEIN

139724	ATU001 664	ATL8C3 4263:2 002..1	gap2	ATCEA4 C802_1 , ATCEA4 S31234 , ATCEA4 S35791	99, 86, 82	ATL8C3 4263:1 910..5 31	0.85	g54401 8	60	1437	4.0e- 145	N IN DUP2- TIF463 2 INTERG ENIC REGION [Sacch aromyc es cerevi siae]
139725	ATU001 665	ATL8C3 7694:2 99..22 14	gap2	ATCEA4 S2957, ATCEA4 C2394_1, ATCEA4 C13147 6_1	99, 98, 95	ATL8C3 7694:1 153..2 057	0.84	g34829 19	60	584	3.9e- 63	(AC003 970) Putati ve protei n kinase [Arabi dopsis thalia na]
139726	ATU001 666	ATL8C2 4289:2 33..47 23	gap2	ATCEA4 C728_1 , ATCEA4 C728_3 , ATCEA4 S32555	99, 97, 95	ATL8C2 4289:6 05..23 99, ATL8C2 4289:2 560..4 574	0.81, 0.90	g16993 70	60	593	7.8e- 50	(S8262 0) prolid ase=pe ptidas e D/imid opepti dase {EC 3.4.13 .9} [Mus

139727	ATU001 667	ATL8C4 5308:6 95...83 22	gap2	ATCEA4 S4599, ATCEA4 S27877	99, 98	ATL8C4 5308:6 95...83 14	0.81	g11291 73, g38778 58	60, 58	486, 64	4.6e- 31, 8.2e- 10	sp.] (X9408 2) KLP2 protei n [Xenop us laevis]; (Z3480 1) Simila rity with drosoph ila MSP- 300 protei n (PIR acc. no. S30431) [Caeno rhabdi tis elegan s]
139728	ATU001 668	ATL8C6 690:49 0...323 7	gap2	ATCEA4 C36799 1, ATCEA4 C23820 1	99, 89	ATL8C6 690:49 0...317 4	0.79	g16518 28	60	660	1.4e- 52	(D9090 0) dihydr olipoa mide dehydr ogenas e [Synec hocyst is sp.]
139729	ATU001 669	ATL8C3 9776:1 ..774	gap2	ATCEA4 S13718	99	ATL8C3 9776:1 03...48	0.73	g33193 41	60	406	1.9e- 42	(AF077 407) simila

139730	ATU001 670	ATL8C4 832:46 88..1	gap2	ATCEA4 C760_1 , ATCEA4 S13200 , ATCEA4 C89870 1, ATCEA4 S1949, ATCEA4 S29605 , ATCEA4 C760_4 , ATCEA4 C17751 1, ATCEA4 C760_2	99, 98, 97, 95, 92, 91, 86, 83	ATL8C4 832:45 29..13 1	0.69	g22621 59	60	684	1.5e- 47	(AC002 329) predic ted protei n simila r to S.pomb e protei n C5H10. 03 [Arabi dopsis thalia na]
139731	ATU001 671	ATL8C1 4626:5 6..150 1	gap2	ATCEA4 C19384 2, ATCEA4 C19384	99, 98	ATL8C1 4626:5 6..130 3	0.67	g37859 83	60	338	2.1e- 31	(AC005 560) hypoth etical protei

139732	ATU001 672	ATL8C4 9507:1 389..1	gap2	ATCEA4 C32768 _1	99	ATL8C4 9507:1 341..5 4	0.62	g45393 70	60	783	1.5e- 76	n [Arabi dopsis thalia na] AL049 525) UDP- galact ose 4- epimer ase- like protei n [Arabi dopsis thalia na]
139733	ATU001 673	ATL8C4 2199:4 720..2 13	gap2	ATCEA4 C18268 _1, ATCEA4 S1979	99, 96	ATL8C4 2199:4 638..2 13	0.57	g34260 51	60	716	5.8e- 37	(AC005 168) hypoth etical protei n [Arabi dopsis thalia na]
139734	ATU001 674	ATL8C4 6601:8 24..17 35	gap2	ATCEA4 C2431 _1	99			g21297 73	60	767	1.0e- 71	xylogl ucan endotr ansgly cosyla se- relate d protei n XTR3 - Arabid opsis thalia na (fragm

139735	ATU001 675	ATL8C2 7568:2 679..1	gap2	ATCEA4 S3277, ATCEA4 C11440 _1	99, 91					g21941 26	60	913	(AC002 062) EST gb T43 335 comes from this gene. [Arabi dopsis thalia na]
139736	ATU001 676	ATL8C3 4329:1 ..774	gap2	ATCEA4 C5332_1	99	ATL8C3 4329:1 22..77 4	0.98			g45394 57	59	219	(AL049 500) heat shock transc riptio n factor -like protei n [Arabi dopsis thalia na]
139737	ATU001 677	ATL8C4 5152:3 04..30 17	gap2	ATCEA4 S1264, ATCEA4 C4063_1	99, 96	ATL8C4 5152:3 04..30 03	0.94			g26513 05	59	296	(AC002 336) hypoth etical protei n [Arabi dopsis thalia na]
139738	ATU001 678	ATL8C3 0719:1	gap2	ATCEA4 C12329	99, 97,	ATL8C3 0719:7	0.89			g28326 25	59	1149	(AL021 711) 5.3e- 111

139745	ATU001 685	ATL8C1 5521:1 871..1	gap2	ATCEA4 C14546 0_1	99	ATL8C1 5521:1 814..1 89	0.61	g29824 52	59	2851	4.6e- 259	[Arabi dopsis thalia na] (AL022 223) recept or protei n kinase -like protei n [Arabi dopsis thalia na]
139746	ATU001 686	ATL8C9 406:15 95..1	gap2	ATCEA4 C29448 1, ATCEA4 C5120_ 1	99, 98	ATL8C9 406:12 23..30 5	0.61	g26550 98	59	1113	1.6e- 102	(AF023 472) peptid e transp orter [Horde um vulgar e]
139747	ATU001 687	ATL8C4 6627:1 892..3 094	gap2	ATCEA4 C30775 1, ATCEA4 S12667	99, 98			g26512 96	59	305	1.4e- 17	(AC002 336) b-zip DNA- bindin g protei n [Arabi dopsis thalia na]
139748	ATU001 688	ATL8C3 5193:1 287..1	gap2	ATCEA4 C16662 1, ATCEA4 S322	99, 99			g41917 75	59	757	4.1e- 24	(AC005 917) putati ve acyl-

139749	ATU001 689	ATL8C2 8063:9 25..1	gap2	ATCEA4 C43593 _1	99					g25831 32	59	114	4.0e- 10	(AC002 387) unknown protein [Arabi dopsis thalia na]	CoA choles terol acyltr ansfer ase [Arabi dopsis thalia na]
139750	ATU001 690	ATL8C3 4148:1 ..1815	gap2	ATCEA4 S5594, ATCEA4 C2261_1, ATCEA4 C64928 _1, ATCEA4 S6141	99, 98, 96, 84					g45860 53	59	683	1.9e- 65	(AC007 020) putati ve lacass e [Arabi dopsis thalia na]	
139751	ATU001 691	ATL8C2 4506:1 180..1 671	gap2	ATCEA4 S34446 , ATCEA4 C6241_1, ATCEA4 S13729 , ATCEA4 S8213	99, 98, 88, 83					g37383 40	59	443	3.2e- 44	(AC005 170) GMP syntha se- like protei n [Arabi dopsis thalia na]	
139752	ATU001 692	ATL8C2 364:22 88..1	gap2	ATCEA4 C2179_1	99					g37859 75	58	248	1.4e- 19	(AC005 560) hypo	

139753	ATU001 693	ATL8C1 9228:1 ..1094	gap2	ATCEA4 S32163	99	ATL8C1 9228:2 13..93 2	0.89	g44552 37	58	729	3.9e- 84	etical protei n [Arabi dopsis thalia na]
139754	ATU001 694	ATL8C3 6600:2 503..4 476	gap2	ATCEA4 S2377	99	ATL8C3 6600:3 067..4 447	0.88	g17341 9	58	703	2.6e- 65	(L1157 4) p68 RNA helica se [Schiz osacch aromyc es pombe]
139755	ATU001 695	ATL8C1 5935:5 425..3 8	gap2	ATCEA4 S469, ATCEA4 C4852 1	99, 94	ATL8C1 5935:5 380..3 8	0.81	g21314 34	58	1704	2.0e- 186	hypoth etical protei n YDR334 w - yeast (Sacch aromyc es cerevi siae) [Sacch aromyc

139760	ATU001 700	ATL8S1 2259:1 ..560	gap2	ATCEA4 S5079	99	ATL8S1 2259:4 7..552	0.50	g29795 56	58	372	1.7e- 39	(AC003 680) unknown protein [Arabi dopsis thalia na]
139761	ATU001 701	ATL8C3 5337:1 ..799	gap2	ATCEA4 C53113 _1	99			g38920 54	58	995	2.5e- 101	(AC002 330) putative glycosyl transfer sferase [Arabi dopsis thalia na]
139762	ATU001 702	ATL8C1 1134:8 84..1	gap2	ATCEA4 C9714_1, ATCEA4 S11205, ATCEA4 S8658	99, 96, 85			g20621 67	58	339	1.8e- 15	(AC001 645) Proline- rich protein in APG isolated [Arabi dopsis thalia na]
139763	ATU001 703	ATL8C3 8999:1 ..1023	gap2	ATCEA4 C4771_1	99	ATL8C3 8999:5 0..881	0.98	g27656 67	57	525	7.4e- 41	(Z8331 2) 3'(2') ,5'- bispho

139764	ATU001 704	ATL8C1 1773:1 ..2644	gap2	ATCEA4 C34740 1, ATCEA4 S26675 , ATCEA4 C12281 1 _	99, 95, 87	ATL8C1 1773:7 7..258 6	0.97	g11433 9	57	1739	2.9e- 120	PLASMA MEMBRANE ATPASE 3 (PROTO N PUMP) [Arabi dopsis thalia na]
139765	ATU001 705	ATL8C2 2117:1 652..6 32	gap2	ATCEA4 C8451_ 1, ATCEA4 S31810	99, 92	ATL8C2 2117:1 343..6 32	0.94	g29807 60	57	191	6.6e- 16	AL022 198) putati ve protei n [Arabi dopsis thalia na]
139766	ATU001 706	ATL8C4 458:26 12..1	gap2	ATCEA4 S1008	99	ATL8C4 458:25 19..74	0.90	g39351 68	57	1234	1.8e- 105	(AC004 557) F17L21 .11 [Arabi dopsis thalia na]
139767	ATU001 707	ATL8C4 5102:1 ..1233	gap2	ATCEA4 S2852, ATCEA4 C23052 1, ATCEA4 C29597 1	99, 97, 86	ATL8C4 5102:8 0..208 , ATL8C4 5102:4 65..10 90	0.87, 0.49	g42042 57	57	1399	3.3e- 132	(AC005 223) 5493 [Arabi dopsis thalia na]

139768	ATU001 708	ATL8C2 4207:1 259..7 7	gap2	ATCEA4 S12709 , ATCEA4 C6507 1, ATCEA4 C68605 1, ATCEA4 C68605 2	99, 99, 94, 93	ATL8C2 4207:1 031..3 98	0.86	g28275 36	57	288	3.8e- 23	(AL021 633) hypoth etical protei n [Arabi dopsis thalia na]
139769	ATU001 709	ATL8C4 5240:1 ..2310	gap2	ATCEA4 S3122, ATCEA4 S10368	99, 98	ATL8C4 5240:7 2..226 4	0.86	g28966 95	57	73	6.7e- 06	(AL021 897) fadD14 [Mycob acteri um tuberc ulosis]
139770	ATU001 710	ATL8C3 5063:9 51..1	gap2	ATCEA4 C1323 1, ATCEA4 S32670	99, 94	ATL8C3 5063:9 01..12 5	0.78	g13619 82	57	1352	1.9e- 125	4- coumar ate-- CoA ligase (EC 6.2.1. 12) - Arabid opsis thalia na [Arabi dopsis thalia na]
139771	ATU001 711	ATL8C9 934:96 5..1	gap2	ATCEA4 C1307 1, ATCEA4 C18551 1	99, 87	ATL8C9 934:87 9..8	0.76	g11684 93	57	776	2.3e- 82	ARGINA SE [Arabi dopsis thalia na]
139772	ATU001 712	ATL8C1 1300:9	gap2	ATCEA4 S4048,	99, 94	ATL8C1 1300:4	0.75	g33866 09	57	507	3.5e- 36	(AC004 665)

139773	ATU001 713	3..967	ATCEA4 C32973 _1	99	ATL8C4 6567:1 27..69 1	82..89 2	0.71	g38772 52	57	139	6.0e- 05	putative DNA- binding protein [Arabidopsis thaliana]
139774	ATU001 714	ATL8C1 2852:1 ..1367	ATCEA4 C12106 _1, ATCEA4 C24414 _1	99, 97	ATL8C1 2852:1 03..13 53	ATL8C1 6567:1 27..69 1	0.65	g42635 27	57	248	1.1e- 20	(AC004 044) hypothetical protein [Arabidopsis thaliana]
139775	ATU001 715	ATL8C9 602:1. ..1518	ATCEA4 C11801 6_1, ATCEA4 C11832 5_1	99, 94	ATL8C9 602:93 ..1489	ATL8C9 602:93 ..1489	0.60	g21601 89	57	867	1.6e- 74	(AC000 132) Similarto A. thaliana receptor- like protein kinase (gb RL K5 ARA

139776	ATU001 716	ATL8C3 1254:2 658..1 38	gap2	ATCEA4 S29583 , ATCEA4 C11848 1, ATCEA4 C13633 2_1	99, 94, 90	ATL8C3 1254:1 422..1 38	0.56	g45392 42	57	141	1.4e- 11	TH). ESTs gb ATT S0475, gb ATT S4362 come from this gene. [Arabi dopsis thalia na]
139777	ATU001 717	ATL8C1 5761:1 460..1	gap2	ATCEA4 C32715 _1	99	ATL8C1 5761:1 264..2 22	0.47	g44907 56	57	680	3.6e- 63	(AL035 708) hypoth etical protei n [Schiz osacch aromyc es pombe]
139778	ATU001 718	ATL8C1 2628:1 124..1	gap2	ATCEA4 S2621	99			g46893 76	57	850	8.9e- 87	(AF138 872) zinc finger protei n 3 [Arabi dopsis thalia na]

139779	ATU001 719	ATL8C3 7043:2 783..7 89	gap2	ATCEA4 C13385 1, ATCEA4 S36138	99, 91				941159 13	57	470		thalia na]
139780	ATU001 720	ATL8C2 6088:4 607..2 819	gap2	ATCEA4 C78152 1 1	99	ATL8C2 6088:3 342..3 089	1.00		945875 85	56	595	1.0e- 47	(AC007 232) hypoth etical protein [Arabi dopsis thalia na]
139781	ATU001 721	ATL8C1 3627:3 26..11 29	gap2	ATCEA4 C14642 1 1	99				923885 83	57	1122	3.1e- 90	(AC000 098) Simila r to Synech ocysti

139782	ATU001 722	ATL8C1 2325:1 98..13 76	gap2	ATCEA4 S3474	99					g32978 21	57	1228	1.5e- 125	(AL031 032) extens in- like protei n [Arabi dopsis thalia na]	s hypo thetical protei n (gb D9 0908). [Arabi dopsis thalia na]
139783	ATU001 723	ATL8C1 7642:5 51..18 99	gap2	ATCEA4 C83015 1, ATCEA4 C52324 1	99, 82	ATL8C1 7642:5 51..18 09	0.97			g31932 96	56	1041	4.3e- 110	(AF069 298) simila r to pectin esterase [Arabi dopsis thalia na]	(AF069 298) simila r to pectin esterase [Arabi dopsis thalia na]
139784	ATU001 724	ATL8C3 2055:9 72..1	gap2	ATCEA4 C11758 1, ATCEA4 S12957 , ATCEA4 S17204	99, 89 96, 89	ATL8C3 2055:8 20..28 5	0.96			g33416 88	56	715	1.5e- 54	(AC003 672) putative casein kinase II beta subunit [Arabi dopsis]	(AC003 672) putative casein kinase II beta subunit [Arabi dopsis]

139785	ATU001 725	ATL8C1 4806:3 337..1	gap2	ATCEA4 S648, ATCEA4 C66138 2, ATCEA4 C66138 1, ATCEA4 C18127 1	99, 96, 91, 84	ATL8C1 4806:3 290..1 459	0.93	g29242 58	56	2531	5.4e- 265	thalia na]
139786	ATU001 726	ATL8C6 933:1. .2022	gap2	ATCEA4 S10651 , ATCEA4 C13355 4_1, ATCEA4 S30167 , ATCEA4 S36250 , ATCEA4 C7470_ 1, ATCEA4 C62456 1	99, 98, 98, 97, 95, 93	ATL8C6 933:86 ..1690	0.84	g38735 50	56	78	0.0062	(Z0004 4) RNA polyme rase beta'' subuni t [Nicot iana tabacu m] (AL033 534) serine -rich protei n [Schiz osacch aromyc es pombe]
139787	ATU001 727	ATL8C7 45:160 ..922	gap2	ATCEA4 S13904	99	ATL8C7 45:160 ..750	0.82	g35401 81	56	622	9.9e- 50	(AC004 122) Unknow n protei n [Arabi dopsis thalia na]
139788	ATU001 728	ATL8C1 3421:1 856..1	gap2	ATCEA4 S1598, ATCEA4 S10619	99, 96	ATL8C1 3421:1 751..1 11	0.80	g29470 63	56	464	1.4e- 43	(AC002 521) putati ve

139789	ATU001 729	ATL8C5 325:42 01..23 01	gap2	ATCEA4 C4155_1, ATCEA4 S11685, ATCEA4 S31223	99, 98 94, 88	ATL8C5 325:41 96..26 95	0.78	g43143 70	56	660	4.0e- 40	Ser/Th r protei n kinase [Arabi dopsis thalia na]
139790	ATU001 730	ATL8C2 4509:1 ..950	gap2	ATCEA4 C45785 1, ATCEA4 S10308	99, 98	ATL8C2 4509:7 9..950	0.76	g44690 22	56	1354	1.3e- 138	(AL035 602) cytoch rome P450- like protei n [Arabi dopsis thalia na]
139791	ATU001 731	ATL8C4 0857:1 ..1869	gap2	ATCEA4 C93106 1, ATCEA4 C5846_1	99, 97	ATL8C4 0857:6 66..18 01	0.72	g48862 82	56	130	1.1e- 07	(AL050 300) putati ve protei n [Arabi dopsis thalia na]
139792	ATU001 732	ATL8C2 8949:7 09..1	gap2	ATCEA4 S31903 1, ATCEA4	99, 98	ATL8C2 8949:5 57..78	0.69	g47411 97	56	271	3.9e- 29	(AL049 746) aldose 1-

139793	ATU001 733	ATL8C4 5257:2 583..2 58	gap2	ATCEA4 C34118 1, ATCEA4 S23299	99, 85	ATL8C4 5257:2 456..3 20	0.69	g44670 98	56	527	4.6e- 33	(AL035 538) putati ve protei n [Arabi dopsis thalia na]
139794	ATU001 734	ATL8C2 4342:9 86..14 94	gap2	ATCEA4 C307_1	99	ATL8C2 4342:1 111..1 357	0.50	g34451 97	56	651	4.8e- 41	(AC004 786) homeob ox protei n, HAT9 [Arabi dopsis thalia na]
139795	ATU001 735	ATL8C1 1730:1 401..1	gap2	ATCEA4 C26205 1, ATCEA4 S34045 , ATCEA4 S2566	99, 89, 86	ATL8C1 1730:9 30..31 0	0.44	g32128 65	56	1424	4.1e- 130	(AC004 005) unknow n protei n [Arabi dopsis thalia na]
139796	ATU001 736	ATL8C3 5626:2 715..1 878	gap2	ATCEA4 S2588	99	ATL8C3 5626:2 631..1 878	0.42	g16522 88	56	142	1.8e- 10	(D9090 4) hypoth etical protei

139797	ATU001 737	ATL8C3 1375:4 03..1	gap2	ATCEA4 C44979 _1	99						g22449 31	56	157	1.7e- 10	(Z9733 9) hypoth etical protei n [Arabi dopsis thalia na]
139798	ATU001 738	ATL8C3 5754:7 55..1	gap2	ATCEA4 C6621_1	99						g24355 11	56	79	0.077	(AF024 504) contai ns simila rity to prolyl 4- hydrox ylase alpha subuni t [Arabi dopsis thalia na]
139799	ATU001 739	ATL8C1 4811:1 ..1418	gap2	ATCEA4 C9126_2, ATCEA4 C9126_1, ATCEA4 S12818	99, 91, 82						g13635 26	56	383	7.0e- 37	plasto quinol -- plasto cyanin reduct ase (EC 1.10.9 9.1) cytoch rome

139800	ATU001 740	ATL8C4 3033:8 93..1	gap2	ATCEA4 C1240_3	99					g48113 2	56	1197	8.0e- 117	b6 - maize chloro plast [Zea mays] sucros e transp ort protei n SUC1 - Arabid opsis thalia na [Arabi dopsis thalia na] (AC004 005) unknow n protei n [Arabi dopsis thalia na]
139801	ATU001 741	ATL8C9 87:112 7..1	gap2	ATCEA4 C14474 _1	99				ATL8C9 87:106 6..302	g32128 51	55	335	5.4e- 26	(AC004 005) unknow n protei n [Arabi dopsis thalia na]
139802	ATU001 742	ATL8C1 2558:1 840..3 790	gap2	ATCEA4 S12442 , ATCEA4 C2666_2, ATCEA4 S12785 , ATCEA4 S34017	99, 99, 89, 88			ATL8C1 2558:2 081..3 555	0.98	g47047 66	55	849	2.2e- 76	(AF131 223) protei n disulf ide isomer ase homolo g; PDI [Datis ca glomer ata]

139803	ATU001 743	ATL8C8 377:10 62..1	gap2	ATCEA4 S8212, ATCEA4 C12602 1, ATCEA4 S7904	99, 98, 85	ATL8C8 377:95 4..146	0.96	g13387 2	55	703	1.0e- 64	30S RIBOSO MAL PROTEI N S1, CHLORO PLAST PRECUR SOR (CS1) [Spina cia olerac ea]
139804	ATU001 744	ATL8C2 907:1. .1425	gap2	ATCEA4 C38367 1	99	ATL8C2 907:28 ..1306	0.94	g22451 30	55	849	2.3e- 65	(Z9734 4) GLABRA 2 homolo g [Arabi dopsis thalia na]
139805	ATU001 745	ATL8C1 6108:6 6..331 8	gap2	ATCEA4 C30366 1	99	ATL8C1 6108:1 64..31 59	0.84	g40564 90	55	661	3.7e- 51	(AC005 896) hypoth etical protei n [Arabi dopsis thalia na]
139806	ATU001 746	ATL8C4 3406:2 621..1 316	gap2	ATCEA4 C84400 1	99	ATL8C4 3406:2 578..1 821	0.84	g25831 22	55	771		(AC002 387) hypoth etical protei n [Arabi dopsis thalia na]
139807	ATU001	ATL8C1	gap2	ATCEA4	99	ATL8C1	0.80	g33353	55	1369	2.2e-	(AC003771)

139811	ATU001 751	ATL8C4 1321:6 19..15 7	gap2	ATCEA4 C13061 1, ATCEA4 C97163 1	99, 97				g32692 96	55	736	2.4e- 74	tula MtN2 (GB:Y1 5293) [Arabi dopsis thalia nal]
139812	ATU001 752	ATL8C1 9717:1 026..1	gap2	ATCEA4 C11959 4 1, ATCEA4 S3609	99, 99				g38596 96	55	171	3.2e- 24	(AL033 497) unknown hypoth etical protei n [Candi da albica ns]
139813	ATU001 753	ATL8C3 3551:1 56..18 28	gap2	ATCEA4 C17076 2, ATCEA4 S16999	99, 96				g42493 85	55	797	3.9e- 64	(AC005 966) T2K10. 11 [Arabi dopsis thalia nal]
139814	ATU001 754	ATL8C4 4653:1 ..433	gap2	ATCEA4 S7255, ATCEA4 C25241 3, ATCEA4 C25241	99, 96, 96, 96	ATL8C4 4653:1 30..23 1	0.99		g28798 11	54	169	6.6e- 17	(AJ223 316) riboso mal protei n L30 [Lupin]

139822	ATU001 762	ATL8C2 8302:9 11..1	gap2	ATCEA4 C26582 2, ATCEA4 C26582 _1	99, 97	ATL8C2 8302:6 60..11 4	0.77	g45389 79	54	368	1.6e- 28	this gene. [Arabi dopsis thalia na]
139823	ATU001 763	ATL8C1 0906:4 779..3 618	gap2	ATCEA4 C95656 _1, ATCEA4 C14960 _1	99, 94	ATL8C1 0906:4 485..3 774	0.75	g16658 17	54	125	0.074	(D8746 6) Simila r to S.cere visiae hypothe tical protein n L3111 (S5931 6) [Homo sapien s]
139824	ATU001 764	ATL8C2 3417:1 011..1	gap2	ATCEA4 S12720	99	ATL8C2 3417:8 99..20 0	0.65	g29824 41	54	842	1.0e- 68	(AL022 224) cytoch rome p450 like protei n [Arabi dopsis thalia na]
139825	ATU001	ATL8C7	gap2	ATCEA4	99	ATL8C7	0.59	g37859	54	606	1.5e-	(AC005

765	565:97 ..2472		C35130 _1		565:97 ..2143	76				39	560) Sec12p -like protei n [Arabi dopsis thalia na]
139826	ATU001 766	ATL8C8 359:11 89..1	gap2	ATCEA4 C27143 _1	99	ATL8C8 359:11 11..90	0.57	g39278 36	54	625	7.7e- 51 (AC005 727) unknow n protei n [Arabi dopsis thalia na]
139827	ATU001 767	ATL8C3 0577:1 ..816	gap2	ATCEA4 C2268_1, ATCEA4 C2268_2, ATCEA4 S25749	99, 86, 85	ATL8C3 0577:2 47..74 0	0.55	g44172 80	54	438	5.3e- 39 (AC007 019) putati ve ATP syntha se [Arabi dopsis thalia na]
139828	ATU001 768	ATL8C3 9854:1 ..1043	gap2	ATCEA4 C58275 _1, ATCEA4 S8967	99, 86	ATL8C3 9854:1 94..28 9	0.52	g41057 98	54	414	4.1e- 36 (AF049 930) PGP237 -11 [Petun ia x hybrid al]
139829	ATU001 769	ATL8C3 7036:4 24..17 51	gap2	ATCEA4 S24650 , ATCEA4 C18003 4, ATCEA4 S24657	99, 94, 92, 88			g41159 28	54	297	(AF118 222) No defini tion line found [Arabi

139830	ATU001 770	ATL8C9 427:11 20..1	gap2	ATCEA4 S24659 ATCEA4 S14044 ATCEA4 C76429 ATCEA4 C15893	99, 96 98, 96	ATL8C9 427:10 76..10 4	0.98	g45875 33	53	89	6.2e- 05	dopsis thalia na] (AC007 060) EST gb AA7 21821 comes from this gene. [Arabi dopsis thalia na]
139831	ATU001 771	ATL8C9 205:1. .1406	gap2	ATCEA4 C45937 ATCEA4 S30035 ATCEA4 S5589	99, 85 88, 85	ATL8C9 205:48 3..137 9	0.82	g37905 81	53	135		(AF079 179) RING- H2 finger protei n RHBla [Arabi dopsis thalia na]
139832	ATU001 772	ATL8C2 6534:1 099..1	gap2	ATCEA4 S27	99	ATL8C2 6534:6 50..12	0.79	g30753 90	53	588	2.7e- 54	(AC004 484) protei n kinase ARSK1 [Arabi dopsis thalia na]
139833	ATU001 773	ATL8C3 2710:9 6..959	gap2	ATCEA4 C31951 _1	99	ATL8C3 2710:1 37..67 3	0.75	g45860 55	53	519	6.9e- 53	(AC007 020) hypoth etical protei n [Arabi

139834	ATU001 774	ATL8C3 8452:8 96..1	gap2	ATCEA4 C2206_1, ATCEA4 C64511_1	99, 82	ATL8C3 8452:8 74..21 2	0.68	g46782 85	53	761	5.7e- 79	dopsis thalia na] (AL049 660) putati ve protei n [Arabi dopsis thalia na]
139835	ATU001 775	ATL8C4 7800:1 048..1	gap2	ATCEA4 C40155 2, ATCEA4 S31890	99, 92	ATL8C4 7800:8 27..41 3	0.61	g28275 54	53	810	1.1e- 46	(AL021 635) putati ve DNA bindin g protei n [Arabi dopsis thalia na]
139836	ATU001 776	ATL8C3 6633:1 ..3263	gap2	ATCEA4 C32320 1, ATCEA4 C683_1 , ATCEA4 S25077 , ATCEA4 S32030	99, 97, 96, 94	ATL8C3 6633:6 3..135 3, ATL8C3 6633:1 712..3 040	0.60, 0.92	g41917 83	53	156	2.0e- 14	(AC005 917) hypoth etical protei n [Arabi dopsis thalia na]
139837	ATU001 777	ATL8C2 7008:1 ..1610	gap2	ATCEA4 S3110	99	ATL8C2 7008:1 90..11 80	0.52	g38738 07	53	272	3.1e- 21	(Z4990 7) B0491. 1 [Caeno rhabdi tis elegan s]

139838	ATU001 778	ATL8C4 9282:1 37..16 10	gap2	ATCEA4 S4233	99	ATL8C4 9282:1 37..14 00	0.51	g21467 39	53	536	1.4e- 39	hexoki nase (EC 2.7.1. 1) 1 - Arabid opsis thalia na [Arabi dopsis thalia na]
139839	ATU001 779	ATL8C2 403:1. .1161	gap2	ATCEA4 S4804	99	ATL8C2 403:44 3..102 2	0.49	g47340 06	53	472	4.0e- 41	(AC007 178) hypoth etical protei n [Arabi dopsis thalia na]
139840	ATU001 780	ATL8C2 8927:2 1..687	gap2	ATCEA4 C18396 1, ATCEA4 S29689 , ATCEA4 C17147 1	99, 96, 88			g25003 76	53	142	9.8e- 15	60S RIBOSO MAL PROTEI N L34 [Arabi dopsis thalia na]
139841	ATU001 781	ATL8C1 8399:1 141..1 747	gap2	ATCEA4 C2037 - 1, ATCEA4 S15276 , ATCEA4 S32923	99, 85, 82			g36950 23	53	644	9.6e- 43	(AF055 850) unknow n [Arabi dopsis thalia na]
139842	ATU001 782	ATL8C3 75:124 6..1	gap2	ATCEA4 C70174 1, ATCEA4 S4901,	99, 84, 82, 82			g23471 92	53	420	9.9e- 42	(AC002 338) splice osomal protei

139843	ATU001 783	ATL8C1 2003:9 16..18 86	gap2	ATCEA4 C16942 1, ATCEA4 S31020	99				g32016 19	53		661	2.8e- 36	n U2B isolog [Arabi dopsis thalia na]
139844	ATU001 784	ATL8S1 9788:5 54..1	gap2	ATCEA4 S13416 , ATCEA4 C20305 1	99, 93	ATL8S1 9788:3 71..12 1	0.97		g44671 16	52		268	7.3e- 18	(AL035 538) hypoth etical protei n [Arabi dopsis thalia na]
139845	ATU001 785	ATL8C8 208:1. .1522	gap2	ATCEA4 C25817 2, ATCEA4 S28797 , ATCEA4 C25817 3	99, 93 95, 93	ATL8C8 208:25 3..113 0	0.97		g29824 63	52		431	4.5e- 28	(AL022 223) putati ve protei n [Arabi dopsis thalia na]
139846	ATU001 786	ATL8C4 3196:1 ..723	gap2	ATCEA4 S8425, ATCEA4 S13444	99, 87	ATL8C4 3196:1 03..59 4	0.95		g22449 39	52		178	1.4e- 10	(Z9733 9) hypoth etical protei

139847	ATU001 787	ATL8C1 4173:1 ..983	gap2	ATCEA4 S27225 , ATCEA4 C24500 _1	99, 95	ATL8C1 4173:1 92..43 8	0.93	g45104 24	52	651	9.8e- 58	(AC006 929) putati ve carbox ypepti dase [Arabi dopsis thalia na]
139848	ATU001 788	ATL8C1 2122:2 380..3 559	gap2	ATCEA4 C4985 _1	99	ATL8C1 2122:2 402..3 463	0.93	g44172 78	52	1977	6.7e- 197	(AC007 019) hypoth etical protei n [Arabi dopsis thalia na]
139849	ATU001 789	ATL8C4 868:46 08..1	gap2	ATCEA4 S16097 , ATCEA4 C56920 _1, ATCEA4 C193_1 , ATCEA4 C84391 _1	99, 97, 97, 96	ATL8C4 868:46 08..14 23, ATL8C4 868:70 4..18	0.92, 0.86	g27915 25	52	29	0.91	(AL021 246) lipQ [Mycob acteri um tuberc ulosis]
139850	ATU001 790	ATL8C2 8876:1 ..1017	gap2	ATCEA4 C21852 _1	99	ATL8C2 8876:1 11..69 5	0.84	g26424 50	52	985	1.0e- 100	(AC002 391) putati ve metal ion transp

139855	ATU001 795	ATL8C4 4504:1 ..1685	gap2	ATCEA4 C98983 1, ATCEA4 C20968 1, ATCEA4 S9368, ATCEA4 S31227 , ATCEA4 S157	99, 96, 92, 91, 82	ATL8C4 4504:1 61..16 85	0.49	g45394 52	52	1714	2.1e- 161	[N9701 9,gb A A39520 3 come from this gene. [Arabi dopsis thalia na]
139856	ATU001 796	ATL8C1 3570:4 60..12 55	gap2	ATCEA4 S2059	99			g45103 98	52	502	9.5e- 30	[AC006 587) hypoth etical protei n [Arabi dopsis thalia na]
139857	ATU001 797	ATL8C1 5015:1 ..900	gap2	ATCEA4 C22685 1, ATCEA4 C17756 1, ATCEA4 C51310 1	99, 99, 96			g45809 90, g10916 78	52, 38	408, 296	1.3e- 38, 8.5e- 29	[AF120 335) putati ve transp osase [Arabi dopsis thalia na]

139858	ATU001 798	ATL8C1 0259:3 556..1 288	gap2	ATCEA4 S3823	99	ATL8C1 0259:3 556..2 075	0.94	g33295 06	51	159		na]; activa tor- like transp osable elemen t [Penni setum glaucu m]
139859	ATU001 799	ATL8C2 185:1. .964	gap2	ATCEA4 C632_1 , ATCEA4 S33436	99, 89	ATL8C2 185:27 6..776	0.92	g21295 83	51	397	5.7e- 29	ferrit in - Arabid opsis thalia na [Arabi dopsis thalia na]
139860	ATU001 800	ATL8S2 2066:3 54..1	gap2	ATCEA4 C6822_1	99	ATL8S2 2066:3 54..15 9	0.92	g49143 24	51	286	4.7e- 22	(AC005 489) F14N23 .10 [Arabi dopsis thalia na]

139861	ATU001 801	ATL8C3 3051:1 ..618	gap2	ATCEA4 C27449 1, ATCEA4 S33974 , ATCEA4 S33070	99, 87, 87, 87	ATL8C3 3051:1 04..56 1	0.91	g30634 44	51	273	5.8e- 30	(AC003 981) F22013 .5 [Arabi dopsis thalia na]
139862	ATU001 802	ATL8C9 928:1. .1192	gap2	ATCEA4 C84206 1, ATCEA4 S19006 , ATCEA4 S25219	99, 87, 92, 87	ATL8C9 928:64 ..605	0.90	g12442 9	51	659	2.1e- 67	37 KD CHLORO PLAST INNER ENVELO PE MEMBRA NE PROTEI N PRECUR SOR (E37) [Spina cia olerac ea]
139863	ATU001 803	ATL8C4 3196:2 942..1 056	gap2	ATCEA4 C18817 1, ATCEA4 S32603	99, 96	ATL8C4 3196:2 704..1 276	0.89	g45586 63	51	166	1.9e- 07	(AC007 063) unknown protei n [Arabi dopsis thalia na]
139864	ATU001 804	ATL8C2 4729:1 ..2382	gap2	ATCEA4 S4235, ATCEA4 C2165_1	99, 97	ATL8C2 4729:1 15..22 01	0.78	g58488 2	51	1657	8.7e- 154	CYCLOA RTENOL SYNTHA SE (2, 3- EPOXYS QUALEN E-- CYCLOA RTENOL

139865	ATU001 805	ATL8C5 499:1. .861	gap2	ATCEA4 S6119	99	ATL8C5 499:91 ..668	0.69	g49143 71	51	765	4.1e- 84	CYCLAS E) [Arabi dopsis thalia na]
139866	ATU001 806	ATL8C9 519:1. .2235	gap2	ATCEA4 S4151	99	ATL8C9 519:12 7..194 3	0.66	g21911 42	51	1008	1.8e- 109	(AF007 269) A IG00 2N01.2 7 gene produc t [Arabi dopsis thalia na]
139867	ATU001 807	ATL8C4 0166:1 44..11 41	gap2	ATCEA4 S1528	99	ATL8C4 0166:1 44..57 1	0.58	g15183 88	51	355	1.3e- 22	(X9117 2) korean - radish isoper oxidase [Rapha nus sativu s]
139868	ATU001 808	ATL8C1 0730:1 ..741	gap2	ATCEA4 S443	99	ATL8C1 0730:5 4..719	0.55	g29110 82	51	998	1.4e- 95	(AL021 960) hypoth etical protei n

139869	ATU001 809	ATL8C3 8779:9 17..1	gap2	ATCEA4 S10623	99	ATL8C3 8779:5 19..10 6	0.54	g28800 49	51	804	2.6e- 69	[Arabi dopsis thalia na] (AC002 340) hypoth etical protei n [Arabi dopsis thalia na]
139870	ATU001 810	ATL8C1 3828:1 ..688	gap2	ATCEA4 C47181 _1	99	ATL8C1 3828:3 07..61 0	0.52	g45080 73	51	619	2.7e- 59	(AC005 882) 43220 [Arabi dopsis thalia na]
139871	ATU001 811	ATL8C4 8217:1 25..19 23	gap2	ATCEA4 C74681 _1, ATCEA4 S7179	99, 85	ATL8C4 8217:4 62..13 25	0.98	g36872 30	50	975	1.9e- 109	(AC005 169) hypoth etical protei n [Arabi dopsis thalia na]
139872	ATU001 812	ATL8C1 1468:1 939..1 388	gap2	ATCEA4 C322_1	99	ATL8C1 1468:1 842..1 388	0.95	g68191 2	50	699	1.9e- 62	(D3171 5) cp33 [Arabi dopsis thalia na]
139873	ATU001 813	ATL8C4 570:11 93..1	gap2	ATCEA4 C4584_1	99	ATL8C4 570:11 58..18 2	0.95	g38853 28	50	526	3.5e- 42	(AC005 623) putati ve serine /threo

139874	ATU001 814	ATL8C1 6319:5 158..3 849	gap2	ATCEA4 S3453	99	ATL8C1 6319:5 087..3 886	0.94	g49144 30	50	1170	2.3e- 119	nine protei n kinase [Arabi dopsis thalia na]
139875	ATU001 815	ATL8C1 1045:1 ..2305	gap2	ATCEA4 C7135_ 1, ATCEA4 S8220	99, 93	ATL8C1 1045:2 49..21 83	0.91	g31840 82	50	298	4.5e- 15	(AL023 781) N- termin al acetyl transf erase 1 [Schiz osacch aromyc es pombel]
139876	ATU001 816	ATL8C1 48:1.. 1709	gap2	ATCEA4 S7012, ATCEA4 S29859 , ATCEA4 C16526 1	99, 93 99, 93	ATL8C1 48:860 ..747	0.88	g48357 89	50	859		(AC007 296) Strong simila rity to []
139877	ATU001 817	ATL8C5 0040:1 584..2 40	gap2	ATCEA4 S12967	99	ATL8C5 0040:1 430..4 54	0.81	g44544 76	50	254	1.1e- 33	(AC006 234) hypothe tical protei

139878	ATU001 818	ATL8C6 526:28 2..117 2	gap2	ATCEA4 S7735, ATCEA4 C18737 _1	99, 98	ATL8C6 526:52 3..110 2	0.81	g29470 70	50	992	4.4e- 84	n [Arabi dopsis thalia na] (AC002 521) putati ve Ser/Th r protei n kinase [Arabi dopsis thalia na]
139879	ATU001 819	ATL8C3 9084:1 ..1628	gap2	ATCEA4 S30678 , ATCEA4 S13335	99, 94	ATL8C3 9084:5 4..128 6	0.81	g45393 05	50	678	1.3e- 59	(AL049 480) putati ve protei n [Arabi dopsis thalia na]
139880	ATU001 820	ATL8C2 3377:1 ..2920	gap2	ATCEA4 S7379, ATCEA4 S33161	99, 86	ATL8C2 3377:9 3..285 7	0.73	g31219 95, g32491 06	50, 35	472, 129	4.2e- 28, 7.1e- 06	DOM34 INTERA CTING PROTEI N 2 [Sacch aromyc es cerevi siae]; (AC003 114) T12M4. 16 [Arabi dopsis thalia

139881	ATU001 821	ATL8C3 7900:3 7..125 1	gap2	ATCEA4 S1606	99	ATL8C3 7900:3 88..11 44	0.66	g45393 32	50	763	6.1e- 80	na] (AL035 539) glycos yltran sferas e like protei n (fragm ent) [Arabi dopsis thalia na]
139882	ATU001 822	ATL8C1 9569:1 246..1	gap2	ATCEA4 C692_1 , ATCEA4 S24649	99, 83	ATL8C1 9569:1 132..8	0.65	g44903 21	50	1193	1.4e- 88	(AJ011 604) nitrat e transp orter [Arabi dopsis thalia na]
139883	ATU001 823	ATL8C4 9316:1 ..2518	gap2	ATCEA4 S26644 , ATCEA4 C5724_2, ATCEA4 S16049 , ATCEA4 C5724_1, ATCEA4 C25876 1	99, 98, 98, 95, 88	ATL8C4 9316:1 112..2 434	0.58	g36412 52	50	667	3.3e- 61	(AF053 127) leucin e-rich recept or- like protei n kinase [Malus domest ica]
139884	ATU001 824	ATL8C3 6317:1 ..752	gap2	ATCEA4 C65369 _1	99	ATL8C3 6317:6 7..752	0.52	g34829 19	50	367	8.0e- 39	(AC003 970) Putati ve protei

139885	ATU001 825	ATL8C3 188:10 09..1	gap2	ATCEA4 C34720 _1	99	ATL8C3 188:97 7..330	0.50	g35102 51	50	1201	1.4e- 122	n kinase [Arabi dopsis thalia na] (AC005 310) unknow n protei n [Arabi dopsis thalia na]
139886	ATU001 826	ATL8C1 8089:1 252..1	gap2	ATCEA4 C16646 _1	99			g49030 18	50	539	2.4e- 57	(AB027 507) ACE [Arabi dopsis thalia na]
139887	ATU001 827	ATL8C4 5586:1 08..10 60	gap2	ATCEA4 C29626 _1, ATCEA4 S2933	99, 98	ATL8C4 5586:1 08..96 8	0.95	g45394 65	49	1036	8.6e- 87	(AL049 500) putati ve protei n [Arabi dopsis thalia na]
139888	ATU001 828	ATL8C1 572:40 5..508 3	gap2	ATCEA4 C314_1	99	ATL8C1 572:40 8..475 6	0.90	g29247 70	49	2649	4.1e- 235	(AC002 334) putati ve myosin heavy chain [Arabi dopsis thalia na]

139889	ATU001 829	ATL8C3 7230:2 723..1 440	gap2	ATCEA4 C2757_1, ATCEA4 C45663_1	99, 98	ATL8C3 7230:2 136..1 583	0.87	g58489 2	49	556	SERINE CARBOX YPEPTI DASE I PRECUR SOR (CARBO XYPEPT IDASE C) [Oryza sativa]
139890	ATU001 830	ATL8C4 8715:2 258..5 49	gap2	ATCEA4 S5216	99	ATL8C4 8715:2 187..7 28	0.82	g35488 06	49	1482	3.2e- 135 unknow n protei n [Arabi dopsis thalia na]
139891	ATU001 831	ATL8C3 2447:1 168..1	gap2	ATCEA4 C1161_1	99	ATL8C3 2447:1 073..2 37	0.80	g21490 21	49	1036	1.8e- 115 ADPG pyroph osphor ylase large subuni t [Arabi dopsis thalia na]
139892	ATU001 832	ATL8C3 4530:1 064..4 261	gap2	ATCEA4 S30304 , ATCEA4 C11599 _1, ATCEA4 S10072	99, 82 96, 82	ATL8C3 4530:1 064..4 052	0.79	g42205 21	49	1655	1.7e- 159 (AL035 356) putati ve protei n [Arabi dopsis thalia

139893	ATU001 833	ATL8C5 0023:1 ..1219	gap2	ATCEA4 C81847 1, ATCEA4 C13110 1	99, 99	ATL8C5 0023:4 07..49 3	0.70	g39280 92	49	319	2.7e- 18	(AC005 770) unknown protein [Arabi dopsis thalia na]
139894	ATU001 834	ATL8C3 3109:7 07..1	gap2	ATCEA4 S13767 , ATCEA4 C40640 1, ATCEA4 S21403	99, 99, 97, 82	ATL8C3 3109:6 22..14 3	0.66	g45103 48	49	887	2.4e- 77	(AC006 921) unknown protein [Arabi dopsis thalia na]
139895	ATU001 835	ATL8C2 4979:1 20..89 9	gap2	ATCEA4 S10919	99	ATL8C2 4979:2 82..67 6	0.60	g44553 61	49	519	7.2e- 45	(AL035 524) putative protein [Arabi dopsis thalia na]
139896	ATU001 836	ATL8C3 6228:9 9..289 8	gap2	ATCEA4 S4522	99	ATL8C3 6228:2 97..26 17	0.54	g45811 49	49	531	1.3e- 44	(AC006 919) hypothetical protein [Arabi dopsis thalia na]
139897	ATU001 837	ATL8C1 0209:1 ..1554	gap2	ATCEA4 C11343 1,	99, 98, 87, 86	ATL8C1 0209:1 14..98	0.98	g22528 65	48	878		(AF013 294) No

139902	ATU001 842	ATL8C3 4305:4 95..11 20	gap2	ATCEA4 S36168	99	ATL8C3 4305:5 39..96 5	0.86	g10417 06	48	211	4.1e- 11	thalia na] (U3048 0) expans in At- EXP6 [Arabi dopsis thalia na]
139903	ATU001 843	ATL8C4 6461:1 ..2629	gap2	ATCEA4 S11208	99	ATL8C4 6461:5 8..261 0	0.86	g24659 23	48	1015	2.7e- 102	(AF024 648) recept or- like serine /threo nine kinase [Arabi dopsis thalia na]
139904	ATU001 844	ATL8C1 3720:1 216..1	gap2	ATCEA4 C29763 _1	99	ATL8C1 3720:6 28..31	0.86	g40564 55	48	447	1.1e- 25	(AC005 990) Simila r to gb L19 255 carbon ic anhydr ase from Nicoti ana tabacu m and a member of the prokar yotic- type

139905	ATU001 845	ATL8C1 5929:1 ..1389	gap2	ATCEA4 S7399, ATCEA4 C8233_ 1	99, 95	ATL8C1 5929:6 5..122 9	0.84	g28275 44	48	1125	1.6e- 68	carbon ic anhydr ase family PF1004 84. EST gb Z23 5745 comes from this gene. [Arabi dopsis thalia na]
139906	ATU001 846	ATL8C4 968:1. .3055	gap2	ATCEA4 S2840, ATCEA4 S6482	99, 96	ATL8C4 968:31 ..2346	0.80	g23351 06, g30045 55	48, 41	186, 316	9.0e- 15, 6.4e- 26	(AC002 339) salt induci ble protei n-like [Arabi dopsis thalia na]; (AC003 673) simila r to salt

139907	ATU001 847	ATL8C3 649:1. .802	gap2	ATCEA4 S36377	99	ATL8C3 649:61 ..707	0.75	g17032 19	48	602	1.1e- 63	inducible protein [Arabi dopsis thalia na]
139908	ATU001 848	ATL8C2 2231:2 544..1	gap2	ATCEA4 C5425_ 1, ATCEA4 C50487 _1	99, 85	ATL8C2 2231:1 857..9 1	0.75	g45859 66	48	620	3.4e- 23	(AC005 287) Putati ve dihyrd olipoa mide acetyl transf erase [Arabi dopsis thalia na]
139909	ATU001 849	ATL8C5 31:1.. 1188	gap2	ATCEA4 S12143 , ATCEA4 S25216 , ATCEA4 C67079 _1	99, 86 95, 86	ATL8C5 31:120 ..1066	0.70	g44159 34	48	563	5.9e- 38	(AC006 418) putati ve auxin respon se factor 1 [Arabi dopsis thalia na]
139910	ATU001 850	ATL8C2 5429:8 84..1	gap2	ATCEA4 C18039 _1,	99, 96	ATL8C2 5429:4 85..70	0.68	g44067 59	48	282	1.5e- 22	(AC006 836) hypoth

139911	ATU001 851	ATL8C2 662:12 70..1	gap2	ATCEA4 S2631	99	ATL8C2 662:12 70..31	0.67	g32890 02	48	218	1.9e- 16	etical protei n [Arabi dopsis thalia na]
139912	ATU001 852	ATL8C6 037:10 02..15 90	gap2	ATCEA4 S6280	99	ATL8C6 037:10 92..15 50	0.57	g11075 26	48	442	2.1e- 42	(AF073 522) CRP1 [Zea mays] (X8793 1) SIEP1L protei n [Beta vulgar is]
139913	ATU001 853	ATL8C2 368:1. .2189	gap2	ATCEA4 S25879 ATCEA4 S2441	99, 98	ATL8C2 368:27 5..182 5	0.56	g32128 59, g22448 16	48, 35	83, 102	3.0e- 10, 2.8e- 08	(AC004 005) hypoth etical protei n [Arabi dopsis thalia na]; (Z9733 6) hypoth etical protei n [Arabi dopsis thalia na]
139914	ATU001 854	ATL8S9 16:1.. 541	gap2	ATCEA4 S12650	99	ATL8S9 16:267 ..435	0.43	g36954 09	48	107	0.0002 2	(AF096 373) No defini tion

139915	ATU001 855	ATL8C4 8333:3 900..1 750	gap2	ATCEA4 C24518 _1	99					g26642 02	48	369	6.8e- 28	(AJ003 217) GT2 [Arabi dopsis thalia na]	line found [Arabi dopsis thalia na]
139916	ATU001 856	ATL8C8 699:1. .1446	gap2	ATCEA4 C31191 _1	99				ATL8C8 699:36 1..125 6	0.91	47	84	0.998	(AB000 113) cation ic amino acid transp orter 3 [Rattu s norveg icus]	
139917	ATU001 857	ATL8C1 8312:1 354..1	gap2	ATCEA4 C27659 _1, ATCEA4 S2624	99, 97				ATL8C1 8312:1 151..2 02	0.82	47	548	1.7e- 53	(AC007 153) 68961 [Arabi dopsis thalia na]	
139918	ATU001 858	ATL8C2 9790:7 4..968	gap2	ATCEA4 S10694	99				ATL8C2 9790:1 93..91 7	0.80	47	292	9.1e- 21	(AC002 340) hypoth etical protei n [Arabi dopsis thalia na]	
139919	ATU001	ATL8C2	gap2	ATCEA4	99, 98				ATL8C2	0.77	47	1601	1.4e-	PATHO	

	859	445:16 28..1		C903_2 , ATCEA4 C903_1		445:14 95..67	90		138	ENESIS - RELATE D HOMEOD OMAIN PROTEI N (PRHA) [Arabi dopsis thalia na]
139920	ATU001 860	ATL8C4 791:36 77..65 76	gap2	ATCEA4 S3110, ATCEA4 C7514_1	99, 95	ATL8C4 791:37 55..64 42	0.76	g38738 07	149	2.4e- 12 B0491. 1 [Caeno rhabdi tis elegan s]
139921	ATU001 861	ATL8C9 691:44 6..165 2	gap2	ATCEA4 S5398	99	ATL8C9 691:48 2..160 9	0.74	g26424 50	1090	4.0e- 97 (AC002 391) putati ve metal ion transp orter (Nramp) [Arabi dopsis thalia na]
139922	ATU001 862	ATL8S2 7811:4 65..1	gap2	ATCEA4 C240_2 , ATCEA4 C240_1	99, 95	ATL8S2 7811:3 62..28	0.72	g32427 06	368	9.0e- 18 (AC003 040) cyclin - depend ent kinase inhibi tor

139923	ATU001 863	ATL8C4 9460:1 302..1	gap2	ATCEA4 C11697 91, ATCEA4 S1802	99, 98	ATL8C4 9460:1 107..6 3	0.70	g22448 59	47	1349	5.6e- 134	protein [Arabi dopsis thalia na]
139924	ATU001 864	ATL8C2 0369:6 06..12 97	gap2	ATCEA4 S13923	99	ATL8C2 0369:6 06..12 00	0.61	g33353 72	47	370	1.0e- 39	(AC003 028) putati ve SRG1 protein [Arabi dopsis thalia na]
139925	ATU001 865	ATL8C4 8056:1 ..1505	gap2	ATCEA4 S13101 , ATCEA4 C21441 _1	99, 98	ATL8C4 8056:1 66..67 3	0.59	g44544 84	47	654	9.1e- 53	(AC006 234) putati ve diacyl glycer ol kinase [Arabi dopsis thalia na]
139926	ATU001 866	ATL8C1 0041:4 4..149 2	gap2	ATCEA4 C24657 _1	99	ATL8C1 0041:1 15..12 92	0.58	g24974 92	47	171		URIDYL ATE KINASE (UK) (URIDI NE

139927	ATU001 867	ATL8C3 6812:1 ..882	gap2	ATCEA4 C45239 _1	99						g27022 68	47	485	3.4e- 38	(AC003 033) putati ve cellul ase [Arabi dopsis thalia na]	MONOPH OSPHAT E KINASE) (UMP KINASE) [Synec hocyst is sp.]
139928	ATU001 868	ATL8C6 336:14 ..1716	gap2	ATCEA4 C12457 _1	99						g26186 86	47	452	3.8e- 50	(AC002 510) hypoth etical protei n [Arabi dopsis thalia na]	(AC002 510) hypoth etical protei n [Arabi dopsis thalia na]
139929	ATU001 869	ATL8C2 5841:1 167..2 460	gap2	ATCEA4 S463, ATCEA4 S31444	99, 92					ATL8C2 5841:1 181..2 285	g18814 12	46	272	3.4e- 14	(Z8333 3) pala [Emeri cella nidula ns]	(Z8333 3) pala [Emeri cella nidula ns]
139930	ATU001 870	ATL8C2 3818:3 425..4 18	gap2	ATCEA4 S4169, ATCEA4 C4327 _1	99, 93					ATL8C2 3818:3 196..4 29	g38823 21	46	615	3.4e- 54	(AB018 343) KIAA08 00 protei n [Homo]	(AB018 343) KIAA08 00 protei n [Homo]

139931	ATU001 871	ATL8C1 0724:1 415..1	gap2	ATCEA4 C2545_1, ATCEA4 C12011 01, ATCEA4 S26604	99, 88 97, 88	ATL8C1 0724:8 11..25 6	0.89	g26421 58	46	337	7.5e- 20	sapien (AC003 000) hypoth etical protei n [Arabi dopsis thalia na]
139932	ATU001 872	ATL8C1 0994:1 580..1	gap2	ATCEA4 C26646 1, ATCEA4 C35629 1, ATCEA4 S16373	99, 86 96, 86	ATL8C1 0994:1 496..8 8	0.83	g31352 71	46	337	9.9e- 27	(AC003 058) putati ve recept or- like protei n kinase [Arabi dopsis thalia na]
139933	ATU001 873	ATL8C2 5326:7 13..55 29	gap2	ATCEA4 S1877	99	ATL8C2 5326:7 13..55 29	0.72	g38602 46	46	220	1.9e- 23	(AC005 824) putati ve revers e- transc riptas e protei n [Arabi dopsis thalia na]
139934	ATU001 874	ATL8C3 2600:7 72..1	gap2	ATCEA4 C4616_1, ATCEA4	99, 82 97, 82 94, 82	ATL8C3 2600:6 79..52	0.58	g45035 23	46	261	4.1e- 29	UNKNOWN [Homo sapien]

139935	ATU001 875	ATL8C1 7682:1 ..1282	gap2	ATCEA4 S6192, ATCEA4 C8823_1	99, 92	ATL8C1 7682:3 87..10 86	0.56	g41036 35	46	219	8.5e- 20	(AF026 538) ABA- respon sive protei n [Horde um vulgar e]
139936	ATU001 876	ATL8C1 9735:1 ..670	gap2	ATCEA4 C76416 1, ATCEA4 C5711_1	99, 98	ATL8C1 9735:1 21..66 0	0.46	g35823 29	46	526	4.8e- 50	(AC005 496) unknow n protei n [Arabi dopsis thalia na]
139937	ATU001 877	ATL8C1 2394:1 266..4 71	gap2	ATCEA4 S3921	99			g45392 93	46	1177	4.2e- 104	(AL049 480) putati ve membra ne transp orter [Arabi dopsis thalia na]
139938	ATU001 878	ATL8C1 0142:1 09..19 90	gap2	ATCEA4 S11985	99			g45444 60	46	116		(AC006 592) putati ve revers

139939	ATU001 879	ATL8C4 2654:2 937..1	gap2	ATCEA4 C12282 2.1, ATCEA4 C45419 _1	99, 94					g43244 70	46	156	1.2e- 08	(AF105 010) LAG1Ce -1 [Caeno rhabdi tis elegan s]	e transc riptas e [Arabi dopsis thalia na]
139940	ATU001 880	ATL8C1 573:90 0..202 7	gap2	ATCEA4 C22502 _1	99					g17711 62	46	1130	1.4e- 105	(X9893 0) SBT2 [lycop ersico n escule ntum]	(X9893 0) SBT2 [lycop ersico n escule ntum]
139941	ATU001 881	ATL8C1 6848:2 140..5 21	gap2	ATCEA4 S1822	99	ATL8C1 6848:1 605..5 21				g32427 08, g34027 57	45, 35	556, 287	8.5e- 56, 3.2e- 32	(AC003 040) putati ve serine /threo nine protei n kinase [Arabi dopsis thalia na]; (AL031 187) recept or- like serine	(AC003 040) putati ve serine /threo nine protei n kinase [Arabi dopsis thalia na]; (AL031 187) recept or- like serine

139942	ATU001 882	ATL8C3 5967:7 74..90	gap2	ATCEA4 C5494_1, ATCEA4 S9358	99, 92	ATL8C3 5967:6 21..13 5	0.94	g23697 66	45	528	6.9e- 59	/three nine protei n kinase ARK3 [Arabi dopsis thalia na]
139943	ATU001 883	ATL8C3 5799:1 ..718	gap2	ATCEA4 S300	99	ATL8C3 5799:7 9..619	0.94	g33282 40	45	407	6.8e- 37	(AJ001 304) hypoth etical protei n [Citru s x paradi sil] (AF064 775) early nodule - specif ic protei n [Medic ago trunca tula]
139944	ATU001 884	ATL8C4 8764:1 02..18 10	gap2	ATCEA4 C1018_1	99	ATL8C4 8764:1 60..14 96	0.92	g39148 26	45	1944	1.4e- 186	DNA- DIRECT ED RNA POLYME RASE CHLORO PLAST PRECUR SOR [Arabi dopsis thalia]

139945	ATU001 885	ATL8C8 457:32 64..14 67	gap2	ATCEA4 S24651 , ATCEA4 C13052 1, ATCEA4 S24660 , ATCEA4 S34225 , ATCEA4 S30776 , ATCEA4 S5758	99, 98, 93, 90, 88, 88	ATL8C8 457:32 13..19 99	0.91	g41159 28	45	354	4.3e- 26	na] (AF118 222) No defini tion line found [Arabi dopsis thalia na]
139946	ATU001 886	ATL8C3 9313:1 ..724	gap2	ATCEA4 S10938	99	ATL8C3 9313:8 3..657	0.90	g13387 2	45	34	0.80	30S RIBOSO MAL PROTEI N S1, CHLORO PLAST PRECUR SOR (CS1) [Spina cia olerac ea]
139947	ATU001 887	ATL8C1 6193:1 642..1	gap2	ATCEA4 S5179	99	ATL8C1 6193:1 637..3 1	0.88	g33866 04	45	171	4.7e- 17	(AC004 665) putati ve protei n kinase [Arabi dopsis thalia na]
139948	ATU001 888	ATL8C1 0199:1	gap2	ATCEA4 C22779	99	ATL8C1 0199:6	0.88	g32876 95	45	835		(AC003 979)

139949	ATU001 889	..2445		gap2	ATL8C2 5579:1 ..1154	ATCEA4 C1782_1	99	ATL8C2 5579:1 56..97 4	0.88	g33959 38	45	690	2.2e- 83	Simila r to hypoth etical protei n C34B7. 2 gb 172 9503 from C. elegan s cosmid gb 283 220. [Arabi dopsis thalia na]
139950	ATU001 890	ATL8C4 4995:2 204..1	gap2	ATCEA4 C4688_4, ATCEA4 C4688_3, ATCEA4 C4688	99, 83, 83, 82	ATL8C4 4995:2 204..6 7	0.86	g10551 30	45	142	1.0e- 12	(U3999 8) coded for by C. elegan s cDNA yk92b1		

139951	ATU001 891	ATL8C1 366:39 52..11 4	gap2	ATCEA4 S2806	99	ATL8C1 366:39 52..11 4	0.85	g33419 80	45	75	2.8e- 08	(AF049 523) huntin gtin- intera cting protei n HYPA/F
												1.3; coded for by C. elegant s cDNA yk92b1 1.5; coded for by C. elegant s cDNA yk78c2 .5; coded for by C. elegant s cDNA cm9a8; coded for by C. elegant s cDNA yk66h8 .3; coded for by C. elegant s cDNA yk78c2 .3 ... []

139952	ATU001 892	ATL8C2 298:1. .1062	gap2	ATCEA4 C7675_1	99	ATL8C2 298:78 ..764	0.77	g30055 76	45	674	1.4e- 60	BP11 [Homo sapien s] (AF047 718) putati ve high affini ty nitrat e transp orter; GmNRT2 [Glyci ne max]
139953	ATU001 893	ATL8C4 580:14 78..1	gap2	ATCEA4 C1117_1	99	ATL8C4 580:14 78..12 0	0.77	g13467 82	45	452	3.1e- 38	SERINE /THREO NINE PROTEI N PHOSPH ATASE PP-X ISOZYM E 1 [Arabi dopsis thalia na]
139954	ATU001 894	ATL8C5 898:52 35..12 9	gap2	ATCEA4 C96238 1, ATCEA4 C14902 1, ATCEA4 S32508	99, 98, 94	ATL8C5 898:52 17..12 9	0.64	g43226 70, g49272 40, g23310 36	45, 36, 35	91, 142, 158	(AF094 508) dentin phosph oryn [Homo sapien sl]; (AF139 986) cleava ge and	

139955	ATU001 895	ATL8C3 452:58 8..1	gap2	ATCEA4 S397	99	ATL8C3 452:55 5..7	0.59	g31842 58	45	226	6.6e- 17	(U8213 0) tumor suscep tibili ty protei n [Homo sapien s]
139956	ATU001 896	ATL8C4 8400:1 ..1628	gap2	ATCEA4 S2653, ATCEA4 C25610 1, ATCEA4 C10657	99, 98, 97	ATL8C4 8400:1 019..1 581	0.58	g22451 07	45	1023	1.8e- 107	(Z9734 3) thioes terase homolo g [Arabi

139957	ATU001 897	ATL8C4 8223:1 ..2178	gap2	5_1	99, 93	ATL8C4 8223:3 39..21 19	0.50	g44671 47	45	429	3.3e- 53	dopsis thalia na] (AL035 540) putati ve protei n [Arabi dopsis thalia na]
139958	ATU001 898	ATL8C4 1148:1 ..821	gap2	ATCEA4 C8114_1, ATCEA4 S5986	99, 85	ATL8C4 1148:2 95..77 9	0.47	g22451 01	45	432	6.0e- 42	(Z9734 3) hypoth etical protei n [Arabi dopsis thalia na]
139959	ATU001 899	ATL8C3 3453:3 268..1 775	gap2	ATCEA4 S26474 , ATCEA4 C41972 _1	99, 91			g38501 29	45	69	0.13	(AL033 391) conser ved hypoth etical protei n [Candi da albica ns]
139960	ATU001 900	ATL8C6 038:48 6..137 8	gap2	ATCEA4 C8944_1, ATCEA4 S30001 , ATCEA4 C13413 1_1, ATCEA4	99, 99, 96, 84			g22136 00	45	650	2.1e- 58	(AC000 348) T7N9.2 0 [Arabi dopsis thalia na]

139961	ATU001 901	ATL8C7 806:11 27..30 7	gap2	S10951 ATCEA4 C5005_2, ATCEA4 C5005_1	99, 97				g38853 31	45	748	2.4e- 76	(AC005 623) putati ve cytoch rome p450 protei n [Arabi dopsis thalia na]
139962	ATU001 902	ATL8C6 025:1. .666	gap2	ATCEA4 C18494 _1	99				g40637 50	45	845	1.1e- 76	(AC005 851) putati ve indole -3- acetat e beta- glucos yltran sferas e synthe tase [Arabi dopsis thalia na]
139963	ATU001 903	ATL8C5 770:23 09..1	gap2	ATCEA4 C85559 _1	99	ATL8C5 770:12 32..10 0	0.97		g41036 35	44	264		(AF026 538) ABA- respon sive protei n [Horde um vulgar e]
139964	ATU001	ATL8C4	gap2	ATCEA4	99	ATL8C4	0.94		g17070	44	298	3.6e-	(U7872 e]

904	0479:1 46..66 6		C5595_1		0479:1 50..46 0		22				29	1) prolin e-rich protei n isolog [Arabi dopsis thalia na]
139965	ATU001 905	ATL8C3 9405:1 74..84 2	gap2	ATCEA4 C11272 1, ATCEA4 C35482 1, ATCEA4 S20404	99, 98, 85	ATL8C3 9405:3 45..83 6	0.90	g29975 91	44	344	7.7e- 28	(AF020 814) glucos e-6- phosph ate/ph osphat e- transl ocator precur sor [Pisum sativu m]
139966	ATU001 906	ATL8C4 4353:1 303..1 77	gap2	ATCEA4 S8262	99	ATL8C4 4353:1 302..1 77	0.89	g45444 34	44	235	2.5e- 24	(AC006 955) putati ve DNA- direct ed RNA polyme rase II [Arabi dopsis thalia na]
139967	ATU001 907	ATL8C3 7316:2 499..1	gap2	ATCEA4 C7400_1, ATCEA4 C35722 1	99, 94	ATL8C3 7316:2 296..2 07	0.89	g46789 24	44	308		(AL049 711) putati ve protei n

139968	ATU001 908	ATL8C1 7626:3 49..34 21	gap2	ATCEA4 S2740, ATCEA4 C33494 1, ATCEA4 C34908 1, ATCEA4 S29613 , ATCEA4 S14700	99, 98, 95, 94, 83	ATL8C1 7626:3 49..32 22	0.88	g25014 57	44	317	6.9e- 26	[Arabi dopsis thalia na] UBIQU TIN CARBOX YL- TERMIN AL HYDROL ASE DUB-1 (UBIQU ITIN THIOLE STERAS E DUB- 1). (UBIQU ITIN- SPECIF IC PROCES SING PROTEA SE DUB-1) (DEUBI QUITIN ATING ENZYME 1) [Mus muscul us]
139969	ATU001 909	ATL8C2 8920:8 68..1	gap2	ATCEA4 C45363 1	99	ATL8C2 8920:6 42..22 6	0.85	g22135 92	44	521	8.4e- 54	[AC000 348) T7N9.1 2 [Arabi dopsis thalia na]
139970	ATU001	ATL8C4	gap2	ATCEA4	99, 98	ATL8C4	0.85	g36881	44	2000	4.2e-	(AL031

	910	829:38 79..1		S537, ATCEA4 S10899		829:37 47..18 1	73			152	804) putati ve protei n [Arabi dopsis thalia na]
139971	ATU001 911	ATL8C2 7749:2 314...9 7	gap2	ATCEA4 C1034__ 1, ATCEA4 S35847 , ATCEA4 C14635 2_1	99, 98, 93	ATL8C2 7749:2 106..9 7	g24628 32	44	844		(AF000 657) simila r to Bacill us CotA [Arabi dopsis thalia na]
139972	ATU001 912	ATL8C1 9823:4 72...29 73	gap2	ATCEA4 S1276, ATCEA4 S1634	99, 86	ATL8C1 9823:5 93..28 44	g18883 57	44	1385	1.9e- 111	(X9813 0) alpha mannos idase [Arabi dopsis thalia na]
139973	ATU001 913	ATL8C2 3800:1 700...4	gap2	ATCEA4 C235_2 , ATCEA4 S13525	99, 98	ATL8C2 3800:1 573..4	g22249 11	44	1065	1.9e- 104	(U9304 8) somati c embryo genesi s recept or- like kinase [Daucu s carota]
139974	ATU001	ATL8C2	gap2	ATCEA4	99, 88	ATL8C2	g30969	44	270	9.7e-	(AL023)

914	1439:1 ..901		C17617 1, ATCEA4 S5167		1439:9 1..863	35			17	094) putative protein [Arabi dopsis thalia na]
139975	ATU001 915	gap2	ATCEA4 C19750 _1	99	ATL8C1 9356:1 041..3 8	g36954 03	44	100	1.8e- 07	(AF096 373) contains similarity to the pfkB family of carbohy- drate kinase s (Pfam: PF0029 4, E=1.6e -75) [Arabi dopsis thalia na]
139976	ATU001 916	gap2	ATCEA4 S4907, ATCEA4 C18115 _1, ATCEA4 C21406 _1	99, 96, 96, 96	ATL8C4 6094:1 896..6 1	g35402 09	44	525	2.1e- 38	(AC004 260) Hypo- thetical protein [Arabi dopsis thalia na]
139977	ATU001 917	gap2	ATCEA4 S8571, ATCEA4	99, 97	ATL8C1 5839:1 220..2	g45859 25	44	677	7.4e- 58	(AC007 211) unknown

		..1315													LIKE PROTEI N KINASE 5 PRECUR SOR [Arabi dopsis thalia na]
139982	ATU001 922	ATL8C2 4866:2 404..1 881	gap2	ATCEA4 S16256	99					g40564 93	44	230	3.7e- 21	(AC005 896) unknow n protei n [Arabi dopsis thalia na]	
139983	ATU001 923	ATL8C1 1909:1 747..1	gap2	ATCEA4 S12176 , ATCEA4 S701, ATCEA4 C13428 0 1	99, 98, 91			ATL8C1 1909:1 719..2 46	0.98	g43226 70	43	110	0.0004 2	(AF094 508) dentin phosph oryn [Homo sapien s]	
139984	ATU001 924	ATL8C3 84:1.. 1845	gap2	ATCEA4 C2387 _ 1	99			ATL8C3 84:135 ..1764	0.96	g32528 25	43	43	0.030	(AC004 382) Unknow n gene produc t [Homo sapien s]	
139985	ATU001 925	ATL8C1 2673:8 804..5 942	gap2	ATCEA4 C30684 1, ATCEA4 S10259 , ATCEA4	99, 99, 98			ATL8C1 2673:8 804..6 167	0.92	g28274 69	43	517	1.8e- 21	(AF044 255) NOSA [Dicty osteli um discoi]	

139990	ATU001 930	ATL8C1 180:32 0..137 8	gap2	ATCEA4 S2351, ATCEA4 C21641 _1	99	ATL8C1 180:48 4..125 4	0.72	g33353 52	43	486	7.1e- 39	ve beta- 1,3- glucan ase [Arabi dopsis thalia na] (AC004 512) Contai ns simila rity to serine /threo nine kinase homolo g PRO25 gb L04 999 from A. thalia na. EST gb Z17 531 comes from this gene. [Arabi dopsis thalia na] (AC003 000) hypoth etical protei
139991	ATU001 931	ATL8C2 2055:1 446..4 93	gap2	ATCEA4 S293, ATCEA4 S35193	99, 93, 87	ATL8C2 2055:1 316..7 29	0.65	g26421 58	43	176	1.4e- 12	

139992	ATU001 932	ATL8C3 2478:1 ..3661	gap2	ATCEA4 C3918_1	99	ATL8C3 2478:2 19..35 03	0.64	g17061 02	43	130	1.9e- 16	n [Arabi dopsis thalia na]
139993	ATU001 933	ATL8S2 0927:1 ..488	gap2	ATCEA4 C80610_1	99	ATL8S2 0927:1 61..38 7	0.51	g49143 17	43	230	1.5e- 21	(AC005 489) F14N23 .3 [Arabi dopsis thalia na]
139994	ATU001 934	ATL8C3 7257:1 ..340	gap2	ATCEA4 C13212_1	99	ATL8C3 7257:1 9..334	0.50	g24990 11	43	251		HYDROX YETHYL THIAZO LE KINASE (4- METHYL -5- BETA- HYDROX YETHYL THIAZO LE

139995	ATU001 935	ATL8S2 6335:5 84..15 7	gap2	ATCEA4 S4609, ATCEA4 S33136 , ATCEA4 S27488	99, 84 95, 84	ATL8S2 6335:5 26..34 2	0.49	g22535 79	43	88				KINASE) (THZ KINASE) (TH KINASE) [Salmo nella typhim urium]
139996	ATU001 936	ATL8C3 6217:3 972..1 423	gap2	ATCEA4 C11036 1, ATCEA4 C72275 1	99, 98			g38941 91	43	454	3.5e- 43			(AC005 662) unknow n protei n [Arabi dopsis thalia na]
139997	ATU001 937	ATL8C2 2851:3 84..28 97	gap2	ATCEA4 S124	99			g24672 72	43	591	1.6e- 64			(Z9975 9) hypoth etical protei n [Schiz osacch aromyc es pombe]
139998	ATU001 938	ATL8C3 481:11 65..23 06	gap2	ATCEA4 S4594	99			g22752 11	43	1528	4.9e- 144			(AC002 337) RNA helica

139999	ATU001 939	ATL8S2 1358:4 81..1	gap2	ATCEA4 C15617 1, ATCEA4 S23315	99, 83	ATL8S2 1358:4 78..25 4	1.00	g37860 08	42	70	6.0e- 09	se isolog [Arabi dopsis thalia nal] (AC005 499) unknow n protei n [Arabi dopsis thalia nal]
140000	ATU001 940	ATL8C2 6563:7 27..1	gap2	ATCEA4 C16207 2, ATCEA4 S3056	99, 87			g72947 8	43	621	2.1e- 60	FERRED OXIN-- NADP REDUCT ASE, LEAF ISOZYM E PRECUR SOR (FNR) [Oryza sativa]
140001	ATU001 941	ATL8C4 0420:8 12..1	gap2	ATCEA4 C35446 1, ATCEA4 C35446 2	99, 99	ATL8C4 0420:7 27..97	0.97	g29567 83	42	351	1.1e- 36	(AL022 103) mannos e-6- phosph ate isomer ase [Schiz osacch aromyc es pombe]
140002	ATU001 942	ATL8C4 1265:1	gap2	ATCEA4 C31171	99, 97, 87	ATL8C4 1265:9	0.93	g30634 65	42	1316	1.5e- 121	(AC003 981)

140007	ATU001 947	ATL8C2 0014:2 13..92 7	gap2	ATCEA4 S30526 , ATCEA4 S33861	99	ATL8C2 0014:2 13..76 4	0.72	g47880 9	42	306		[Arabi dopsis thalia na]
140008	ATU001 948	ATL8C3 0171:1 167..1	gap2	ATCEA4 S13742 , ATCEA4 S20408	99, 84	ATL8C3 0171:9 90..45 6	0.70	g44159 12	42	444	5.2e- 24	(AC006 282) putati ve protea se [Arabi dopsis thalia na]
140009	ATU001 949	ATL8C2 6309:1 919..1	gap2	ATCEA4 C2907 - 1, ATCEA4 S4670, ATCEA4 S4176	99, 95, 94	ATL8C2 6309:1 831..2 69	0.68	g39288 71, g44328 27	42, 41	167, 198	3.0e- 16, 2.0e- 18	(AF093 627) poly(A DP)- ribose polyme rase [Zea mays]; (AC006 593) putati ve ADP- ribose polyme rase [Arabi dopsis

140014	ATU001 954	ATL8C1 1437:3 472..2 739	gap2	ATCEA4 S27302	99					g29110 53	42	672	1.2e- 46	[Homo sapien s] (AL021 961) hypoth etical protei n [Arabi dopsis thalia na]
140015	ATU001 955	ATL8C1 6953:1 383..2 85	gap2	ATCEA4 S31550	99					g49144 23	42	1053	5.1e- 105	(AL050 351) putati ve recept or- like protei n kinase [Arabi dopsis thalia na]
140016	ATU001 956	ATL8C2 9766:3 42..75 8	gap2	ATCEA4 C11686 1_2, ATCEA4 C11686 1_1	99, 97					g29822 83	42	273	4.5e- 29	(AF051 226) PREG- like protei n [Picea marian a]
140017	ATU001 957	ATL8C2 5786:1 ..719	gap2	ATCEA4 S33827 , ATCEA4 C13044 2, ATCEA4 C13052 7_1	99, 95 98, 95					g32362 46	42	518	3.1e- 52	(AC004 684) putati ve expans in protei n [Arabi

140018	ATU001 958	ATL8C9 734:15 26..1	gap2	ATCEA4 S6998	99	ATL8C9 734:14 36..40 1	0.94	g91322 7	41	134	9.1e- 11	dopsis thalia na]
140019	ATU001 959	ATL8C2 6213:2 154..2 648	gap2	ATCEA4 C8592 1	99	ATL8C2 6213:2 154..2 637	0.88	g22448 05	41	396	1.1e- 36	(Z9733 6) hypoth etical protei n [Arabi dopsis thalia na]
140020	ATU001 960	ATL8C6 319:1. .1141	gap2	ATCEA4 S3973	99	ATL8C6 319:45 2..579	0.85	g38763 53	41	82	4.7e- 06	(Z6831 5) Simila rity to Human cleava ge stimul ation factor 50 KD subuni t (SW:CS T3 HUM AN); cDNA

140021	ATU001 961	ATL8C2 5138:8 04..1	gap2	ATCEA4 S11980	99	ATL8C2 5138:2 32..40	0.84	g45811 40	41	532	2.1e- 44	EST yk423h 11.3 comes from this gene; cDNA EST yk423h 11.5 comes from this gene [Caeno rhabdi tis elegan s]
140022	ATU001 962	ATL8C2 84:148 4..641	gap2	ATCEA4 S4891, ATCEA4 C29787 _1	99, 98	ATL8C2 84:134 9..641	0.79	g22450 87	41	251	1.7e- 15	(Z9734 3) hypoth etical protei n [Arabi dopsis thalia na]
140023	ATU001 963	ATL8C2 349:54 ..2718	gap2	ATCEA4 C25149 _1, ATCEA4 S15297	99, 92	ATL8C2 349:54 ..1246	0.76	g26232 96	41	715	6.7e- 33	(AC002 409) hypoth etical protei

140024	ATU001 964	ATL8C2 1002:1 713..1	gap2	ATCEA4 S43	99	ATL8C2 1002:1 658..4 08	0.74	g31525 77	41	1357	2.7e- 128	n [Arabi dopsis thalia na]
140025	ATU001 965	ATL8C3 2333:8 2..190 2	gap2	ATCEA4 C25555 _1	99	ATL8C3 2333:8 2..186 8	0.71	g28326 46	41	573	9.2e- 56	(AL021 710) MuDR transp osable elemen t - like protei n [Arabi dopsis thalia na]
140026	ATU001 966	ATL8C3 3410:1 670..4 86	gap2	ATCEA4 S132	99	ATL8C3 3410:1 593..4 86	0.68	g26424 48	41	887	5.8e- 86	(AC002 391) hypothe tical protei

140027	ATU001 967	ATL8C2 301:1. .1255	gap2	ATCEA4 S26764	99		ATL8C2 301:21 4..112 6	0.66	g45845 33	41	913	6.7e- 96	n [Arabi dopsis thalia na]
140028	ATU001 968	ATL8C1 4899:5 86..1	gap2	ATCEA4 S1399	99		ATL8C1 4899:4 93..31	0.65	g27085 32	41	477	2.8e- 50	(AF029 351) putati ve RNA bindin g protei n [Nicot iana tabacu m]
140029	ATU001 969	ATL8C1 2891:1 ..2428	gap2	ATCEA4 C29152 1, ATCEA4 C12441 4, ATCEA4 C29152 2	99, 93, 88		ATL8C1 2891:6 21..19 76	0.65	g19463 58, g19463 59	41, 36	191, 942	4.7e- 07, 1.7e- 89	(U9321 5) unknow n protei n [Arabi dopsis thalia na]; (U9321 5) unknow n protei n [Arabi dopsis

140030	ATU001 970	ATL8C2 0968:5 00..1	gap2	ATCEA4 C29064 _1	99	ATL8C2 0968:3 49..15 3	0.59	g44907 25	41	416	4.5e- 43	thalia na] (AL035 709) endo- xylogl ucan transf erase- like protei n [Arabi dopsis thalia na]
140031	ATU001 971	ATL8C1 081:36 28..14 08	gap2	ATCEA4 C29050 _1	99	ATL8C1 081:35 01..17 74	0.57	g30753 99	41	345	0.093	(AC004 484) SF16- like protei n [Arabi dopsis thalia na]
140032	ATU001 972	ATL8C4 2220:1 181..1	gap2	ATCEA4 S1973	99	ATL8C4 2220:1 181..1 1	0.57	g44328 46	41	542	7.1e- 54	(AC006 283) unknow n protei n [Arabi dopsis thalia na]
140033	ATU001 973	ATL8C5 602:31 6..913	gap2	ATCEA4 S3319	99	ATL8C5 602:31 6..912	0.45	g48743 06	41	360		(AC006 053) hypoth etical protei n [Arabi dopsis thalia na]

140034	ATU001 974	ATL8C4 3062:3 01..13 72	gap2	ATCEA4 C4526_1	99					g45859 98	41	1632	1.0e- 148	na] (AC005 287) Hypoth etical protei n [Arabi dopsis thalia na]
140035	ATU001 975	ATL8S2 5224:4 98..1	gap2	ATCEA4 S7992	99					g36680 83	41	780	1.2e- 54	(AC004 667) hypoth etical protei n [Arabi dopsis thalia na]
140036	ATU001 976	ATL8C1 6647:2 444..1	gap2	ATCEA4 C15514 _1, ATCEA4 C15514 _2_	99, 99					g33675 69	41	157	0.87	(AL031 135) putati ve protei n [Arabi dopsis thalia na]
140037	ATU001 977	ATL8C2 4393:1 ..2330	gap2	ATCEA4 S36333 , ATCEA4 S36332 , ATCEA4 C144 1	99, 99, 99	ATL8C2 4393:7 7..205 7				g22040 89	40	1195	1.8e- 76	(Z8298 9) FCA gamma [Arabi dopsis thalia na]
140038	ATU001 978	ATL8C2 2780:2 33..22 24	gap2	ATCEA4 C1709_1	99	ATL8C2 2780:3 70..19 47				g32427 89	40	1481	2.5e- 138	(AF055 357) respir atory burst

140039	ATU001 979	ATL8C9 638:92 2..1	gap2	ATCEA4 S7396	99	ATL8C9 638:56 3..56	0.95	g34137 12	40	438	3.8e- 42	oxidase protein D [Arabi dopsis thalia na]
140040	ATU001 980	ATL8C4 0538:1 86..10 39	gap2	ATCEA4 C35546 _1	99	ATL8C4 0538:2 32..10 26	0.93	g45860 58	40	498	6.4e- 22	(AC007 020) unknown protein [Arabi dopsis thalia na]
140041	ATU001 981	ATL8C2 4492:3 315..1	gap2	ATCEA4 C91651 _1, ATCEA4 S8269, ATCEA4 S8270	99, 98, 87	ATL8C2 4492:2 987..4 9	0.93	g24594 24, g45394 58	40, 35	178, 248	6.4e- 07, 2.0e- 14	(AC002 332) unknown protein [Arabi dopsis thalia na]; (AL049 500) hypothetical protein [Arabi

140042	ATU001 982	ATL8C9 53:126 0..1	gap2	ATCEA4 C21672 _1	99	ATL8C9 53:113 4..493	0.93	g35102 53	40	415	7.5e- 30	dopsis thalia na]
140043	ATU001 983	ATL8C2 0407:2 859..1 70	gap2	ATCEA4 C71176 _1, ATCEA4 C71176 _3, ATCEA4 C43575 _1, ATCEA4 S5004	99, 96, 93, 87	ATL8C2 0407:2 859..2 43	0.92	g88580 1	40	107	2.7e- 07	(U1834 0) D6R [Vario la virus]
140044	ATU001 984	ATL8S2 1962:1 ..527	gap2	ATCEA4 C11810 5_1	99	ATL8S2 1962:6 2..394	0.87	g43712 80	40	184	3.0e- 16	(AC006 260) hypoth etical protei n [Arabi dopsis thalia na]
140045	ATU001 985	ATL8C1 6289:1 247..3 062	gap2	ATCEA4 C7184_1, ATCEA4 C18934 _2, ATCEA4 C4718_2	99, 98, 86	ATL8C1 6289:1 247..2 744	0.76	g28298 93	40	845	6.2e- 68	(AC002 311) phosph oglucose mutase [Arabi dopsis thalia na]
140046	ATU001	ATL8C4	gap2	ATCEA4	99,	ATL8C4	0.76	g22447	40	1209	1.6e-	(Z9733

986	2560:1 125..8 5		C68741 1, ATCEA4 S3292, ATCEA4 C7069 1	98, 83	2560:1 081..8 9	72				115	5) transp ort protei n [Arabi dopsis thalia na]	
140047	ATU001 987	ATL8C3 6875:5 93..1	gap2	ATCEA4 S30229 , ATCEA4 C24136 1	99, 96	ATL8C3 6875:5 01..29 3	0.73	g10775 81	40	118	1.5e- 07	probab le membra ne protei n YDR126 w - yeast (Sacch aromyc es cerevi siae) []
140048	ATU001 988	ATL8C5 0165:4 031..1	gap2	ATCEA4 C4641 1, ATCEA4 S1558	99, 96	ATL8C5 0165:3 829..2 1	0.72	g21911 44	40	262	7.3e- 18	(AF007 269) A IG00 2N01.2 4 gene produc t [Arabi dopsis thalia na]
140049	ATU001 989	ATL8C4 1497:1 ..1017	gap2	ATCEA4 S26398 , ATCEA4 C21434 1	99, 97	ATL8C4 1497:6 62..10 06	0.70	g24988 96	40	99	1.5e- 05	SYNAPT ONEMAL COMPLE X PROTEI N 1 (SCP1 PROTEI N) (MEIOT

140050	ATU001 990	ATL8C1 487:45 5..146 9	gap2	ATCEA4 S4768	99	ATL8C1 487:56 7..144 9	0.67	g38222 23	40	336	5.5e- 31	(AF077 955) branch ed- chain alpha keto- acid dehydr ogenas e El alpha subuni t [Arabi dopsis thalia na]	IC CHROMO SOME SYNAPT IC PROTEI N) [Mesoc ricetu s auratu s]
140051	ATU001 991	ATL8S9 360:19 3..757	gap2	ATCEA4 C46698 _1	99	ATL8S9 360:19 3..466	0.64	g42261 29	40	65	5.8e- 06	(AF125 459) No defini tion line found [Caeno rhabdi tis elegan s]	
140052	ATU001 992	ATL8C3 1888:1 ..3618	gap2	ATCEA4 S30098	99, 94 98, 94	ATL8C3 1888:2 97..36	0.64	g19316 54	40	135	5.0e- 08	(U9597 3) BRCA1-	

140053	ATU001 993	ATL8C9 675:24 93..1	gap2	ATCEA4 S12902 , ATCEA4 S13081	18	ATL8C9 675:24 93..23 9	0.57	g42493 91	40	516	2.6e- 41	(AC005 966) Simila r to [Arabi dopsis thalia na]
140054	ATU001 994	ATL8C4 6756:1 644..1	gap2	ATCEA4 C22276 1, ATCEA4 C919_1 , ATCEA4 S29820	99, 93 98, 96	ATL8C4 6756:1 510..3 25	0.43	g21547 15	40	552	1.1e- 31	(Y0941 8) CDPK- relate d protei n kinase [Arabi dopsis thalia na]
140055	ATU001 995	ATL8C2 5844:8 48..1	gap2	ATCEA4 C28553 _1	99			g32876 80	40	425	3.4e- 28	(AC003 979) T22J18 .4 [Arabi dopsis thalia na]
140056	ATU001 996	ATL8C3 9801:6 2..697	gap2	ATCEA4 S7363, ATCEA4 S31629 , ATCEA4	99, 88 88, 88			g44552 95	40	433	1.5e- 35	(AL035 528) isofla vone reduct ase-

140057	ATU001 997	ATL8S1 8150:4 82..1	gap2	ATCEA4 C1041_1, ATCEA4 S25783	99, 93					g24993 27	40	372	1.6e- 26	NADH- UBIQUI NONE OXIDOR EDUCTA SE 20 KD SUBUNIT PRECUR SOR (COMPL EX I- 20KD) (CI- 20KD) [Arabi dopsis thalia na]
140058	ATU001 998	ATL8C1 1190:6 10..1	gap2	ATCEA4 C22306_2	99					g28282 52	40	398	1.3e- 43	(AJ003 137) CYP1 [Lycop ersico n escule ntum]
140059	ATU001 999	ATL8C4 5626:1 ..1082	gap2	ATCEA4 S5137	99	ATL8C4 5626:8 ..1048	0.99			g44553 02	39	522	2.1e- 48	(AL035 528) putati ve protei n [Arabi dopsis thalia na]

140060	ATU002 000	ATL8C3 7275:2 37..91 9	gap2	ATCEA4 C4944_1	99	ATL8C3 7275:3 44..84 1	0.95	g25059 40	39	347	(Y1307 1) 26S protea some, non- ATPase subuni t [Mus muscul us]
140061	ATU002 001	ATL8C1 3124:1 ..1571	gap2	ATCEA4 S1721	99	ATL8C1 3124:1 87..15 71	0.93	g31423 00	39	1897	(AC002 411) Contai ns simila rity to pre- mRNA proces sing protei n PRP39 gb L29 224 from S. cerevi siae. ESTs gb R64 908 and gb T88 158, gb N38 703 and gb AA6 51043 come from this

	009	3901:6 571..7 497		S995		3901:7 438..7 236		88				11	371) No defini tion line found [Arabi dopsis thalia na]
140070	ATU002 010	ATL8C7 655:1. .1720	gap2	ATCEA4 S7855, ATCEA4 C592_1	99, 88	ATL8C7 655:25 7..172 0	0.53	g33675 80	39	591	6.3e- 56	(AL031 135) cyclin 2b protei n [Arabi dopsis thalia na]	
140071	ATU002 011	ATL8C2 6164:1 ..1527	gap2	ATCEA4 C2277_1	99	ATL8C2 6164:1 08..12 76	0.44	g24594 44	39	120	0.022	(AC002 332) hypoth etical protei n [Arabi dopsis thalia na]	
140072	ATU002 012	ATL8S3 0405:1 ..717	gap2	ATCEA4 C1362_1, ATCEA4 S19957	99, 99			g21296 13	39	1019	6.8e- 20	homeot ic protei n BEL1 - Arabid opsis thalia na [Arabi dopsis thalia na]	
140073	ATU002 013	ATL8C4 2798:1	gap2	ATCEA4 C49208	99	ATL8C4 2798:8	0.99	g22249 11	38	757	5.9e- 46	(U9304 8)	

140074	ATU002 014	..1222	gap2	ATCEA4 C16271 1, ATCEA4 S670	99, 95	21..95 2	0.99	g45875 50	38	492	6.1e- 38	somati c embryo genesi s recept or- like kinase [Daucu s carota]
		ATL8C1 4962:5 67..13 33	gap2			ATL8C1 4962:5 96..12 63	0.99	g45875 50	38	492	6.1e- 38	(AC006 577) EST gb R64 848 comes from this gene. [Arabi dopsis thalia na]
140075	ATU002 015	ATL8C4 9705:7 886..3 617	gap2	ATCEA4 C72 1, ATCEA4 S33058	99, 96	ATL8C4 9705:6 908..4 867	0.98	g45388 96	38	324	1.4e- 10	(AL049 482) putati ve protei n [Arabi dopsis thalia na]
140076	ATU002 016	ATL8S1 018:1. .522	gap2	ATCEA4 C42001 1, ATCEA4 S32011	99, 92	ATL8S1 018:72 ..499	0.98	g21911 35	38	607	1.1e- 61	(AF007 269) A IG00 2N01.1 4 gene produc t [Arabi dopsis

140077	ATU002 017	ATL8C8 050:96 0..216	gap2	ATCEA4 C680_1	99	ATL8C8 050:83 0..548	0.98	g37760 07	38	425	9.5e- 27	thalia nal (AJ010 467) RNA helica se [Arabi dopsis thalia nal]
140078	ATU002 018	ATL8C2 8942:8 11..1	gap2	ATCEA4 C2045_ 1, ATCEA4 S33680	99, 98	ATL8C2 8942:6 74..51 0	0.98	g30245 16	38	250	4.4e- 24	RAS- RELATE D PROTEI N RAB11C [Arabi dopsis thalia nal]
140079	ATU002 019	ATL8C3 5926:8 89..1	gap2	ATCEA4 C6663_ 3, ATCEA4 S30964 , ATCEA4 C6663_ 4	99, 98 99, 95	ATL8C3 5926:5 67..15 3	0.96	g45389 11	38	257	4.2e- 17	(AL049 482) hypoth etical protei n [Arabi dopsis thalia nal]
140080	ATU002 020	ATL8C3 864:27 4..379 1	gap2	ATCEA4 S3964, ATCEA4 C35195 1, ATCEA4 C79750 1, ATCEA4 S23514	99, 97, 97, 86	ATL8C3 864:66 7..351 1	0.93	g23988 08	38	67	0.9999	(Z9909 1) pre- ribops omal partic le assemb ly protei n. [Schiz osacch aromyc

140088	ATU002 028	ATL8C1 0853:6 08...35 44	gap2	ATCEA4 S27273 , ATCEA4 C12289 3_1, ATCEA4 S33546	99, 94, 91	ATL8C1 0853:6 42...13 41, ATL8C1 0853:3 008...3 544	0.67, 0.62	g22451 17	38	214	1.5e- 17	(Z9734 3) hypoth etical protein [Arabi dopsis thalia na]
140089	ATU002 029	ATL8C9 243:33 85...1	gap2	ATCEA4 C7044_1, ATCEA4 C15552 _1	99, 99	ATL8C9 243:33 85...75	0.63	g28092 46	38	320		(AC002 560) F2401. 15 [Arabi dopsis thalia na]
140090	ATU002 030	ATL8C8 100:17 31...1	gap2	ATCEA4 C48905 _1	99	ATL8C8 100:14 15...71	0.61	g45860 33	38	759	2.7e- 68	(AC007 109) unknown protein [Arabi dopsis thalia na]
140091	ATU002 031	ATL8C3 442:34 5...1	gap2	ATCEA4 C32292 _1	99	ATL8C3 442:34 5...48	0.59	g42205 31	38	130	2.5e- 08	(AL035 356) hypoth etical protein

140092	ATU002 032	ATL8C9 725:69 5..1	gap2	ATCEA4 S1212, ATCEA4 C22629 _1, ATCEA4 S35609	99, 93, 89	ATL8C9 725:46 0..238	0.57	g29110 49	38	622	5.2e- 65	[Arabi dopsis thalia na] (AL021 961) glucos yltran sferas e - like protei n [Arabi dopsis thalia na]
140093	ATU002 033	ATL8C1 4047:1 ..864	gap2	ATCEA4 C63855 _1	99	ATL8C1 4047:1 25..69 1	0.43	g19316 55	38	1073	5.3e- 99	(U9597 3) recept or - kinase isolog [Arabi dopsis thalia na]
140094	ATU002 034	ATL8C2 6675:7 21..10 4	gap2	ATCEA4 C7281_1	99	ATL8C2 6675:6 62..10 4	1.00	g38745 63	37	191	1.2e- 17	(Z8104 2) simila r to Yeast hypoth etical protei n YFY6 like; cDNA EST yk206h 5.3 comes from this gene;

140097	ATU002 037	ATL8C1 5989:3 492..2 01	gap2	ATCEA4 S25932 , ATCEA4 S22493	99, 88	ATL8C1 5989:3 492..1 675	0.88	g78650 2	37	50	0.16	na] GABP beta 1- 1=hete rotetr americ transc ription factor [mice, 129svJ , Peptid e, 382 aa]
140098	ATU002 038	ATL8C2 9697:8 97..21 67	gap2	ATCEA4 C17727 2, ATCEA4 C17727 3, ATCEA4 S13958	99, 93 98, 93	ATL8C2 9697:1 128..2 161	0.83	g55565 5	37	199	5.8e- 07	(U0671 2) DNA- bindin g protei n [Nicot iana tabacu m]
140099	ATU002 039	ATL8C1 5978:2 555..1	gap2	ATCEA4 S2597, ATCEA4 C76992 1, ATCEA4 S16822 , ATCEA4 S10800	99, 98, 89, 88	ATL8C1 5978:2 555..2 09	0.74	g26684 92	37	342	4.3e- 26	(D8998 1) metal- transp orting P-type ATPase [Arabi dopsis thalia na]
140100	ATU002 040	ATL8C4 9785:1 ..1264	gap2	ATCEA4 C1529 1, ATCEA4 S35356	99, 90	ATL8C4 9785:1 246..7 25	0.71	g22858 85	37	980	2.2e- 76	(D8963 1) sulfat e transp orter

140101	ATU002 041	ATL8C2 6449:2 460..1	gap2	ATCEA4 C9184_1, ATCEA4 C11734 7_1, ATCEA4 S19619	99, 92, 86	ATL8C2 6449:2 324..6 2	0.66	942205 32	37	604	3.6e- 27	[Arabi dopsis thalia na] (AL035 356) putati ve protei n [Arabi dopsis thalia na]
140102	ATU002 042	ATL8C2 1727:2 477..6 1	gap2	ATCEA4 C18071 1, ATCEA4 C33386 _1	99, 97	ATL8C2 1727:2 270..3 69	0.58	938740 39	37	248	1.2e- 20	(Z7552 6) Weak simila rity to Staphy lococcus autoly sin gene (TR:G7 65072) ; cDNA EST EMBL:M 89336 comes from this gene; cDNA EST yk505d 12.3 comes from this gene [Caeno rhabdi

140103	ATU002 043	ATL8C3 0896:1 ..1247	gap2	ATCEA4 C23755 _1	99					g45586 64	37	499	2.6e- 51	(AC007 063) hypo- thetical protein [Arabi- dopsis thalia na]	tis elegan- s]
140104	ATU002 044	ATL8C2 4146:2 156..1 327	gap2	ATCEA4 S26998 , ATCEA4 S32807	99, 93					g42638 20	37	249	1.9e- 19	(AC006 067) hypo- thetical protein [Arabi- dopsis thalia na]	
140105	ATU002 045	ATL8C2 6984:3 599..3 102	gap2	ATCEA4 C26994 _1	99					g33554 71	37	450	2.6e- 43	(AC004 218) putati- ve lysoph- osphol- ipase [Arabi- dopsis thalia na]	
140106	ATU002 046	ATL8C4 9448:1 606..1 918	gap2	ATCEA4 C23678 _1, ATCEA4 S35891	99, 99					g13634 87	37	369	2.0e- 35	IAA7 protei- n - Arabid- opsis thalia na [Arabi- dopsis thalia na]	

140107	ATU002 047	ATL8C2 9573:1 616..1	gap2	ATCEA4 S540, ATCEA4 C48936 1, ATCEA4 S5931	99, 83 86, 83				g22451 07	37	376	5.8e- 31	(Z9734 3) thioes terase homolo g [Arabi dopsis thalia na]
140108	ATU002 048	ATL8C1 0711:1 ..792	gap2	ATCEA4 C1873_1	99	ATL8C1 0711:3 6..778	0.90		g42046 97	36	1165	1.4e- 91	(AF117 063) putati ve inosit ol polyph osphat e 5- phosph atase At5P2 [Arabi dopsis thalia na]
140109	ATU002 049	ATL8C3 9465:6 07..10 11	gap2	ATCEA4 C1756_1, ATCEA4 S30839	99, 94	ATL8C3 9465:6 07..94 9	0.83		g31426 98	36	369	2.9e- 27	(AF064 542) protei n farnes yltran sferas e subuni t A [Arabi dopsis thalia na]
140110	ATU002 050	ATL8C4 3714:1 727..1	gap2	ATCEA4 S1230	99	ATL8C4 3714:1 667..4 0	0.81		g48368 91	36	2369		(AC007 369) Hypoth etical protei

140111	ATU002 051	ATL8C5 430:24 86..1	gap2	ATCEA4 C18336 1, ATCEA4 S1293, ATCEA4 C5256_1	99, 85, 84	ATL8C5 430:24 86..34	0.77	g35601 43	36	177	1.2e- 06	n [Arabi dopsis thalia na] (AL031 534) putati ve vacuol ar protei n sortin g- associ ated protei n [Schiz osacch aromyc es pombel]
140112	ATU002 052	ATL8C7 984:1. .1088	gap2	ATCEA4 S155	99	ATL8C7 984:80 ..1039	0.76	g45392 91	36	1327	8.0e- 98	(AL049 480) putati ve protei n [Arabi dopsis thalia na] (AF007 269) contai ns weak simila rity to nebuli n [Arabi
140113	ATU002 053	ATL8C3 8738:6 93..13 87	gap2	ATCEA4 C31405 _1	99	ATL8C3 8738:7 00..13 37	0.76	g21911 32	36	847	4.1e- 81	

140114	ATU002 054	ATL8S2 4133:6 70..1	gap2	ATCEA4 C7979_2, ATCEA4 S3131, ATCEA4 C7979_1	99, 93 95, 93	ATL8S2 4133:5 40..40 0	0.75	g45862 48	36	351	3.3e- 26	dopsis thalia na] (AL049 640) growth factor like protei n [Arabi dopsis thalia na]
140115	ATU002 055	ATL8C1 3388:1 ..1130	gap2	ATCEA4 C76808 1, ATCEA4 S4673	99, 98	ATL8C1 3388:8 0..113 0	0.75	g48502 91	36	550	2.5e- 56	(AL049 876) putati ve transl ation elonga tion factor ts [Arabi dopsis thalia na]
140116	ATU002 056	ATL8C1 7525:1 040..1	gap2	ATCEA4 C18105 _1	99	ATL8C1 7525:1 040..1 6	0.71	g42622 26	36	465	6.5e- 39	(AC006 200) putati ve protei n kinase [Arabi dopsis thalia na]
140117	ATU002 057	ATL8C4 4331:1 336..6 78	gap2	ATCEA4 S10761 , ATCEA4 S13102	99, 98	ATL8C4 4331:1 128..8 07	0.66	g31281 95	36	574	7.1e- 48	(AC004 521) putati ve phosph oribos

140118	ATU002 058	ATL8C4 9467:1 565..2 729	gap2	ATCEA4 C2413 1, ATCEA4 S17963 , ATCEA4 S5647, ATCEA4 S5651	99, 98, 92, 83	ATL8C4 9467:1 614..2 340	0.47	g11728 73	36	505	3.6e- 54	CYSTEI NE PROTEI NASE RD21A PRECUR SOR [Arabi dopsis thalia na]	yl pyroph osphat e synthe tase [Arabi dopsis thalia na]
140119	ATU002 059	ATL8C3 7721:2 004..1	gap2	ATCEA4 S29837 , ATCEA4 C79788 1, ATCEA4 C19361 1, ATCEA4 S29975	99, 97, 88, 87	ATL8C3 7721:1 792..1 265	0.44	g40068 78	36	827	1.3e- 69	(Z9970 7) MAP3K- like protei n kinase [Arabi dopsis thalia na]	
140120	ATU002 060	ATL8C3 5471:1 383..1	gap2	ATCEA4 S1686	99			g43372 00	36	252	9.9e- 31	(AC006 403) putati ve NAM protei n [Arabi dopsis thalia na]	
140121	ATU002 061	ATL8C4 5291:4 97..1	gap2	ATCEA4 S12095	99			g34618 14	36	758	3.6e- 74	(AC004 138) hypoth	

140122	ATU002 062	ATL8C7 700:1. .814	gap2	ATCEA4 S4249	99	ATL8C7 700:63 .723	0.96	g34510 74	35	698	2.5e- 72	etical protei n [Arabi dopsis thalia na]
140123	ATU002 063	ATL8C4 8101:4 38..95 4	gap2	ATCEA4 C31270 _1	99	ATL8C4 8101:7 73..66 9	0.96	g37380 93	35	102	2.1e- 05	(AC005 617) hypoth etical protei n [Arabi dopsis thalia na]
140124	ATU002 064	ATL8C4 4084:1 187..1 19	gap2	ATCEA4 C1330_ 13, ATCEA4 C1330_ 6	99, 98	ATL8C4 4084:6 82..17 3	0.95	g21295 49	35	864	1.1e- 89	calciu m- depend ent protei n kinase (EC 2.7.1. -) CDPK19 - Arabid opsis thalia na [Arabi dopsis

140132	ATU002 072	ATL8C4 9054:1 ..1209	gap2	ATCEA4 S4823, ATCEA4 S34519 , ATCEA4 S29662 , ATCEA4 C65210 _1	99, 95, 94, 93	ATL8C4 9054:7 6..107 0	0.74	924629 31	35	856	1.6e- 70	(Z8383 3) UDP- glucos e:ster ol glucos yltran sferas e [Arabi dopsis thalia na]
140133	ATU002 073	ATL8C3 7498:3 196..1	gap2	ATCEA4 C28840 1, ATCEA4 C4640 _1, ATCEA4 S5108, ATCEA4 C5544 _2	99, 99, 97, 95	ATL8C3 7498:1 957..1 81	0.73	911840 77	35	521		(U4244 5) Cf- 2.2 [Lycop ersico n pimpin ellifol ium]
140134	ATU002 074	ATL8C2 6978:1 ..1370	gap2	ATCEA4 S2582, ATCEA4 S16778	99, 90	ATL8C2 6978:1 61..90 0	0.70	931354 93	35	1447	1.6e- 130	(AF060 248) unknow n [Arabi dopsis thalia na]
140135	ATU002 075	ATL8C3 1954:4 81..11 62	gap2	ATCEA4 C30128 1, ATCEA4 S2128	99, 95	ATL8C3 1954:1 053..7 03	0.69	928275 46	35	425	2.4e- 32	(AL021 635) cytoch rome P450 like protei n [Arabi dopsis thalia na]

140136	ATU002 076	ATL8C2 621:59 2..247 5	gap2	ATCEA4 C24506 1_	99	ATL8C2 621:59 2..203 3	0.68	g22450 40	35	197	0.34	(Z9734 2) hypoth etical protei n [Arabi dopsis thalia na]
140137	ATU002 077	ATL8C4 453:20 9..318 1	gap2	ATCEA4 C5421_ 1, ATCEA4 S7842, ATCEA4 C87029 1, ATCEA4 S17385 , ATCEA4 S9778, ATCEA4 S3447	99, 92, 89, 87, 86, 83	ATL8C4 453:25 97..30 05, ATL8C4 453:26 2..228 6	0.56, 0.91	g45126 63	35	844	6.2e- 75	(AC006 931) hypoth etical protei n [Arabi dopsis thalia na]
140138	ATU002 078	ATL8C3 7239:1 782..1 61	gap2	ATCEA4 S14637	99	ATL8C3 7239:1 782..4 45	0.54	g45672 20	35	145		(AC007 119) hypoth etical protei n, 3' partia l [Arabi dopsis thalia na]
140139	ATU002 079	ATL8C4 5361:1 ..1197	gap2	ATCEA4 S16839	99			g30045 64	35	311	8.0e- 29	(AC003 673) putati ve recept or Ser/Th r

140140	ATU002 080	ATL8C3 516:10 1..964	gap2	ATCEA4 C35376 _1	99					937575 22	35	337	3.8e- 14	protein kinase [Arabidopsis thaliana] (AC005167) putative splicing factor [Arabidopsis thaliana] (AC007017) hypothetical protein [Arabidopsis thaliana] (AC006841)
140141	ATU002 081	ATL8C3 4806:1 ..1409	gap2	ATCEA4 C19752 _1	99					945103 67	35	135	5.0e- 10	beta-fructo furanosidase (EC 3.2.1.26) - Arabidopsis thaliana [Arabidopsis thaliana] (AC006841)
140142	ATU002 082	ATL8C3 9094:1 ..609	gap2	ATCEA4 C1168_1, ATCEA4 S29102	99, 84					948072 5	35	845	1.2e- 87	beta-fructo furanosidase (EC 3.2.1.26) - Arabidopsis thaliana [Arabidopsis thaliana] (AC006841)
140143	ATU002 083	ATL8C2 2674:1	gap2	ATCEA4 S1299	99	ATL8C2 2674:1	0.98			945672 71	34	1203	2.5e- 78	(AC006841)

140148	087	2915:8 05..22 52		S30694		2915:9 95..19 18	64	18	534) hypo- thetical protein [Arabi- dopsis thaliana]
140149	ATU002 088	ATL8C3 7070:1 510..1	gap2	ATCEA4 S5747	99	ATL8C3 7070:1 510..5 00	g28092 32	584	(AC002 560) F21B7. 1 [Arabi- dopsis thaliana]
140150	ATU002 089	ATL8C3 8186:1 131..1	gap2	ATCEA4 C47842 _1	99	ATL8C3 8186:1 069..3 37	g17076 57	295	(Z7164 0) DnaJ homolo- gue [Pisum sativum]
140151	ATU002 090	ATL8C1 5482:1 ..1413	gap2	ATCEA4 S2742, ATCEA4 C26752 _1	99, 92	ATL8C1 5482:1 33..14 13	g46789 27	40	(AL049 711) hypo- thetical protein [Arabi- dopsis thaliana]
140152	ATU002 091	ATL8C2 4554:6 17..1	gap2	ATCEA4 C1994_1, ATCEA4 S27527, ATCEA4 C1994_5	99, 96, 87	ATL8C2 4554:4 20..20 7	g21297 40	665	small nuclear ribonu- cleopro- tein - Arabid- opsis thaliana

140152	ATU002 092	ATL8C2 8444:1 ..1059	gap2	ATCEA4 C5671_1, ATCEA4 C23107_1	99, 94	ATL8C2 8444:1 05..10 01	0.78	g45876 15	34	992	3.4e- 104	na [Arabi dopsis thalia na] (AC006 951) putati ve acyl- CoA synthe tase [Arabi dopsis thalia na]
140153	ATU002 093	ATL8C1 1224:7 8..277 1	gap2	ATCEA4 C5382_1, ATCEA4 S5149	99, 85	ATL8C1 1224:1 11..24 49	0.74	g45824 59	34	1015	3.7e- 98	(AC007 071) putati ve RanBP7 /impor tin protei n [Arabi dopsis thalia na]
140154	ATU002 094	ATL8C2 3803:1 397..1 894	gap2	ATCEA4 S2169	99	ATL8C2 3803:1 630..1 482	0.74	g17314 75	34	339	1.0e- 33	(U3561 9) ribulo se-1,5 bispho sphate carbox ylase/ oxygen ase large subuni t N- methyl transf

140155	ATU002 095	ATL8C4 8760:1 72..20 65	gap2	ATCEA4 S1033, ATCEA4 C13570 2_1	99, 98	ATL8C4 8760:1 232..1 989	0.67	g22135 36	34	50	0.81	(X9873 8) DNA- bindin g protei n PD1 [Pisum sativu m]
140156	ATU002 096	ATL8C2 5854:8 57..1	gap2	ATCEA4 C2318_1	99	ATL8C2 5854:3 74..14 3	0.62	g45390 05	34	230	3.5e- 14	(AL049 481) putati ve oxidor educta se [Arabi dopsis thalia na]
140157	ATU002 097	ATL8C1 4922:1 88..12 18	gap2	ATCEA4 C4761_1	99	ATL8C1 4922:7 88..89 2	0.49	g19347 56	34	423	1.9e- 32	(Y1245 9) cytoso lic glutam ine synthe tase [Brass ica napus]
140158	ATU002 098	ATL8S2 482:39 ..552	gap2	ATCEA4 S10686	99	ATL8S2 482:48 ..522	0.46	g34618 17	34	172	7.3e- 18	(AC004 138) unknow n protei n [Arabi dopsis]

140159	ATU002 099	ATL8C1 834:71 9..1	gap2	ATCEA4 S841	99	ATL8C1 834:71 9..12	0.42	g31933 02	34	292	6.8e- 22	thalia na] (AF069 298) contai ns simila rity to a protei n kinase domain (Pfam: pkinas e.hmm, score: 166.20) and to legume lectin s beta domain (Pfam: lectin legB. hmm, score: 139.32) [Arabi dopsis thalia na]
140160	ATU002 100	ATL8C4 8587:1 286..2 7	gap2	ATCEA4 C84348 1, ATCEA4 C20537 1	99, 98	ATL8C4 8587:1 261..2 7	0.42	g10014 78	34	197	1.3e- 15	(D6399 9) hypoth etical protei n [Synec hocyst is sp.]

140161	ATU002 101	ATL8C1 494:11 2..109 0	gap2	ATCEA4 S928	99				g28282 84	34	308	5.6e- 33	(AL021 687) hypoth etical protei n [Arabi dopsis thalia na]
140162	ATU002 102	ATL8C4 3809:4 77..1	gap2	ATCEA4 C11252 1, ATCEA4 S28687	99, 83				g14320 56	34	138		(U5683 4) WRKY3 [Petro selinu m crispu m]
140163	ATU002 103	ATL8C2 268:1. .767	gap2	ATCEA4 C27671 1	99				g45585 64	34	179	9.3e- 19	(AC007 138) predic ted protei n of unknow n functi on [Arabi dopsis thalia na]
140164	ATU002 104	ATL8C1 7487:1 ..1261	gap2	ATCEA4 C46471 1	99	ATL8C1 7487:5 5..125 8	1.00		g45389 28	33	191	1.5e- 12	(AL049 483) putati ve protei n [Arabi dopsis thalia na]
140165	ATU002 105	ATL8C4 5334:1 263..1	gap2	ATCEA4 C25829 1	99				g14917 10	34	103	0.089	(X9650 6) alpha

140166	ATU002 106	ATL8C4 021:98 ..720	gap2	ATCEA4 C68647 _1	99						g23885 69	34	611	3.2e- 42	(AC000 098) Simila r to hypoth etical protei n PID1e3 27464 (gb Z9 7338). [Arabi dopsis thalia na]	subuni t; forms hetero dimer with NC2 alpha/ Dr1 [Homo sapien s]
140167	ATU002 107	ATL8C2 0467:7 89..13 85	gap2	ATCEA4 C27911 _1, ATCEA4 S10766	99, 83						940975 47	33	111	0.0002 9	(U6490 6) ATFP3 [Arabi dopsis thalia na]	
140168	ATU002 108	ATL8S2 9333:5 52..1	gap2	ATCEA4 C31361 _1	99						g13302 54	33	391	9.7e- 38	(D8503 9) calciu m- depend ent protei n kinase [Zea	

140169	ATU002 109	ATL8C2 0876:2 2..262 3	gap2	ATCEA4 C4252_1, ATCEA4 S2641, ATCEA4 C69697 2, ATCEA4 S938	99, 99, 98, 88	ATL8C2 0876:2 79..24 73	0.94	g28298 94	33	1379	1.9e- 85	mays] (AC002 311) Unknown protein [Arabi dopsis thalia na]
140170	ATU002 110	ATL8C2 4134:8 44..1	gap2	ATCEA4 C22_1	99	ATL8C2 4134:7 38..60	0.93	g21296 77	33	537	3.4e- 55	probab lel N- acetyl transf erase hookle ss 1 - Arabid opsis thalia na [Arabi dopsis thalia na]
140171	ATU002 111	ATL8C3 6372:7 74..1	gap2	ATCEA4 C26639 1, ATCEA4 C26639 4	99, 95	ATL8C3 6372:7 73..58	0.85	g47419 29	33	314	1.6e- 36	(AF130 253) membra ne relate d protei n CP5 [Arabi dopsis thalia na]
140172	ATU002 112	ATL8C3 5537:1 223..1	gap2	ATCEA4 C25518 _1	99	ATL8C3 5537:1 089..6 6	0.85	g42043 09	33	966	4.0e- 83	(AC003 027) lcl pr t_seq No defini tion

140173	ATU002 113	ATL8S1 3270:4 63..1	gap2	ATCEA4 C35680 _1	99	ATL8S1 3270:3 89..88	0.85	g45390 08	33	284	1.4e- 28	line found [Arabi dopsis thalia na] (AL049 481) lipase -like protei n [Arabi dopsis thalia na]
140174	ATU002 114	ATL8C2 3293:1 ..2239	gap2	ATCEA4 S4149, ATCEA4 S29491 , ATCEA4 S32774	99, 99, 89	ATL8C2 3293:1 01..21 02	0.82	g44553 50	33	715	2.1e- 55	(AL035 524) putati ve protei n [Arabi dopsis thalia na]
140175	ATU002 115	ATL8C2 3591:1 530..9 8	gap2	ATCEA4 S29803	99	ATL8C2 3591:1 515..9 8	0.72	g41851 39	33	590	1.3e- 53	(AC005 724) putati ve diacyl glycer ol kinase [Arabi dopsis thalia na]
140176	ATU002 116	ATL8C1 4:263. .1266	gap2	ATCEA4 S5177	99	ATL8C1 4:550. .985	0.70	g34510 75	33	254	6.0e- 09	(AL031 326) putati ve protei n [Arabi

140177	ATU002 117	ATL8C4 2:1305 ..1	gap2	ATCEA4 C5317_1, ATCEA4 S30328 , ATCEA4 S2536	99, 95, 89	ATL8C4 2:1192 ..84	0.69	g22449 04	33	139	2.0e- 09	dopsis thalia nal (Z9733 9) simila r to hypoth etical protei n C02F5. 7 - Caenor ha [Arabi dopsis thalia nal
140178	ATU002 118	ATL8C5 910:70 ..1839	gap2	ATCEA4 S15422 , ATCEA4 C11991 9_1	99, 92	ATL8C5 910:76 2..135 9	0.66	g39154 63	33	68		HYPOTH ETICAL 33.1 KD PROTEI N SLR159 2 [Synec hocyst is sp.]
140179	ATU002 119	ATL8C1 3068:2 609..1 49	gap2	ATCEA4 C32380 _1, ATCEA4 C11823 _2, ATCEA4 C11823 _1	99, 95 97, 95	ATL8C1 3068:2 509..1 49	0.61	g37860 17	33	62	0.98	(AC005 499) putati ve non- green plasti d inner envelo pe membra ne protei

140180	ATU002 120	ATL8C2 7052:1 ..2457	gap2	ATCEA4 C23307 1, ATCEA4 C23307 2, ATCEA4 C11000 1, ATCEA4 S35148 , ATCEA4 S28219	99, 99, 97, 95, 83	ATL8C2 7052:1 13..24 38	0.52	g44068 19	33	232	5.8e- 21	n [Arabi dopsis thalia na] (AC006 201) unknow n protei n [Arabi dopsis thalia na]
140181	ATU002 121	ATL8C4 8332:1 959..1 324	gap2	ATCEA4 C31561 1 _	99	ATL8C4 8332:1 948..1 324	0.45	g62358 4	33	229	6.0e- 20	(L2927 2) putati ve [Nicot iana tabacu m]
140182	ATU002 122	ATL8C3 5205:4 98..18 04	gap2	ATCEA4 C2165 1 _	99	ATL8C3 5205:5 25..12 55	0.43	g37790 33	33	889	1.9e- 88	(AC005 171) cycloa rtlenol syntha se [Arabi dopsis thalia na]
140183	ATU002 123	ATL8C1 4148:3 58..10 94	gap2	ATCEA4 C31825 1 _	99			g37790 28	33	978	5.5e- 93	(AC005 171) putati ve recept or kinase [Arabi

140184	ATU002 124	ATL8C3 59:135 4..201 5	gap2	ATCEA4 C2719_1	99					g45126 51	33	208	3.5e- 15	(AC007 048) putati ve tyrosi ne transa minase [Arabi dopsis thalia na]
140185	ATU002 125	ATL8C1 7064:1 435..1	gap2	ATCEA4 C6500_1	99					g16735 20	33	55	0.11	(U7251 5) C3f [Homo sapien s]
140186	ATU002 126	ATL8C1 4912:1 276..2 91	gap2	ATCEA4 C13346 7_1, ATCEA4 S5153	99, 84					g45812 07	33	1112	1.8e- 98	(Y1791 4) cyclic nucleo tide and calmod ulin- regula ted ion channe l [Arabi dopsis thalia na]
140187	ATU002 127	ATL8C3 5221:6 31..1	gap2	ATCEA4 C30943 2, ATCEA4 C30943 1, ATCEA4 S35408	99, 98, 87					g27393 81	33	606	8.8e- 61	(AC002 505) putati ve patati n [Arabi dopsis na]

140188	ATU002 128	ATL8C3 2520:2 238..1 216	gap2	ATCEA4 C17040 _1	99					g34027 01	33	155	1.3e- 06	(AC004 261) unknown protein [Arabi dopsis thalia na]
140189	ATU002 129	ATL8C4 9275:1 ..794	gap2	ATCEA4 C12414 _1, ATCEA4 S25033	99, 95	ATL8C4 9275:9 1..763	0.93			g45799 13	32	898	7.3e- 92	(AB023 423) sulfate transporter [Arabi dopsis thalia na]
140190	ATU002 130	ATL8C3 9853:3 53..20 36	gap2	ATCEA4 C18680 _1	99	ATL8C3 9853:3 53..20 06	0.93			g30804 26	32	366	9.7e- 37	(AL022 604) putative protein [Arabi dopsis thalia na]
140191	ATU002 131	ATL8C4 96:1.. 1006	gap2	ATCEA4 C12464 _1, ATCEA4 S20944 , ATCEA4 C12464 _2	99, 91, 87	ATL8C4 96:734 ..840	0.91			g40564 18	32	379	8.1e- 31	(AC005 322) T7A14. 5 [Arabi dopsis thalia na]
140192	ATU002 132	ATL8C2 9119:9 58..18	gap2	ATCEA4 S10619	99	ATL8C2 9119:9 67..17	0.84			g29470 63	32	354	2.7e- 23	(AC002 521) putative

140193	ATU002 133	ATL8C4 6352:4 56..13 80	gap2	ATCEA4 C6841_1	99	ATL8C4 6352:6 23..13 73	0.81	g30986 03	32	150	2.1e- 07	(AF052 191) katani n p60 subuni t [Stron gyloce ntrotu s purpur atus]
140194	ATU002 134	ATL8C2 8304:9 1..793	gap2	ATCEA4 C16731_1	99	ATL8C2 8304:6 59..46 3	0.73	g25296 83	32	704	2.5e- 56	(AC002 535) unknown protein [Arabi dopsis thalia na]
140195	ATU002 135	ATL8C3 5937:1 ..1999	gap2	ATCEA4 C70124_1	99	ATL8C3 5937:7 8..187 1	0.71	g27393 86	32	1275	5.5e- 113	(AC002 505) unknown protein [Arabi dopsis thalia na]
140196	ATU002 136	ATL8C4 7270:3 16..77	gap2	ATCEA4 C1044_3	99	ATL8C4 7270:3 37..74	0.69	g11717 70	32	461	2.6e- 47	NITRIL ASE 3 [Arabi na]

		1				4											dopsis thaliana]
140197	ATU002 137	ATL8C3 7360:3 44..14 32	gap2	ATCEA4 C5997_1	99		ATL8C3 7360:4 89..79 0	0.66	g42205 14	32	486						(AL035 356) putative protein [Arabidopsis thaliana]
140198	ATU002 138	ATL8C4 7938:1 887..2 663	gap2	ATCEA4 S36225	99		ATL8C4 7938:1 887..2 220	0.63	g28287 3	32	556						transferring protein (myb) homolog - Arabidopsis thaliana [Arabidopsis thaliana]
140199	ATU002 139	ATL8C3 1673:5 13..1	gap2	ATCEA4 C703_1 , ATCEA4 S4404	99, 82		ATL8C3 1673:4 50..14 5	0.59	g43143 68	32	143						(AC006 340) hypothetical protein [Arabidopsis thaliana]
140200	ATU002 140	ATL8C1 6300:1 ..3501	gap2	ATCEA4 C6666_1	99		ATL8C1 6300:2 62..31 63	0.55	g41658 61, g44551 31	32, 30	310, 431						(AF006 603) histone deacetylase mHDA2

140201	ATU002 141	ATL8C3 9671:2 448..1	gap2	ATCEA4 C89169 1, ATCEA4 S2348	99, 84	ATL8C3 9671:2 189..5 4	0.51	g30435 96	32	744	1.5e- 69	[Mus muscul us]; (AF129 433) histon e deacet ylase HDA2 [Droso phila melano gaster]
140202	ATU002 142	ATL8C2 6011:7 61..1	gap2	ATCEA4 C10068 6_1	99	ATL8C2 6011:5 85..22 7	0.41	g32275 2	32	729	1.4e- 78	auxin- indepe ndent growth promot er - Nicoti ana tabacu m [Nicot iana tabacu m]
140203	ATU002 143	ATL8C4 7296:1 ..1564	gap2	ATCEA4 C32401 1, ATCEA4 S4350, ATCEA4 S3691,	99, 89, 88, 85			g46783 23	32	2431	1.1e- 207	(AL049 658) putati ve protei n [Arabi

140208	ATU002 148	ATL8C3 8691:1 441..1	gap2	ATCEA4 C2391_1, ATCEA4 S30361	99, 98	ATL8C3 8691:1 433..7 74	0.98	g23533 33	31	173	0.86	tional enzyme [Schiz osacch aromyc es pombel] (AF016 513) Ce-LEA [Caeno rhabdi tis elegan s] []
140209	ATU002 149	ATL8C9 99:1.. 754	gap2	ATCEA4 C2882_1	99	ATL8C9 99:74. .703	0.98	g35824 36	31	621	6.6e- 64	(AB017 502) beta- D- glucan exohyd rolase [Nicot iana tabacu m]
140210	ATU002 150	ATL8C2 6448:1 ..803	gap2	ATCEA4 C9674_1, ATCEA4 C6889_1	99, 98	ATL8C2 6448:5 7..677	0.94	g21941 37	31	279	9.4e- 20	(AC002 062) ESTs gb1R29 947,gb 1H7670 2 come from this gene. [Arabi dopsis thalia na]
140211	ATU002 151	ATL8C4 8420:1 ..716	gap2	ATCEA4 C2757_1	99	ATL8C4 8420:1 66..59 4	0.89	g58489 2	31	523	1.8e- 56	SERINE CARBOX YPEPTI DASE I PRECUR

140212	ATU002 152	ATL8C3 8095:1 374..1	gap2	ATCEA4 S309, ATCEA4 C3119_1	99, 98	ATL8C3 8095:1 053..1 83	0.88	g26705 5	31	1067	2.5e- 88	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRAN SFERASE) [Arabidopsis thaliana]
140213	ATU002 153	ATL8C3 5917:1 704..3 09	gap2	ATCEA4 C30731 _1	99	ATL8C3 5917:1 548..3 09	0.85	g17056 58	31	157	0.0054	CCAAT-BINDING FACTOR (CBF) [Homo sapiens]
140214	ATU002 154	ATL8C9 830:12 82..1	gap2	ATCEA4 S1066	99	ATL8C9 830:10 86..28	0.84	g41386 50	31	425	1.6e- 19	(Z84207) polynucleotide phosphorylase [Thermophilus]
140215	ATU002 155	ATL8C5 512:29	gap2	ATCEA4 C1806	99	ATL8C5 512:28	0.83	g21911 80	31	1184	9.0e- 109	(AF007270)

		82..16 70		1				74..18 54								Similar r to kinesi n; coded for by A. thalia na cDNA W43760 [Arabi dopsis thalia na]
140216	ATU002 156	ATL8C1 963:26 36..11 31	gap2	ATCEA4 C34844 1, ATCEA4 S35156 , ATCEA4 C3424_1, ATCEA4 S19886	99, 95, 91, 86	ATL8C1 963:25 08..14 04	0.77	g24628 26	31	1462	7.8e- 133	(AF000 657) unknown protei n [Arabi dopsis thalia na]				
140217	ATU002 157	ATL8C1 7726:4 692..1 01	gap2	ATCEA4 C1880_1, ATCEA4 C2011_1	99, 97	ATL8C1 7726:4 582..1 01	0.76	g40975 57	31	147	1.2e- 11	(U6491 1) ATFP8 [Arabi dopsis thalia na]				
140218	ATU002 158	ATL8C1 3239:2 77..28 52	gap2	ATCEA4 S1782	99	ATL8C1 3239:4 49..28 52	0.73	g32016 56	31	86	0.062	(AF005 933) galact okinas e [Lacto bacill us casei]				
140219	ATU002 159	ATL8C4 7695:2 45..11	gap2	ATCEA4 S10714	99	ATL8C4 7695:2 45..73	0.72	g31845 60	31	109	9.3e- 06	(AF052 290) c-type				

140220	ATU002 160	95	gap2	ATCEA4 C30809 _1	99	ATL8C7 884:49 9..744	0.68	g21911 97	31	485	1.3e- 50	cytochrome biogenesis protein [Synecchococcus PCC7002]
												(AF007271) contains similarity to Synecchococcus PCC7942 chromosomal region used as basis of neutral siteI recombinational cloning vector (PID:g1174192) [Arabidopsis thaliana]

140221	ATU002 161	ATL8C4 0991:1 088..3 00	gap2	ATCEA4 C1622_1	99	ATL8C4 0991:1 036..4 95	0.67	g23351 92	31	780	7.2e- 73	na] (AF013 465) bHLH protei n [Arabi dopsis thalia na]
140222	ATU002 162	ATL8C3 6999:1 ..2139	gap2	ATCEA4 S14238 , ATCEA4 C26824 _1	99, 97	ATL8C3 6999:4 48..18 84	0.67	g31655 70	31	164	5.2e- 08	(AF067 946) simila r to Drosop hila ring canal protei n (kelch) (SW:Q0 4652) [Caeno rhabdi tis elegan s]
140223	ATU002 163	ATL8C1 4936:1 ..1157	gap2	ATCEA4 S1670	99	ATL8C1 4936:4 8..114 2	0.67	g48369 17	31	451	1.6e- 43	(AC007 153) 80099 [Arabi dopsis thalia na]
140224	ATU002 164	ATL8C1 0255:1 304..1	gap2	ATCEA4 C30157 _1	99	ATL8C1 0255:1 245..3 3	0.66	g31767 14	31	1365		(AC002 392) putati ve tRNA- splici ng endonu clease

140225	ATU002 165	ATL8C2 3758:2 501..3 060	gap2	ATCEA4 C21905 2, ATCEA4 C21905 1_	99, 98	ATL8C2 3758:3 012..2 740	0.66	g34260 39	31	365	7.8e- 37	(AC005 168) unknown protein [Arabi dopsis thalia na]
140226	ATU002 166	ATL8C1 378:16 79..1	gap2	ATCEA4 S27198 , ATCEA4 S32269 , ATCEA4 C60835 1_	99, 88 92, 88	ATL8C1 378:10 02..66 1	0.52	g45393 89	31	214	1.2e- 17	(AL035 526) putative protein kinase [Arabi dopsis thalia na]
140227	ATU002 167	ATL8C3 7957:1 ..682	gap2	ATCEA4 C16164 1_	99	ATL8C3 7957:1 02..58 2	0.51	g28326 25	31	445	3.2e- 39	(AL021 711) putative protein [Arabi dopsis thalia na]
140228	ATU002 168	ATL8C1 0189:9 19..1	gap2	ATCEA4 C6391_1	99	ATL8C1 0189:7 61..14 0	0.50	g45126 66	31	483		(AC006 931) putative mei2 protein

140229	ATU002 169	ATL8C7 951:15 05..1	gap2	ATCEA4 C4648__ 1	99	ATL8C7 951:42 7..29	0.50	g36680 69	31	306	1.5e- 29	n [Arabi dopsis thalia na]
140230	ATU002 170	ATL8C1 0692:8 30..34 1	gap2	ATCEA4 S9372	99			g13519 7	31	189		TYROSY L-TRNA SYNTH TASE (TYROS INE-- TRNA LIGASE) (TYRRS) []
140231	ATU002 171	ATL8C4 9150:6 58..1	gap2	ATCEA4 C6388__ 1	99			g22450 68	31	242	0.088	(Z9734 2) serine protea se homolo g [Arabi dopsis thalia na]
140232	ATU002 172	ATL8C1 9053:2 518..8 51	gap2	ATCEA4 S26490	99			g33775 07	31	483	1.6e- 24	(AF056 026) auxin transp ort protei n EIR1 [Arabi

140233	ATU002 173	ATL8S6 014:53 8..1	gap2	ATCEA4 C35539 _1	99					g46789 46	31	634	3.9e- 58	(AL049 711) putati ve protei n [Arabi dopsis thalia na]
140234	ATU002 174	ATL8C1 2480:9 05..1	gap2	ATCEA4 C35230 _2, ATCEA4 C35230 _1	99, 96					g44551 69	31	104	2.0e- 07	(AL035 521) putati ve aldehy de dehydr ogenas e [Arabi dopsis thalia na]
140235	ATU002 175	ATL8C2 1840:2 562..2 040	gap2	ATCEA4 S10907 , ATCEA4 S22358 , ATCEA4 S1451	99, 84, 83					g11716 42	31	218	1.8e- 19	PROEAB LE SERINE /THREO NINE- PROTEI N KINASE NAK [Arabi dopsis thalia na]
140236	ATU002 176	ATL8C1 1297:5 22..1	gap2	ATCEA4 C19789 _1	99					g45875 26	31	300	6.5e- 28	(AC007 060) Strong simila rity to

140237	ATU002 177	ATL8C4 5854:1 ..1158	gap2	ATCEA4 C10977 _1	99	ATL8C4 5854:8 5..115 8	0.99	938742 14	30	559	1.2e- 56	F19I3. 2 [] (Z8321 7) Simila rity to Yeast E1-E2 ATPase YEI031 W (SW:YE D1_YEA ST); CDNA EST EMBL:D 27574 comes from this gene; CDNA EST EMBL:D 33757 comes from this gene; CDNA EST EMBL:D 34256 comes from this gene; CDNA EST EMBL:D 37288 comes from..
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140238	ATU002 178	ATL8C1 5865:1 ..3165	gap2	ATCEA4 C10063 3_1, ATCEA4 C10063 3_2	99, 93	ATL8C1 5865:2 01..10 69, ATL8C1 5865:2 252..1 764	0.94, 0.71	948369 17	30	222	2.3e- 21	(AC007 153) 80099 [Arabi dopsis thalia na]
140239	ATU002 179	ATL8C1 3457:1 0323.. 1	gap2	ATCEA4 S11022 , ATCEA4 C1950 1	99, 98	ATL8C1 3457:1 0255.. 168	0.92	934026 97	30	1051	4.7e- 98	(AC004 261) putati ve phosph atidyl inosit ol-4- phosph ate 5- kinase [Arabi dopsis thalia na]
140240	ATU002 180	ATL8C8 46:239 ..1129	gap2	ATCEA4 C33981 _1	99	ATL8C8 46:239 ..1083	0.91	948357 80	30	593	7.0e- 54	(AC007 296) Strong simila rity to gb AF0 49347 berber ine bridge enzyme from Berber is stolon ifera. [Arabi dopsis thalia na]

140241	ATU002 181	ATL8S2 3441:5 85..1	gap2	ATCEA4 C23679 _1	99	ATL8S2 3441:2 97..14 0	0.90	g38853 31	30	371	3.7e- 35	(AC005 623) putati ve cytoch rome p450 protei n [Arabi dopsis thalia na]
140242	ATU002 182	ATL8C2 1763:9 36..13 80	gap2	ATCEA4 C31641 _1	99	ATL8C2 1763:1 352..9 50	0.89	g42042 71	30	293	1.1e- 23	(AC005 223) Unknow n protei n [Arabi dopsis thalia na]
140243	ATU002 183	ATL8C3 8605:4 19..1	gap2	ATCEA4 C29317 _1	99	ATL8C3 8605:3 48..11 7	0.89	g14029 16	30	227	2.1e- 19	(X9831 9) peroxi dase [Arabi dopsis thalia na]
140244	ATU002 184	ATL8C2 3302:2 739..1 02	gap2	ATCEA4 C39593 _1	99	ATL8C2 3302:2 633..1 02	0.83	g49268 27	30	435	5.0e- 40	(AC004 135) T17H7. 12 [Arabi dopsis thalia na]
140245	ATU002 185	ATL8C3 8709:7 06..1	gap2	ATCEA4 C7112_1	99	ATL8C3 8709:6 30..12 1	0.82	g42622 22	30	588	7.9e- 49	(AC006 200) putati ve RNA helica se A,

140246	ATU002 186	ATL8C4 3105:1 ..1094	gap2	ATCEA4 S1060	99	ATL8C4 3105:9 73..10 25	0.81	g37383 39	30	291	2.5e- 17	partia l [Arabi dopsis thalia na]
140247	ATU002 187	ATL8C2 3702:1 ..691	gap2	ATCEA4 C5138_1, ATCEA4 C57180_1	99, 82	ATL8C2 3702:2 49..64 1	0.78	g28110 28	30	572	5.5e- 59	HYPOTH ETICAL 47.9 KD PROTEI N M021B0 4.12 [Arabi dopsis thalia na]
140248	ATU002 188	ATL8C1 0450:2 755..1	gap2	ATCEA4 C11231 _1, ATCEA4 S27469	99, 96	ATL8C1 0450:2 444..7 58	0.77	g38452 48	30	123		(AE001 410) hypoth etical protei n [Plasm odium falcip arum]
140249	ATU002 189	ATL8C1 1655:1 522..1	gap2	ATCEA4 S27201	99	ATL8C1 1655:1 331..4 46	0.77	g28326 18	30	1193	5.8e- 104	(AL021 711) putati ve protei n [Arabi

140255	ATU002 195	ATL8C5 508:1. .747	gap2	ATCEA4 C70705 _1	99				g22136 00	30	509	6.7e- 51	uvate decarb oxylas e [Metha nobact erium thermo autotr ophicu m]
140256	ATU002 196	ATL8C1 0435:1 325..1	gap2	ATCEA4 S12913 , ATCEA4 C11130 _1	99, 96				g31691 71	30	374		(AC004 401) putati ve serine carbox ypepti dase I [Arabi dopsis thalia na]
140257	ATU002 197	ATL8C4 7272:1 207..1	gap2	ATCEA4 C24851 1, ATCEA4 S3411, ATCEA4 C24851 2, ATCEA4 S34250	99, 97, 92, 84				g10768 21	30	141	1.le- 13	probab le 1- acyl- glycer ol-3- phosph ate acyltr ansfer ase - maize [Zea mays]
140258	ATU002	ATL8C3	gap2	ATCEA4	99	ATL8C3	1.00						

140259	198	0139:2 47..20 52		C28034 1		0139:2 47..20 52						
	ATU002 199	ATL8S2 0156:1 ..544	gap2	ATCEA4 C8405 1, ATCEA4 S4948	99, 94	ATL8S2 0156:1 1..544	1.00					
140260	ATU002 200	ATL8C1 0677:1 54..89 5	gap2	ATCEA4 C15241 3, ATCEA4 C15241 1	99, 94	ATL8C1 0677:1 87..88 9	1.00					
140261	ATU002 201	ATL8C8 153:98 2..352	gap2	ATCEA4 C5738 1, ATCEA4 S22909	99, 83	ATL8C8 153:51 3..352	1.00					
140262	ATU002 202	ATL8C7 074:17 03..43 0	gap2	ATCEA4 S29797 94, 93, 85 ATCEA4 C16630 1, ATCEA4 C62904 1, ATCEA4 S6408	99, 94, 93, 85	ATL8C7 074:16 52..59 4	1.00					
140263	ATU002 203	ATL8C9 062:15 34..31 2	gap2	ATCEA4 S890	99	ATL8C9 062:15 32..31 2	1.00					
140264	ATU002 204	ATL8C4 1145:3 52..54 6	gap2	ATCEA4 C4825 2	99	ATL8C4 1145:4 74..54 6	1.00					
140265	ATU002 205	ATL8C4 9032:1 ..1651	gap2	ATCEA4 S14339 ATCEA4 C16026 1	99, 98	ATL8C4 9032:3 42..15 11	1.00					

140266	ATU002 206	ATL8C1 1903:1 ..737	gap2	ATCEA4 C5154_2, ATCEA4 C5154_1	99, 95	ATL8C1 1903:1 15..26 5	1.00					
140267	ATU002 207	ATL8C4 2182:3 177..3 989	gap2	ATCEA4 C14253 _1	99	ATL8C4 2182:3 766..3 987	1.00					
140268	ATU002 208	ATL8C4 1517:2 00..23 30	gap2	ATCEA4 C2224_1, ATCEA4 S7914	99, 98	ATL8C4 1517:4 73..23 30	1.00					
140269	ATU002 209	ATL8C3 5749:1 076..1	gap2	ATCEA4 C461_1	99	ATL8C3 5749:9 56..12 7	0.99					
140270	ATU002 210	ATL8C1 6641:3 737..2 337	gap2	ATCEA4 C4969_1, ATCEA4 S23815 , ATCEA4 S486, ATCEA4 S32779 , ATCEA4 C4969_2	99, 97, 96, 91, 87	ATL8C1 6641:3 574..2 489	0.99					
140271	ATU002 211	ATL8C2 8719:1 ..523	gap2	ATCEA4 C560_1	99	ATL8C2 8719:2 13..42 5	0.99					
140272	ATU002 212	ATL8C3 3327:4 48..67 4	gap2	ATCEA4 C6798_1	99	ATL8C3 3327:5 94..67 4	0.99					
140273	ATU002 213	ATL8C2 6951:2 293..8	gap2	ATCEA4 C13530 1,	98, 92	ATL8C2 6951:2 155..1	0.99	g32692 88, g45593	100, 99	743, 425	1.5e- 68, 3.5e-	(AL030 978) putati

	38		ATCEA4 S21534		574	86	35	ve protei n [Arabi dopsis thalia na]; (AC006 526) putati ve polyga lactur onase [Arabi dopsis thalia na]
140274	ATU002 214	ATL8C3 210:50 22..72 05	gap2	98, 86	ATL8C3 210:51 38..72 05	0.99	1698	(L2748 4) calciu m- depend ent protei n kinase [Zea mays]
140275	ATU002 215	ATL8C2 0103:1 010..4 91	gap2	99, 84	ATL8C2 0103:8 38..57 9	0.99		
140276	ATU002 216	ATL8C2 1370:1 393..2 496	gap2	99	ATL8C2 1370:1 405..2 496	0.99		
140277	ATU002 217	ATL8C4 2863:1 196..3 057	gap2	99, 97	ATL8C4 2863:2 166..3 057	0.99		

140278	ATU002 218	ATL8S7 75:326 ..1	gap2	ATCEA4 C13335 5 1	99	ATL8S7 75:326 ..50	0.99				
140279	ATU002 219	ATL8C7 017:12 90..39 5	gap2	ATCEA4 S11788	99	ATL8C7 017:12 67..39 5	0.99				
140280	ATU002 220	ATL8C4 3529:7 01..81	gap2	ATCEA4 C22912 2, ATCEA4 C22912 1	99, 97	ATL8C4 3529:3 75..59 6	0.99				
140281	ATU002 221	ATL8C4 8008:2 944..3 903	gap2	ATCEA4 C155_1	99	ATL8C4 8008:3 002..3 771	0.99				
140282	ATU002 222	ATL8C4 8714:1 771..4 631	gap2	ATCEA4 C1713_1, ATCEA4 S28954 , ATCEA4 S33676 , ATCEA4 S33883	99, 92, 89, 89	ATL8C4 8714:1 784..4 445	0.99				
140283	ATU002 223	ATL8C9 959:11 87..14 80	gap2	ATCEA4 C1871_1	99	ATL8C9 959:12 96..14 80	0.99				
140284	ATU002 224	ATL8C4 9860:5 44..1	gap2	ATCEA4 C4119_4, ATCEA4 C4119_1, ATCEA4 C4119_6, ATCEA4 S13116	99, 99, 97, 97, 94, 82	ATL8C4 9860:4 13..7	0.99				

	232	9716:1		C22613		9716:3						
140293	ATU002 233	9716:1 ..558 ATL8C9 372:23 6..140 5	gap2	ATCEA4 C1255_1	99	ATL8C9 372:23 6..116 4	0.98					
140294	ATU002 234	ATL8C1 3528:1 ..574	gap2	ATCEA4 C1175_1, ATCEA4 C1175_2	99, 87	ATL8C1 3528:3 46..43 8	0.98					
140295	ATU002 235	ATL8C1 8987:1 788..1 202	gap2	ATCEA4 C80748_1	99	ATL8C1 8987:1 697..1 338	0.98					
140296	ATU002 236	ATL8C1 0856:1 966..1 53	gap2	ATCEA4 S1502	99	ATL8C1 0856:1 961..1 53	0.98					
140297	ATU002 237	ATL8C4 7994:2 446..5 01	gap2	ATCEA4 C594_1	99	ATL8C4 7994:2 227..7 32	0.98					
140298	ATU002 238	ATL8C4 2671:5 63..10 96	gap2	ATCEA4 C21365_1	99	ATL8C4 2671:6 18..10 96	0.98					
140299	ATU002 239	ATL8C3 2229:3 195..4 817	gap2	ATCEA4 C268_1	99	ATL8C3 2229:3 240..4 817	0.98					
140300	ATU002 240	ATL8C2 1567:2 023..1 392	gap2	ATCEA4 S5088	99	ATL8C2 1567:1 879..1 392	0.98					
140301	ATU002 241	ATL8C2 2971:1 51..10 66	gap2	ATCEA4 C1331_4, ATCEA4 S2373, ATCEA4 C1331_3	99, 93, 92	ATL8C2 2971:2 13..10 66	0.98					

140302	ATU002 242	ATL8C4 5424:2 363..3 901	gap2	ATCEA4 C3418_1	98	ATL8C4 5424:2 795..3 898	0.98	g21299 44	100	529	5.2e- 39	RNA- bindin g protei n RZ-1 - wood tobacc o [Nicot iana sylv tris]
140303	ATU002 243	ATL8S3 921:15 3..488	gap2	ATCEA4 C12172 2_1	99	ATL8S3 921:48 6..340	0.98					
140304	ATU002 244	ATL8C1 2151:1 94..77 1	gap2	ATCEA4 C911_2 , ATCEA4 S35896 , ATCEA4 C911_1 , ATCEA4 S28361	99, 89, 89, 83	ATL8C1 2151:1 94..58 2	0.98					
140305	ATU002 245	ATL8C3 1727:5 23..70 2	gap2	ATCEA4 C4368_2, ATCEA4 S2651	99, 83	ATL8C3 1727:5 62..70 2	0.98					
140306	ATU002 246	ATL8C1 0342:1 874..1	gap2	ATCEA4 S24684 , ATCEA4 C1657_1, ATCEA4 S30721 , ATCEA4 S32228 , ATCEA4 S24607	99, 99, 95, 91, 89	ATL8C1 0342:1 453..2 52	0.98					

140307	ATU002 247	ATL8C1 8792:2 874..1 204	gap2	ATCEA4 C7334_1 ATCEA4 S31604 , ATCEA4 S31603 , ATCEA4 S34073 , ATCEA4 C46318 1, ATCEA4 C7334_2	98, 98, 90, 84, 83, 83	ATL8C1 8792:2 776..1 312	0.98	g33428 02	100	1852	7.6e- 193	(AF061 838) putati ve cytoso lic 6- phosph ogluco nate dehydr ogenas e [Zea mays]
140308	ATU002 248	ATL8C3 0619:9 0..101 5	gap2	ATCEA4 C14915 2, ATCEA4 C12411 1, ATCEA4 C14915 1	99, 99, 95	ATL8C3 0619:2 74..18 5	0.98					
140309	ATU002 249	ATL8C5 984:24 66..92 5	gap2	ATCEA4 C58190 1	98	ATL8C5 984:18 54..92 5	0.98	g38941 93	100	1125		(AC005 662) putati ve strict osidin e syntha se [Arabi dopsis thalia na]
140310	ATU002 250	ATL8C8 382:29 17..58 3	gap2	ATCEA4 C1350_1 ATCEA4 S13366	99, 99, 98	ATL8C8 382:27 51..74 3	0.98					

140318	ATU002 258	ATL8C1 5815:1 70..52 0	gap2	ATCEA4 S29784	99	ATL8C1 5815:1 70..40 9	0.98					educta ses (Pfam: PF0067 1, Score= 297.8, E=1.3e -85, N=1) [Arabi dopsis thalia na]
140319	ATU002 259	ATL8C4 8765:4 5..437	gap2	ATCEA4 C96834 1	99	ATL8C4 8765:4 8..280	0.98					
140320	ATU002 260	ATL8C2 349:30 80..17 08	gap2	ATCEA4 S2051	99	ATL8C2 349:29 97..17 08	0.98					
140321	ATU002 261	ATL8C4 8212:4 93..84 5	gap2	ATCEA4 C35172 1	99	ATL8C4 8212:6 37..82 3	0.98					
140322	ATU002 262	ATL8C2 8551:6 74..19 9	gap2	ATCEA4 S15554	99	ATL8C2 8551:6 58..19 9	0.98					
140323	ATU002 263	ATL8C1 7686:9 53..32 69	gap2	ATCEA4 S11785	99	ATL8C1 7686:9 53..23 55	0.98					
140324	ATU002 264	ATL8C2 0874:3 242..6 034	gap2	ATCEA4 S938	99	ATL8C2 0874:3 242..6 034	0.98					
140325	ATU002 265	ATL8C3 6211:2 175..5	gap2	ATCEA4 C26107 1,	99, 98, 93	ATL8C3 6211:2 287..4	0.98, 0.49					

140369	ATU002 309	ATL8C5 0073:4 07..17 45	gap2	S3502, ATCEA4 S12346	99	ATL8C5 0073:5 06..16 59	0.96												
140370	ATU002 310	ATL8C2 2103:2 053..3 41	gap2	ATCEA4 S2863	99	ATL8C2 2103:1 670..3 41	0.96												
140371	ATU002 311	ATL8C2 5505:1 379..1	gap2	ATCEA4 S29785 , ATCEA4 S6372	99, 96	ATL8C2 5505:1 323..2 9	0.96												
140372	ATU002 312	ATL8C9 429:19 23..10 53	gap2	ATCEA4 S36373	99	ATL8C9 429:13 84..12 87	0.96												
140373	ATU002 313	ATL8C3 5852:6 12..15 30	gap2	ATCEA4 C1379 1	99	ATL8C3 5852:7 39..15 30	0.96												
140374	ATU002 314	ATL8C4 1797:1 ..1341	gap2	ATCEA4 S26284 , ATCEA4 C22071 2, ATCEA4 S18655 , ATCEA4 S10660 , ATCEA4 C12586 1	99, 98, 88, 85, 83	ATL8C4 1797:2 18..10 40	0.96												
140375	ATU002 315	ATL8C2 2800:9 05..1	gap2	ATCEA4 S30642 , ATCEA4 C12039	99, 98	ATL8C2 2800:9 00..60 7	0.96												

140384	ATU002 324	ATL8C4 869:30 43..50 41	gap2	ATCEA4 C30843 1, ATCEA4 S26544	98, 88	ATL8C4 869:31 12..47 51	0.96	g41917 74	100	1067	4.3e- 115	(AC005 917) putati ve beta- 1,3- endogl ucanas e [Arabi dopsis thalia na]
140385	ATU002 325	ATL8C8 712:19 01..97 0	gap2	ATCEA4 S26753	99	ATL8C8 712:19 01..97 0	0.96					
140386	ATU002 326	ATL8C3 5071:8 59..1	gap2	ATCEA4 C6770_2	99	ATL8C3 5071:8 59..23 2	0.96					
140387	ATU002 327	ATL8C1 1754:1 ..970	gap2	ATCEA4 C1221_1	99	ATL8C1 1754:2 48..80 7	0.96					
140388	ATU002 328	ATL8C3 9423:6 36..47	gap2	ATCEA4 C1950_1, ATCEA4 S23928	99, 95	ATL8C3 9423:6 36..77	0.96					
140389	ATU002 329	ATL8C4 0089:4 79..1	gap2	ATCEA4 S1048	99	ATL8C4 0089:4 79..14 6	0.96					
140390	ATU002 330	ATL8C7 930:13 54..15 2	gap2	ATCEA4 S11255	99	ATL8C7 930:12 85..15 2	0.96					
140391	ATU002 331	ATL8C4 502:12 90..1	gap2	ATCEA4 C616_1	99	ATL8C4 502:11 03..22 2	0.96					
140392	ATU002 332	ATL8C4 4757:1	gap2	ATCEA4 C14559	99, 94	ATL8C4 4757:1	0.96					

140393	ATU002 333	767..1 70	gap2	1, ATCEA4 C93247 1	99, 97, 88, 86	ATL8C1 5914:1 162..2 682	533..5 81	0.96	g24627 44, g31079 05	100, 57	341, 105	3.5e- 37, 4.2e- 12	(AC002 292) Hypoth etical protei n [Arabi dopsis thalia nal; (D8510 1) leaf protei n [Ipomo ea nil]
140394	ATU002 334	ATL8C1 5914:1 162..2 682	gap2	ATCEA4 C5380 2, ATCEA4 C18430 1, ATCEA4 S34607 , ATCEA4 S10647	99, 97, 88, 86	ATL8C1 5914:1 162..2 682	ATL8C3 262:16 35..37 01	0.96	g24627 44, g31079 05	100, 57	341, 105	3.5e- 37, 4.2e- 12	(AC002 292) Hypoth etical protei n [Arabi dopsis thalia nal; (D8510 1) leaf protei n [Ipomo ea nil]
140395	ATU002 335	ATL8C5 943:89 4..606 1	gap2	ATCEA4 C35032 1, ATCEA4 S4867, ATCEA4 S2331, ATCEA4 C72777 1, ATCEA4 C11900	99, 97, 95, 93, 87	ATL8C5 943:13 32..60 61	ATL8C5 943:13 32..60 61	0.95	g24627 44, g31079 05	100, 57	341, 105	3.5e- 37, 4.2e- 12	(AC002 292) Hypoth etical protei n [Arabi dopsis thalia nal; (D8510 1) leaf protei n [Ipomo ea nil]

140409	ATU002 349	ATL8C9 362:15 34..14 9	gap2	ATCEA4 C62_1, ATCEA4 S31168	99, 90	ATL8C9 362:14 30..31 3	0.95					
140410	ATU002 350	ATL8C4 3630:8 78..1	gap2	ATCEA4 C23871 2, ATCEA4 C23871 1	99, 86	ATL8C4 3630:5 38..13 4	0.95					
140411	ATU002 351	ATL8C4 092:56 4..239 5	gap2	ATCEA4 S4129	99	ATL8C4 092:23 95..56 4	0.95					
140412	ATU002 352	ATL8C1 9237:2 99..24 31	gap2	ATCEA4 C1588_1, ATCEA4 C47605 1, ATCEA4 S21234	99, 87	ATL8C1 9237:8 70..22 24	0.95					
140413	ATU002 353	ATL8C1 3744:8 43..1	gap2	ATCEA4 C11430 3	99	ATL8C1 3744:8 43..7	0.95					
140414	ATU002 354	ATL8C4 7646:1 891..1 79	gap2	ATCEA4 C824_1	99	ATL8C4 7646:1 735..1 79	0.95					
140415	ATU002 355	ATL8C1 6271:2 22..26 68	gap2	ATCEA4 S2110	99	ATL8C1 6271:2 22..26 68	0.95					
140416	ATU002 356	ATL8C2 1192:1 224..4 031	gap2	ATCEA4 C5692_1, ATCEA4 S1503	98, 83	ATL8C2 1192:1 292..4 014	0.95	g23426 85	100	518	2.5e- 37	(AC000 106) Contai ns simila rity to Rhodoc occus amidas e

140417	ATU002 357	ATL8C6 912:57 5..1	gap2	ATCEA4 C26392 2, ATCEA4 C26392 3, ATCEA4 S8484	99, 97, 83	ATL8C6 912:44 9..365	0.95						(gb D1 6207). ESTs gb T20 504,gb H3665 0,gb N 97423, gb H36 595 come from this gene. [Arabi dopsis thalia na]
140418	ATU002 358	ATL8C6 384:15 19...35 7	gap2	ATCEA4 S348, ATCEA4 C19487 1, ATCEA4 S22999	99, 96, 86	ATL8C6 384:14 75..35 7	0.95						
140419	ATU002 359	ATL8C4 6660:1 34..49 79	gap2	ATCEA4 C8669 1, ATCEA4 C31658 1, ATCEA4 C33811 1, ATCEA4 S5674	98, 98, 97, 94	ATL8C4 6660:1 411..1 34, ATL8C4 6660:2 416..4 340	0.95, 0.68	g48772 87, g16522 03, g15316 51	100, 57, 45	204, 96, 51	1.1e- 20, 0.021, 0.025	(AJ133 749) deoxyg uanosi ne kinase 1 [Mus muscul us]; (D9090 3)	

140420	ATU002 360	ATL8C4 8961:2 570..1 816	gap2	ATCEA4 C10044 1_1	99	ATL8C4 8961:2 570..1 922	0.95									hypothetical protein [Synecocystis sp.]; (U67083) KRAB-zinc finger protein KZF-2 [Rattus norvegicus]
140421	ATU002 361	ATL8C9 993:20 69..1	gap2	ATCEA4 C27755 1, ATCEA4 S8065, ATCEA4 C55893 1	99, 98, 92	ATL8C9 993:19 61..12 2	0.95									
140422	ATU002 362	ATL8C2 3612:1 023..1 14	gap2	ATCEA4 C7239 1, ATCEA4 S10331	99, 99	ATL8C2 3612:9 38..11 4	0.95									
140423	ATU002 363	ATL8C1 9145:2 444..1	gap2	ATCEA4 S36275	99	ATL8C1 9145:2 382..1 6	0.95									
140424	ATU002 364	ATL8C2 1916:7 46..1	gap2	ATCEA4 C11625 7 1,	99, 98	ATL8C2 1916:6 78..54	0.95									

140441	ATU0002 381	ATL8C9 443:11 31..28 58	gap2	C821_3 ATCEA4 C7205_1 ATCEA4 S7505	98, 89	ATL8C9 443:11 31..28 58	0.94	g46789 35	100	948	3.9e- 84	(AL049 711) putati ve protei n [Arabi dopsis thalia na]
140442	ATU0002 382	ATL8C3 8336:1 457..1	gap2	ATCEA4 C14451 ATCEA4 S964, ATCEA4 S17606	99, 98, 85	ATL8C3 8336:1 307..1 53	0.94					
140443	ATU0002 383	ATL8S1 8980:2 96..1	gap2	ATCEA4 C26543 1	99	ATL8S1 8980:1 58..17	0.94					
140444	ATU0002 384	ATL8C3 4121:1 ..1388	gap2	ATCEA4 S12649 , ATCEA4 S14182 , ATCEA4 C2251_1 ATCEA4 S19695	99, 94, 93, 87	ATL8C3 4121:2 90..13 65	0.94					
140445	ATU0002 385	ATL8C4 3205:1 370..1	gap2	ATCEA4 C1375_1 ATCEA4 S35376	99, 93	ATL8C4 3205:1 283..1 61	0.94					
140446	ATU0002 386	ATL8C1 6649:6 60..19 54	gap2	ATCEA4 S13394 , ATCEA4 S13474	99, 87	ATL8C1 6649:7 10..19 54	0.94					
140447	ATU0002 387	ATL8C3 4554:2	gap2	ATCEA4 C46966	98, 93,	ATL8C3 4554:2	0.94	g29814 75	100	1234	2.4e- 113	(AF053 084)

140453	ATU002 393	ATL8C4 2807:4 17..32 70	gap2	1 ATCEA4 C39078 1	98	ATL8C4 2807:9 11..30 35	0.94	g16444 02	100	591	1.5e- 47	(U7352 4) putati ve ATP/GT P- bindin g protei n [Homo sapien s]
140454	ATU002 394	ATL8C1 970:1. .2108	gap2	ATCEA4 C1364 1	99	ATL8C1 970:37 6..189 6	0.94					
140455	ATU002 395	ATL8C3 2599:9 5..872	gap2	ATCEA4 S36307 , ATCEA4 S12381 , ATCEA4 S36372 , ATCEA4 C742 1	99, 97, 83, 83	ATL8C3 2599:9 5..842	0.94					
140456	ATU002 396	ATL8C3 6201:1 657..5 1	gap2	ATCEA4 S30617	98	ATL8C3 6201:1 657..8 8	0.94	g33865 98	100	1931	3.8e- 197	(AC004 665) putati ve cytoch rome p450 [Arabi dopsis thalia na]
140457	ATU002 397	ATL8C1 3414:3 62..14 33	gap2	ATCEA4 S1513, ATCEA4 C33899	99, 94	ATL8C1 3414:3 62..14 33	0.94					

140458	ATU002 398	ATL8C1 7055:4 37..21 46	gap2	1 ATCEA4 C154_1	99	ATL8C1 7055:4 37..21 46	0.94										
140459	ATU002 399	ATL8C6 005:30 6..123 2	gap2	ATCEA4 S10782	99	ATL8C6 005:30 6..123 2	0.94										
140460	ATU002 400	ATL8C1 2079:1 ..711	gap2	ATCEA4 C16549 1	99	ATL8C1 2079:9 9..502	0.94										
140461	ATU002 401	ATL8C1 039:11 87..40 6	gap2	ATCEA4 S13643 , ATCEA4 S32450	99, 98	ATL8C1 039:11 76..51 7	0.94										
140462	ATU002 402	ATL8C1 1140:2 71..62 6	gap2	ATCEA4 C1916_ 1, ATCEA4 S34082 , ATCEA4 S32647 , ATCEA4 S2284, ATCEA4 S6176	99, 97, 95, 93, 83	ATL8C1 1140:3 00..60 6	0.94										
140463	ATU002 403	ATL8C4 6108:1 ..1273	gap2	ATCEA4 C8385_ 1, ATCEA4 S13788 , ATCEA4 S31135 , ATCEA4 S33177	99, 96, 88, 88	ATL8C4 6108:1 00..11 01	0.94										
140464	ATU002 404	ATL8S1 6818:5 91..10	gap2	ATCEA4 S663	99	ATL8S1 6818:5 57..41	0.94										

140475	ATU002 415	ATL8C3 6244:4 548...9 06	gap2	ATCEA4 C1025_1, ATCEA4 S14863 , ATCEA4 S15473 , ATCEA4 S26303 , ATCEA4 S14862	99, 98, 97, 88, 86	ATL8C3 6244:4 495...1 184	0.93									
140476	ATU002 416	ATL8C1 0675:9 ..700	gap2	ATCEA4 C11432 6 1	99	ATL8C1 0675:1 5...555	0.93									
140477	ATU002 417	ATL8C4 8061:8 87...10	gap2	ATCEA4 C6000_2, ATCEA4 C6000_1	99, 90	ATL8C4 8061:6 36...10	0.93									
140478	ATU002 418	ATL8C4 1285:1 ..1186	gap2	ATCEA4 C7370_1	99	ATL8C4 1285:2 7...107 2	0.93									
140479	ATU002 419	ATL8C4 3973:1 711...1	gap2	ATCEA4 C403_2 , ATCEA4 S17959	99, 95	ATL8C4 3973:1 326...1 42	0.93									
140480	ATU002 420	ATL8C2 4707:1 383...2 338	gap2	ATCEA4 S6823	99	ATL8C2 4707:1 589...2 338	0.93									
140481	ATU002 421	ATL8C4 1576:1 097...1 59	gap2	ATCEA4 C63316 ,_1	99	ATL8C4 1576:1 097...1 59	0.93									
140482	ATU002 422	ATL8C2 847:22 24...13	gap2	ATCEA4 C27708 1,	99, 91	ATL8C2 847:21 77...15	0.93									

140483	ATU002 423	99	gap2	ATCEA4 C15042 2_1	99, 98, 84	63	0.93							
		ATL8C2 6914:1 425...1		ATCEA4 C889_1 , ATCEA4 S31523 , ATCEA4 S10577 , ATCEA4 S10863		ATL8C2 6914:1 059...1 9								
140484	ATU002 424	ATL8C4 6754:2 901...4 840	gap2	ATCEA4 S1974	99	ATL8C4 6754:2 901...4 840	0.93							
140485	ATU002 425	ATL8C3 1135:1 45...31 85	gap2	ATCEA4 C6430_1, ATCEA4 S1088, ATCEA4 S28314 , ATCEA4 C11835 3_1, ATCEA4 C7137_1	99, 99, 99, 95, 94	ATL8C3 1135:4 55...29 91	0.93							
140486	ATU002 426	ATL8C4 6718:1 402...3 918	gap2	ATCEA4 C895_1 , ATCEA4 S1784	99, 99	ATL8C4 6718:1 825...3 630	0.93							
140487	ATU002 427	ATL8C3 3056:1 ...2676	gap2	ATCEA4 S2869, ATCEA4 S2344	99, 96	ATL8C3 3056:7 6...267 6	0.93							
140488	ATU002 428	ATL8C1 5782:1 ...1795	gap2	ATCEA4 S516	99	ATL8C1 5782:1 05...17	0.93							

140489	ATU002 429	ATL8C4 1213:6 6..995	gap2	ATCEA4 C92305 1, ATCEA4 C5804_1	99, 98	95 ATL8C4 1213:6 6..630	0.93												
140490	ATU002 430	ATL8C9 242:1. .1942	gap2	ATCEA4 C9393_1, ATCEA4 S29919 , ATCEA4 C9393_3	99, 94, 85	ATL8C9 242:36 3..146 9	0.93												
140491	ATU002 431	ATL8C3 3739:3 38..17 13	gap2	ATCEA4 C28258 _1	99	ATL8C3 3739:9 46..15 38	0.93												
140492	ATU002 432	ATL8C4 8609:1 54..10 62	gap2	ATCEA4 S1287, ATCEA4 C65342 _1	99, 96	ATL8C4 8609:1 76..96 3	0.93												
140493	ATU002 433	ATL8C3 3430:1 ..1101	gap2	ATCEA4 S36217 , ATCEA4 S25098	99, 89	ATL8C3 3430:1 54..61 7	0.93												
140494	ATU002 434	ATL8C8 830:1. .2440	gap2	ATCEA4 S25218 , ATCEA4 C70733 _2, ATCEA4 S34717	99, 97, 94	ATL8C8 830:20 9..230 7	0.93												
140495	ATU002 435	ATL8C4 926:28 94..34 5	gap2	ATCEA4 C33444 _1	99	ATL8C4 926:28 94..49 1	0.93												
140496	ATU002 436	ATL8C3 7460:6	gap2	ATCEA4 C3960	99	ATL8C3 7460:6	0.93												

140509	ATU002 449	ATL8S1 9695:1 14..61 1	gap2	ATCEA4 S7714, ATCEA4 C29305 1	99, 97	ATL8S1 9695:2 29..37 0	0.92									l-CoA reductase [Rattus norvegicus]; (AB018412) chloroplast phosphoglycerate kinase [Populus nigra]
140510	ATU002 450	ATL8C3 4862:5 765..4 137	gap2	ATCEA4 S13705 , ATCEA4 C17570 1	99, 98	ATL8C3 4862:5 765..4 307	0.92									
140511	ATU002 451	ATL8C8 526:23 67..83 6	gap2	ATCEA4 S6331, ATCEA4 S474	98, 85	ATL8C8 526:23 67..90 1	0.92	g3492806	100	750	3.1e-75	(AJ225045) adventitious rooting related oxygenase [Malus domestica]				
140512	ATU002 452	ATL8C1 1788:1 ..955	gap2	ATCEA4 S36262 ,	99, 88	ATL8C1 1788:1 84..82	0.92									

140513	ATU002 453	ATL8S9 231:51 6..90	gap2	ATCEA4 C566 1	99, 89	ATL8S9 231:36 2..90	0.92	g48357 60	100	1018	4.5e-94	(AC007 202) Strong similarity to gb Y14 272 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase from Pisum sativum. ESTs gb AA0 67485 and gb AI1 00551 come from this gene. [Arabis dopsis thaliana]
140514	ATU002 454	ATL8C3 4838:9 ..2349	gap2	ATCEA4 S12134	98	ATL8C3 4838:1 37..22 16	0.92	g48357 60	100	1018	4.5e-94	(AC007 202) Strong similarity to gb Y14 272 3-deoxy-D-manno-2-octulosonate-8-phosphate synthase from Pisum sativum. ESTs gb AA0 67485 and gb AI1 00551 come from this gene. [Arabis dopsis thaliana]

140515	ATU002 455	ATL8C3 8637:2 416..8 71	gap2	ATCEA4 S30689 , ATCEA4 S2240, ATCEA4 S3175, ATCEA4 C8180_1	98, 98, 89 96, 89	ATL8C3 8637:2 344..1 044	0.92	g22528 66	100	478	2.3e- 23	(AF013 294) contai ns region of simila rity to SYT [Arabi dopsis thalia na]
140516	ATU002 456	ATL8C1 0302:1 380..8 2	gap2	ATCEA4 S1409, ATCEA4 S29719	99, 96	ATL8C1 0302:1 380..8 2	0.92					
140517	ATU002 457	ATL8C4 522:11 2..671	gap2	ATCEA4 S12944	99	ATL8C4 522:11 2..528	0.92					
140518	ATU002 458	ATL8C8 645:13 02..98	gap2	ATCEA4 C498_1	99	ATL8C8 645:92 1..98	0.92					
140519	ATU002 459	ATL8C3 4334:2 784..7 81	gap2	ATCEA4 C1490_1	99	ATL8C3 4334:2 479..9 46	0.92					
140520	ATU002 460	ATL8C6 216:18 6..123 3	gap2	ATCEA4 C6687_1, ATCEA4 S13692	99, 99	ATL8C6 216:18 6..105 2	0.92					
140521	ATU002 461	ATL8C3 4331:1 ..1169	gap2	ATCEA4 C1816_2, ATCEA4 C1816_1	99, 94	ATL8C3 4331:1 35..89 8	0.92					
140522	ATU002 462	ATL8C4 948:21 35..43 61	gap2	ATCEA4 C14265_1	98	ATL8C4 948:24 54..43 61	0.92	g28299 11	100	1526	5.9e- 152	(AC002 291) Unknow n protei n

[illegible]

140538	ATU002 478	193..4 439	gap2	ATCEA4 C12300 8_1, ATCEA4 C36534 1	98, 91 97, 91	282..4 439	0.92	g45859 88	100	1754	3.1e- 141	(AC005 287) Simila r to phosph oprote in phosph atase 2A regula tory subuni t [Arabi dopsis thalia na]
140539	ATU002 479	ATL8C4 3815:8 88..10	gap2	ATCEA4 C5785_1	99	ATL8C4 3815:8 68..10	0.92					
140540	ATU002 480	ATL8C1 6591:2 011..3 143	gap2	ATCEA4 S13341	99	ATL8C1 6591:2 011..3 143	0.92					
140541	ATU002 481	ATL8C4 6813:1 741..1 37	gap2	ATCEA4 C1932_1, ATCEA4 C6977_1	99, 97	ATL8C4 6813:1 600..3 01	0.92					
140542	ATU002 482	ATL8C2 2464:1 635..4 85	gap2	ATCEA4 C681_1	99	ATL8C2 2464:1 529..7 07	0.91					
140543	ATU002 483	ATL8C1 7472:1	gap2	ATCEA4 C1383	99	ATL8C1 7472:1	0.91					

		29		ATCEA4 S11451		14									
140552	ATU002 492	ATL8C6 147:10 .1819	gap2	ATCEA4 C62751 1, ATCEA4 C4947_1, ATCEA4 S1895	99, 97, 94	ATL8C6 147:10 61..170 4	0.91								
140553	ATU002 493	ATL8C4 231:16 29..1	gap2	ATCEA4 C1933_1, ATCEA4 C1934_1, ATCEA4 S14340	99, 82, 82	ATL8C4 231:14 57..11	0.91								
140554	ATU002 494	ATL8C1 0568:3 15..14 20	gap2	ATCEA4 S2977, ATCEA4 S12840	99, 99	ATL8C1 0568:3 35..14 20	0.91								
140555	ATU002 495	ATL8C2 957:14 59..1	gap2	ATCEA4 C22529 1, ATCEA4 S19267 , ATCEA4 S26522	99, 92, 82	ATL8C2 957:14 59..22	0.91								
140556	ATU002 496	ATL8C9 953:48 61..45 8	gap2	ATCEA4 C10969 3_1, ATCEA4 C4230_1, ATCEA4 C23970 1, ATCEA4 C8282_1	99, 99, 97, 96	ATL8C9 953:48 61..71 6	0.91								
140557	ATU002 497	ATL8C2 9326:2	gap2	ATCEA4 S1772	99	ATL8C2 9326:2	0.91								

		2..112 9		ATCEA4 C64233 1		2..106 0									
140595	ATU002 535	ATL8C1 0941:2 082..4 065	gap2	ATCEA4 C11515 1, ATCEA4 C77821 1	99, 95	ATL8C1 0941:2 184..3 929	0.90								
140596	ATU002 536	ATL8C4 1630:5 98..57	gap2	ATCEA4 C20649 1	99	ATL8C4 1630:5 76..57	0.90								
140597	ATU002 537	ATL8C4 6571:3 80..14 36	gap2	ATCEA4 C28233 1	99	ATL8C4 6571:4 54..14 36	0.90								
140598	ATU002 538	ATL8C3 6392:1 114..3 3	gap2	ATCEA4 S10702	99	ATL8C3 6392:1 114..3 3	0.90								
140599	ATU002 539	ATL8C1 6375:3 831..4 799	gap2	ATCEA4 C19758 1, ATCEA4 S18285	99, 88	ATL8C1 6375:3 896..4 662	0.90								
140600	ATU002 540	ATL8C3 8823:7 88..1	gap2	ATCEA4 C1540 1	99	ATL8C3 8823:5 44..18 0	0.90								
140601	ATU002 541	ATL8C2 8678:5 07..73 5	gap2	ATCEA4 C11906 8 1	99	ATL8C2 8678:5 61..73 5	0.90								
140602	ATU002 542	ATL8C5 224:17 46..75 1	gap2	ATCEA4 C1457 1, ATCEA4 S32559	99, 91	ATL8C5 224:17 32..93 3	0.90								
140603	ATU002 543	ATL8C4 4369:5 55..26 09	gap2	ATCEA4 C801 1	99	ATL8C4 4369:6 10..24 94	0.90								
140604	ATU002	ATL8C4	gap2	ATCEA4	99	ATL8C4	0.89								

140612	ATU002 552		954..1 07	gap2	3, ATCEA4 C12633 2, ATCEA4 S1312, ATCEA4 S23940 , ATCEA4 C12783 8 1, ATCEA4 S2769, ATCEA4 C34502 1	97, 93, 92, 85, 82	890..4 02					putati ve protei n [Arabi dopsis thalia na]
140613	ATU002 553		ATL8C5 64:429 0..108 9	gap2	ATCEA4 C4467 1	99	ATL8C5 64:409 5..108 9	0.89				
140614	ATU002 554		ATL8C3 8128:1 411..2 187	gap2	ATCEA4 S29507	99	ATL8C3 8128:1 485..2 187	0.89				
140615	ATU002 555		ATL8C2 6971:6 28..36 44	gap2	ATCEA4 S6343	99	ATL8C2 6971:6 28..31 41	0.89				
140616	ATU002 556		ATL8C2 6115:9 77..31 9	gap2	ATCEA4 C889_1 , ATCEA4 S9954	99, 85	ATL8C2 6115:8 93..52 5	0.89				
140617	ATU002 557		ATL8C1 1583:2 588..1 32	gap2	ATCEA4 C5355_ 1, ATCEA4 S6440, ATCEA4 S7757	99, 96, 94	ATL8C1 1583:1 805..1 32	0.89				
140618	ATU002 558		ATL8C1 3474:1 053..2	gap2	ATCEA4 C30740 1,	99, 94, 91	ATL8C1 3474:1 053..2	0.89				

140634	ATU002 574	39 ATL8C3 0345:2 922..2 090	gap2	S12309 ATCEA4 S36374	99	39 ATL8C3 0345:2 764..2 254	0.89	g32491 07	100	122	1.5e-07	(AC003114) Contain similarity to phloem-specific lectin PP2gb Z17331 from Cucurbita maxima. [Arabidopsis thaliana]
140635	ATU002 575	ATL8C2 5617:5 09..26 62	gap2	ATCEA4 C25911 1, ATCEA4 C65764 1, ATCEA4 S31912	98, 94, 90	ATL8C2 5617:8 69..26 62	0.89					
140636	ATU002 576	ATL8C3 4677:5 39..13 63	gap2	ATCEA4 C1113 1	99	ATL8C3 4677:5 61..13 63	0.89					
140637	ATU002 577	ATL8C2 2863:1 86..73 4	gap2	ATCEA4 C19958 2, ATCEA4 C19958 1	99, 88	ATL8C2 2863:1 87..55 4	0.89					
140638	ATU002 578	ATL8C4 191:42 9..1	gap2	ATCEA4 C20804 1	99	ATL8C4 191:42 8..36	0.89					
140639	ATU002 579	ATL8C2 2400:1	gap2	ATCEA4 C675 1	99	ATL8C2 2400:1	0.89					

140640	ATU002 580	..2540	gap2	ATCEA4 S23231 , ATCEA4 C53164 1, ATCEA4 C53164 2	99, 93 98, 93	80..25 40 ATL8C2 4722:2 717..2 05	0.89	g22530 10	100	838	1.1e- 63	(Y1419 9) MAP3K delta- 1 n protei n kinase [Arabi dopsis thalia na]
140641	ATU002 581	ATL8C4 2033:1 73..37 36	gap2	ATCEA4 C9557 1, ATCEA4 S4784, ATCEA4 C81636 1, ATCEA4 C48671 1	98, 98, 92, 83	ATL8C4 2033:1 73..33 61	0.88	g22530 10	100	838	1.1e- 63	(Y1419 9) MAP3K delta- 1 n protei n kinase [Arabi dopsis thalia na]
140642	ATU002 582	ATL8C1 4559:1 ..575	gap2	ATCEA4 C35540 1	99	ATL8C1 4559:6 9..575	0.88					
140643	ATU002 583	ATL8C4 1325:1 ..855	gap2	ATCEA4 C45591 1, ATCEA4 S29705	99, 96	ATL8C4 1325:2 26..85 5	0.88					
140644	ATU002 584	ATL8C4 9835:1 16..74 5	gap2	ATCEA4 C532 1	99	ATL8C4 9835:1 19..53 1	0.88					
140645	ATU002 585	ATL8C1 4692:1 ..910	gap2	ATCEA4 C1528 1, ATCEA4 S17979 , ATCEA4 S9645	99, 97, 96	ATL8C1 4692:1 81..61 9	0.88					
140646	ATU002	ATL8C9	gap2	ATCEA4	99	ATL8C9	0.88					

	586	743:19 98..32 1	S2214		743:19 98..32 1							
140647	ATU002 587	ATL8C1 8309:1 295..2 667	gap2	ATCEA4 S11855	99	ATL8C1 8309:1 295..2 667	0.88					
140648	ATU002 588	ATL8C4 47:122 5..598 9	gap2	ATCEA4 C22894 1, ATCEA4 S3242, ATCEA4 S24160	99, 98	ATL8C4 47:156 4..598 9	0.88					
140649	ATU002 589	ATL8C3 897:10 8..637	gap2	ATCEA4 S10	99	ATL8C3 897:63 7..108	0.88					
140650	ATU002 590	ATL8C1 8729:1 ..329	gap2	ATCEA4 S11377	99	ATL8C1 8729:1 01..32 9	0.88					
140651	ATU002 591	ATL8C3 8723:2 08..97 6	gap2	ATCEA4 C9055_ 1, ATCEA4 S13592	98, 98	ATL8C3 8723:2 54..97 4	0.88	932692 93	100	964	7.7e- 70	(AL030 978) putati ve protei n [Arabi dopsis thalia na]
140652	ATU002 592	ATL8C3 0284:9 60..40 4	gap2	ATCEA4 C79926 1_ 1	99	ATL8C3 0284:8 05..72 2	0.88					
140653	ATU002 593	ATL8C3 8014:1 ..1000	gap2	ATCEA4 S15374 , ATCEA4 C391_1 , ATCEA4 S9397	99, 98, 84	ATL8C3 8014:1 09..70 3	0.88					
140654	ATU002	ATL8C1	gap2	ATCEA4	99, 99	ATL8C1	0.88					

140660	ATU002 600	ATL8C2 9112:4 0..144 0	gap2	ATCEA4 S22417 , ATCEA4 C12375 1, ATCEA4 C12375 4, ATCEA4 S31930 , ATCEA4 S32305 , ATCEA4 S34062 , ATCEA4 S29132 , ATCEA4 S31125 , ATCEA4 S10539	99, 99, 96, 96, 95, 94, 85, 84, 83	ATL8C2 9112:5 34..12 54	0.88				
140661	ATU002 601	ATL8C2 5580:1 35..17 30	gap2	ATCEA4 S760	99	ATL8C2 5580:1 35..15 61	0.88				
140662	ATU002 602	ATL8C6 042:46 ..819	gap2	ATCEA4 S26970	99	ATL8C6 042:46 ..595	0.88				
140663	ATU002 603	ATL8C3 6025:5 01..16 78	gap2	ATCEA4 S12845 , ATCEA4 S1526	99, 92	ATL8C3 6025:5 01..16 78	0.88				
140664	ATU002 604	ATL8S2 4298:3 96..1	gap2	ATCEA4 C1124 1	99	ATL8S2 4298:3 95..14 5	0.88				
140665	ATU002 605	ATL8C1 0399:1	gap2	ATCEA4 C1090	99, 92	ATL8C1 0399:9	0.88				

		0114.. 5716		1, ATCEA4 S32623		932..5 716						
140666	ATU002 606	ATL8C3 2532:2 005..5 87	gap2	ATCEA4 C1234 1, ATCEA4 S30803 92, 82	99, 95, 94, 94, 92, 82	ATL8C3 2532:1 749..7 52	0.88					
140667	ATU002 607	ATL8C1 7018:1 366..6 35	gap2	ATCEA4 S1749	99	ATL8C1 7018:1 346..6 35	0.88					
140668	ATU002 608	ATL8C1 6036:1 ..306	gap2	ATCEA4 S34648	99	ATL8C1 6036:4 7..152	0.88					
140669	ATU002 609	ATL8C2 6027:5 87..1	gap2	ATCEA4 S13377 94, 82 ATCEA4 S24844 ATCEA4 C41425 1	99, 94, 82	ATL8C2 6027:4 23..30 1	0.88					
140670	ATU002 610	ATL8C2 7294:9 3..132 9	gap2	ATCEA4 S8136	99	ATL8C2 7294:9 3..100 3	0.88					
140671	ATU002 611	ATL8C6 907:12 3..162 8	gap2	ATCEA4 S15076 ATCEA4	99, 95, 82	ATL8C6 907:12 3..886	0.88					

140686	ATU002 626	ATL8C7 812:10 53..35 6	gap2	ATCEA4 C6602_1	99	ATL8C7 812:10 53..35 6	0.87					
140687	ATU002 627	ATL8C3 2501:1 559..2 15	gap2	ATCEA4 C5917_1	99	ATL8C3 2501:1 479..2 15	0.87					
140688	ATU002 628	ATL8C4 5375:2 973..1 347	gap2	ATCEA4 C1825_1	99	ATL8C4 5375:2 930..1 514	0.87					
140689	ATU002 629	ATL8C8 419:1. .3825	gap2	ATCEA4 C1604_1	99	ATL8C8 419:58 0..359 1	0.87					
140690	ATU002 630	ATL8C3 8109:1 166..1	gap2	ATCEA4 S26608 , ATCEA4 C22769 1, ATCEA4 S2413	99, 96, 93	ATL8C3 8109:1 013..2 8	0.87					
140691	ATU002 631	ATL8C3 7405:1 737..1	gap2	ATCEA4 S36322 , ATCEA4 C593_1 , ATCEA4 S18773	99, 99, 95	ATL8C3 7405:1 673..2 02	0.87					
140692	ATU002 632	ATL8C4 29:343 4..1	gap2	ATCEA4 S4180, ATCEA4 C4718_2, ATCEA4 C18934 1, ATCEA4 C18934 2, ATCEA4	99, 97, 95, 87, 86, 86	ATL8C4 29:342 2..53	0.87					

140693	ATU002 633	ATL8S1 5998:2 42..10 5	gap2		C7184_1, ATCEA4 C47919 1	99, 85	ATL8S1 5998:2 27..10 5	0.87					
140694	ATU002 634	ATL8C4 9808:5 53..18 99	gap2		ATCEA4 S842	99	ATL8C4 9808:5 53..18 99	0.87					
140695	ATU002 635	ATL8C3 9188:1 ..2023	gap2		ATCEA4 C6624_1, ATCEA4 C6624_2, ATCEA4 S32108	99, 97, 83	ATL8C3 9188:3 24..20 23	0.87					
140696	ATU002 636	ATL8C3 7837:2 508..1 1	gap2		ATCEA4 C23943 _1	99	ATL8C3 7837:2 508..1 1	0.87					
140697	ATU002 637	ATL8C1 4523:1 1619.. 1922	gap2		ATCEA4 S4446	98	ATL8C1 4523:1 1619.. 1922	0.87					
							g48951 69, g48951 68			100, 100	5776, 1937	0.0, 2.7e- 190	(AC007 662) putati ve helica se [Arabi dopsis thalia nal; (AC007 662) putati ve replac ation protei n Al

140698	ATU002 638	ATL8C4 558:31 42..44 94	gap2	ATCEA4 C5779_1	98	ATL8C4 558:31 44..44 94	0.87	g46789 28	100	692	4.7e- 70	[Arabi dopsis thalia na]
140699	ATU002 639	ATL8C3 3401:1 ..987	gap2	ATCEA4 C1277_1, ATCEA4 S17804	99, 85	ATL8C3 3401:7 61..44 3	0.87					
140700	ATU002 640	ATL8C4 5610:1 ..1800	gap2	ATCEA4 C1632_1	99	ATL8C4 5610:1 51..15 84	0.87					
140701	ATU002 641	ATL8C4 5399:1 78..10 51	gap2	ATCEA4 C4925_1	99	ATL8C4 5399:1 82..10 51	0.87					
140702	ATU002 642	ATL8C2 3880:1 256..1 1	gap2	ATCEA4 C3628_1	99	ATL8C2 3880:1 256..1 1	0.87					
140703	ATU002 643	ATL8C2 4162:1 247..1	gap2	ATCEA4 C1709_1	99	ATL8C2 4162:1 232..2 44	0.87					
140704	ATU002 644	ATL8C4 188:26 06..1	gap2	ATCEA4 S3404, ATCEA4 C17102_1	99, 97	ATL8C4 188:26 06..31 0	0.87					

140705	ATU002 645	ATL8C4 5752:1 133..1 99	gap2	ATCEA4 C1201_1, ATCEA4 S31324	99, 87	ATL8C4 5752:1 129..3 60	0.87				
140706	ATU002 646	ATL8S1 5347:4 55..21 0	gap2	ATCEA4 C11922 9_1	99	ATL8S1 5347:4 24..21 0	0.87				
140707	ATU002 647	ATL8C2 8691:1 ..439	gap2	ATCEA4 C12850 _1	99	ATL8C2 8691:1 43..43 9	0.87				
140708	ATU002 648	ATL8C2 2785:1 ..1717	gap2	ATCEA4 C1051_1, ATCEA4 S15080 , ATCEA4 S36345	99, 99, 86	ATL8C2 2785:2 80..14 73	0.87				
140709	ATU002 649	ATL8C3 7172:5 7..300 9	gap2	ATCEA4 C1552_1	99	ATL8C3 7172:5 8..283 9	0.87				
140710	ATU002 650	ATL8C4 5205:4 875..9 55	gap2	ATCEA4 S3471	99	ATL8C4 5205:4 875..9 55	0.87				
140711	ATU002 651	ATL8C2 476:46 92..15 5	gap2	ATCEA4 C432_1	99	ATL8C2 476:46 50..38 4	0.87				
140712	ATU002 652	ATL8C1 9934:1 ..597	gap2	ATCEA4 C24980 1, ATCEA4 S36081 , ATCEA4 C11580 7_1	99, 96, 94	ATL8C1 9934:7 1..540	0.87				
140713	ATU002 653	ATL8C4 5093:1	gap2	ATCEA4 C7089	99	ATL8C4 5093:9	0.87				

140723	ATU002 663	ATL8C3 0176:1 216..1	gap2	ATCEA4 C2753_1	99	ATL8C3 0176:1 216..8 88	0.86					
140724	ATU002 664	ATL8C3 4477:6 852..1	gap2	ATCEA4 C1039_1	99	ATL8C3 4477:6 734..1 26	0.86					
140725	ATU002 665	ATL8C2 2661:9 01..70	gap2	ATCEA4 C20919_1	99	ATL8C2 2661:8 87..70	0.86					
140726	ATU002 666	ATL8C3 8478:2 975..9 55	gap2	ATCEA4 S1869	99	ATL8C3 8478:2 975..9 55	0.86					
140727	ATU002 667	ATL8C2 2807:1 160..2 458	gap2	ATCEA4 S12132	99	ATL8C2 2807:2 458..1 160	0.86					
140728	ATU002 668	ATL8C1 5418:4 59..23 0	gap2	ATCEA4 C4650_1	99	ATL8C1 5418:4 51..23 0	0.86					
140729	ATU002 669	ATL8C4 9173:8 2..183 1	gap2	ATCEA4 C13807_1, ATCEA4 S35044 , ATCEA4 S11905 , ATCEA4 C66487_1	99, 96, 93, 86	ATL8C4 9173:8 2..161 4	0.86					
140730	ATU002 670	ATL8C2 4526:1 600..1 40	gap2	ATCEA4 S1909	99	ATL8C2 4526:1 600..4 26	0.86					
140731	ATU002 671	ATL8C8 433:25 2..131 3	gap2	ATCEA4 C1515_1, ATCEA4 S6305	99, 96	ATL8C8 433:29 0..101 1	0.86					

140732	ATU002 672	ATL8C3 0605:2 17..20 68	gap2	ATCEA4 C940_1 , ATCEA4 S25994 , ATCEA4 S35126	99, 98, 92	ATL8C3 0605:2 17..19 29	0.86					
140733	ATU002 673	ATL8C1 0286:4 395..6 290	gap2	ATCEA4 C511_1 , ATCEA4 C511_2 , ATCEA4 S31515	99, 97, 92	ATL8C1 0286:4 395..5 867	0.86					
140734	ATU002 674	ATL8S2 6481:3 78..37	gap2	ATCEA4 S30659	99	ATL8S2 6481:3 46..37	0.86					
140735	ATU002 675	ATL8C4 6143:2 63..33 68	gap2	ATCEA4 C38207 1, ATCEA4 C13213 1	99, 97	ATL8C4 6143:2 63..33 68	0.86					
140736	ATU002 676	ATL8C2 1734:2 655..1	gap2	ATCEA4 C5709_4, ATCEA4 S3374, ATCEA4 C5709_2, ATCEA4 C5709_1, ATCEA4 S34102 , ATCEA4 S7503, ATCEA4 S7981, ATCEA4 S30837	99, 97, 94, 90, 88, 85, 85, 82	ATL8C2 1734:2 655..1 70	0.86					

140737	ATU002 677	ATL8C1 5550:2 9..184 1	gap2	ATCEA4 S426	99	ATL8C1 5550:1 841..2 9	0.86						
140738	ATU002 678	ATL8C9 671:1. .555	gap2	ATCEA4 C22758 1	99	ATL8C9 671:2. .555	0.86						
140739	ATU002 679	ATL8C2 7964:6 55..58	gap2	ATCEA4 C631_2 , ATCEA4 C631_1	99, 99	ATL8C2 7964:6 26..14 4	0.86						
140740	ATU002 680	ATL8C4 5493:1 285..3 2	gap2	ATCEA4 C16313 _1	99	ATL8C4 5493:9 17..32	0.86						
140741	ATU002 681	ATL8C1 8608:1 330..2 2	gap2	ATCEA4 C14429 1, ATCEA4 S32072	99, 93	ATL8C1 8608:1 000..2 2	0.86						
140742	ATU002 682	ATL8C4 9819:8 2..156 7	gap2	ATCEA4 C14115 1, ATCEA4 S28153 , ATCEA4 S33096 , ATCEA4 S32469	99, 95, 90, 88	ATL8C4 9819:9 7..111 9	0.86						
140743	ATU002 683	ATL8C4 7868:4 261..1 979	gap2	ATCEA4 C57_7, ATCEA4 S7780, ATCEA4 S9733, ATCEA4 S6314	99, 94, 93, 85	ATL8C4 7868:4 230..1 979	0.85						
140744	ATU002 684	ATL8C3 8050:2 754..2 066	gap2	ATCEA4 C10068 6_1	99	ATL8C3 8050:2 705..2 449	0.85						

140788	ATU002 728	ATL8C4 6487:6 892..3 724	gap2	ATCEA4 S8184, ATCEA4 S1024, ATCEA4 C7741_1	98, 94	ATL8C4 6487:6 892..4 093	0.84	g17066 95	100	161	1.2e- 10	PHOSPH OMEVAL ONATE KINASE [Sacch aromyc es cerevi siae]
140789	ATU002 729	ATL8C1 047:15 5..135 9	gap2	ATCEA4 S1161	99	ATL8C1 047:15 5..135 9	0.84					
140790	ATU002 730	ATL8C5 312:49 40..23 84	gap2	ATCEA4 C1734_1, ATCEA4 C1734_2, ATCEA4 S16252	99, 90	ATL8C5 312:47 53..28 40	0.84					
140791	ATU002 731	ATL8C3 5374:3 264..1 967	gap2	ATCEA4 C1722_1	99	ATL8C3 5374:3 189..2 159	0.84					
140792	ATU002 732	ATL8C1 3166:4 173..2 925	gap2	ATCEA4 S34391, ATCEA4 S14252	99, 97	ATL8C1 3166:4 173..3 170	0.84					
140793	ATU002 733	ATL8C3 0210:1 18..12 69	gap2	ATCEA4 S3906, ATCEA4 C20516_1, ATCEA4 S19540	99, 84	ATL8C3 0210:1 18..66 3	0.84					
140794	ATU002 734	ATL8C9 763:31 19..35 8	gap2	ATCEA4 S2611	99	ATL8C9 763:27 74..35 8	0.84					
140795	ATU002 735	ATL8C1 960:15 53..1	gap2	ATCEA4 C28315_1,	98, 91	ATL8C1 960:13 94..97	0.84	g35488 01	100	689	2.0e- 58	(AC005 313) putati

140803	ATU002 743	90 ATL8C3 6534:4 809..4 7	gap2	ATCEA4 S17953 , ATCEA4 S805, ATCEA4 C2017_1, ATCEA4 S35066 , ATCEA4 S34823 , ATCEA4 S24588 , ATCEA4 S33659 , ATCEA4 S28629	99, 99, 99, 97, 96, 94, 86, 83	133 ATL8C3 6534:4 761..4 7	0.84					
140804	ATU002 744	ATL8C2 4985:9 70..22 8	gap2	ATCEA4 C351_1	99	ATL8C2 4985:8 29..58 9	0.84					
140805	ATU002 745	ATL8S1 1020:1 28..67 0	gap2	ATCEA4 S12814	99	ATL8S1 1020:3 91..54 9	0.84					
140806	ATU002 746	ATL8C1 4712:7 06..10 13	gap2	ATCEA4 C22660 _1	99	ATL8C1 4712:7 69..82 8	0.84					
140807	ATU002 747	ATL8C3 0584:2 427..1 820	gap2	ATCEA4 C20674 _1	99	ATL8C3 0584:2 427..1 981	0.84					
140808	ATU002 748	ATL8C1 2570:4 795..1 101	gap2	ATCEA4 C12001 0_1	99	ATL8C1 2570:4 795..1 101	0.84					
140809	ATU002	ATL8S2	gap2	ATCEA4	99, 83	ATL8S2	0.84					

	749	8956:1 56..58 8		C8006_ 1, ATCEA4 C8006_ 2		8956:1 60..58 8						
140810	ATU002 750	ATL8C1 1828:1 934..1	gap2	ATCEA4 C172_1	99	ATL8C1 1828:1 892..1 142	0.84					
140811	ATU002 751	ATL8C3 3531:2 95..14 87	gap2	ATCEA4 S26705	99	ATL8C3 3531:4 02..14 87	0.84					
140812	ATU002 752	ATL8C3 6420:3 07..11 24	gap2	ATCEA4 S6072, ATCEA4 S31714	99, 92	ATL8C3 6420:4 06..11 20	0.84					
140813	ATU002 753	ATL8C2 0917:1 156..7 19	gap2	ATCEA4 S4100	99	ATL8C2 0917:9 03..71 9	0.84					
140814	ATU002 754	ATL8C3 2789:2 5..112 6	gap2	ATCEA4 C97213 _1	99	ATL8C3 2789:2 5..104 5	0.84					
140815	ATU002 755	ATL8C2 4320:6 021..2 9	gap2	ATCEA4 S5420, ATCEA4 S3063, ATCEA4 S33795	99, 94 99, 94	ATL8C2 4320:6 021..2 9	0.84					
140816	ATU002 756	ATL8C1 2375:1 ..459	gap2	ATCEA4 C67582 _1	99	ATL8C1 2375:8 3..459	0.84					
140817	ATU002 757	ATL8C3 4954:2 85..29 66	gap2	ATCEA4 C1702_5, ATCEA4 C6995_1, ATCEA4 C86071_1, ATCEA4	98, 98, 86 89, 86	ATL8C3 4954:1 448..2 758	0.84	g25418 76	100	1148	5.7e- 116	(D2601 5) CND41, chloro plast nucleo id DNA bindin g protei

					S35872													n [Nicotiana tabacum]
140818	ATU002 758	ATL8C2 0564:1 629..4 271	gap2		ATCEA4 S11246 , ATCEA4 C12431 1, ATCEA4 S20153	99, 97, 94	ATL8C2 0564:2 092..4 271	0.84										
140819	ATU002 759	ATL8C4 5029:1 ..1303	gap2		ATCEA4 C4687 - 1, ATCEA4 S448, ATCEA4 S10870	99, 97, 88	ATL8C4 5029:1 7..130 3	0.84										
140820	ATU002 760	ATL8C3 7024:2 6..521	gap2		ATCEA4 S1153	99	ATL8C3 7024:1 11..52 1	0.84										
140821	ATU002 761	ATL8C4 8143:1 ..457	gap2		ATCEA4 C13528 8_1, ATCEA4 S14323	99, 85	ATL8C4 8143:1 46..26 4	0.83										
140822	ATU002 762	ATL8C6 345:17 80..82	gap2		ATCEA4 C17858 1	99	ATL8C6 345:16 32..82	0.83										
140823	ATU002 763	ATL8C5 0256:1 513..1	gap2		ATCEA4 C4455 - 1, ATCEA4 S3991	99, 92	ATL8C5 0256:1 513..5	0.83										
140824	ATU002 764	ATL8S7 179:39 4..66	gap2		ATCEA4 C28792 2	99	ATL8S7 179:39 4..245	0.83										
140825	ATU002 765	ATL8C4 5273:1 445..1	gap2		ATCEA4 C1133 - 1	99	ATL8C4 5273:1 392..1 26	0.83										

140836	ATU002 776	ATL8S2 246:20 4..432	gap2	ATCEA4 C11530 1	99	ATL8S2 246:20 4..360	0.83					
140837	ATU002 777	ATL8S1 3501:1 3..608	gap2	ATCEA4 C12603 1	99	ATL8S1 3501:1 3..347	0.83					
140838	ATU002 778	ATL8C1 4451:1 268..4 784	gap2	ATCEA4 C742_1 , ATCEA4 S12254 , ATCEA4 S34789 , ATCEA4 S36372	99, 98, 95, 84	ATL8C1 4451:2 553..4 405	0.83					
140839	ATU002 779	ATL8C1 3682:5 09..11 83	gap2	ATCEA4 C9483_1 , ATCEA4 S5947	99, 90	ATL8C1 3682:6 28..11 65	0.83					
140840	ATU002 780	ATL8C4 9777:2 583..3 042	gap2	ATCEA4 C16931 _1	99	ATL8C4 9777:2 827..2 658	0.83					
140841	ATU002 781	ATL8C1 2931:7 8..107 9	gap2	ATCEA4 C7957_1 , ATCEA4 S15024	99, 88	ATL8C1 2931:7 8..101 0	0.83					
140842	ATU002 782	ATL8C8 787:30 4..124 9	gap2	ATCEA4 S290, ATCEA4 S11943 , ATCEA4 C67712 _1	99, 98, 94	ATL8C8 787:10 23..12 49	0.83					
140843	ATU002 783	ATL8C2 1152:1 2092.. 3243	gap2	ATCEA4 S20350 , ATCEA4 S32918	99, 96, 94	ATL8C2 1152:1 2092.. 3667	0.83					

140844	ATU002 784	ATL8C2 461:21 08..16 0	gap2	ATCEA4 C92784 1	99, 92	ATL8C2 461:21 08..16 0	0.83						
140845	ATU002 785	ATL8S2 1759:1 ..490	gap2	ATCEA4 C1173 1	99	ATL8S2 1759:1 22..42 5	0.83						
140846	ATU002 786	ATL8C4 8871:9 70..52	gap2	ATCEA4 S29502	99	ATL8C4 8871:7 24..52	0.83						
140847	ATU002 787	ATL8C2 1486:2 838..8 38	gap2	ATCEA4 C1729 1, ATCEA4 S18436 ATCEA4 S25905	99, 95, 91	ATL8C2 1486:2 803..1 049	0.83						
140848	ATU002 788	ATL8C1 6389:9 77..24 2	gap2	ATCEA4 S36218	99	ATL8C1 6389:9 68..24 2	0.83						
140849	ATU002 789	ATL8C1 1385:1 665..2 34	gap2	ATCEA4 C12259 1	99	ATL8C1 1385:1 665..2 34	0.83						
140850	ATU002 790	ATL8C3 6871:1 41..31 95	gap2	ATCEA4 S7705, ATCEA4 C52145 1	99, 98	ATL8C3 6871:1 41..31 95	0.83						
140851	ATU002 791	ATL8C3 5745:1 858..1	gap2	ATCEA4 C67889 1, ATCEA4 C24181 1	99, 96	ATL8C3 5745:9 89..35	0.83						
140852	ATU002	ATL8C4	gap2	ATCEA4	99	ATL8C4	0.83						

140874	ATU002 814		14		ATCEA4 S16573		64												
		gap2	ATL8C8 804:21 44..1		ATCEA4 S34978 , ATCEA4 S36, ATCEA4 C5884_1	99, 98	ATL8C8 804:18 83..16 6	0.82											
140875	ATU002 815	gap2	ATL8C6 758:1. .6077		ATCEA4 C26115 _1	99	ATL8C6 758:16 8..607 7	0.82											
140876	ATU002 816	gap2	ATL8C1 3107:1 611..3 23		ATCEA4 S26305 , ATCEA4 C12708 _1, ATCEA4 C12708 3	99, 97	ATL8C1 3107:1 611..5 00	0.82											
140877	ATU002 817	gap2	ATL8C6 050:35 1..191 5		ATCEA4 C11779 6_2	99	ATL8C6 050:35 1..151 2	0.82											
140878	ATU002 818	gap2	ATL8C4 5028:1 615..1		ATCEA4 C220_1 , ATCEA4 S34651	99, 89	ATL8C4 5028:1 557..8 4	0.82											
140879	ATU002 819	gap2	ATL8C1 7923:1 96..10 86		ATCEA4 S32727 , ATCEA4 C2487_4, ATCEA4 C2487_5	99, 92	ATL8C1 7923:2 98..10 86	0.82											
140880	ATU002 820	gap2	ATL8C2 7154:5 71..1		ATCEA4 S14200	99	ATL8C2 7154:2 91..20	0.82											

140881	ATU002 821	ATL8C4 4477:1 ..988	gap2	ATCEA4 C7883_1, ATCEA4 S71	99, 99	0	0.82													
140882	ATU002 822	ATL8S2 488:49 0..181	gap2	ATCEA4 C13958 1	99	ATL8S2 488:47 8..181	0.82													
140883	ATU002 823	ATL8C1 0377:1 460..4 53	gap2	ATCEA4 C1001_1, ATCEA4 S32432	99, 82	ATL8C1 0377:1 379..6 30	0.82													
140884	ATU002 824	ATL8C3 5365:2 160..7 6	gap2	ATCEA4 C27310 _1	99	ATL8C3 5365:2 160..2 76	0.82													
140885	ATU002 825	ATL8C2 4225:1 ..2661	gap2	ATCEA4 C1938_1	99	ATL8C2 4225:2 08..19 71	0.82													
140886	ATU002 826	ATL8C1 6598:1 328..1	gap2	ATCEA4 C28155 _1	99	ATL8C1 6598:9 30..77 8	0.82													
140887	ATU002 827	ATL8C1 0802:5 8..168 5	gap2	ATCEA4 C84428 1, ATCEA4 C48483 1	99, 86	ATL8C1 0802:5 8..122 5	0.81													
140888	ATU002 828	ATL8C3 1866:9 171..2 774	gap2	ATCEA4 C20327 1, ATCEA4 C460_1 ATCEA4 C6448_1, ATCEA4 S15540	99, 99, 98, 98, 96	ATL8C3 1866:9 171..2 883	0.81													

140897	ATU002 837	ATL8C1 5613:2 771..2 99	gap2	ATCEA4 S33089 , ATCEA4 C13024 01, ATCEA4 S34095 , ATCEA4 C1760_1	98, 95, 92, 83	ATL8C1 5613:2 653..8 81	0.81	g31725 38	100	1133	5.3e- 106	[Synec hocyst is sp.]; homeot ic protei n - Arabid opsis thalia na [Arabi dopsis thalia na]
140898	ATU002 838	ATL8C1 303:58 6..569 3	gap2	ATCEA4 C1254_1, ATCEA4 S12734 , ATCEA4 S4858, ATCEA4 C42928 1	99, 97, 97, 83	ATL8C1 303:58 6..558 8	0.81					[AF067 789) tSNARE AtTLG2 P [Arabi dopsis thalia na]
140899	ATU002 839	ATL8C2 6553:1 755..2 48	gap2	ATCEA4 C22412 1, ATCEA4 C74620	98, 89, 82	ATL8C2 6553:1 749..5 12	0.81	g36500 33	100	279	9.1e- 23	(AC005 396) unknow n protei

140908	ATU002 848	8681:1 571..1 74	ATL8C2 8705:9 68..10 1	gap2	C9872_ 1	ATCEA4 C811_1	99	8681:1 571..1 74	ATL8C2 8705:9 68..10 2	0.81							
140909	ATU002 849	8681:1 571..1 74	ATL8C2 1188:3 110..6 111	gap2	ATCEA4 C30273 1, ATCEA4 S6154, ATCEA4 C10329 7 1	99, 92, 89	0.81	ATL8C2 1188:3 203..6 026									
140910	ATU002 850	ATL8C3 0507:9 24..33 6	ATL8C3 0507:9 24..33 6	gap2	ATCEA4 C10792 1	99	0.81	ATL8C3 0507:7 40..33 6									
140911	ATU002 851	ATL8C1 8410:7 37..19 3	ATL8C1 8410:7 37..19 3	gap2	ATCEA4 S13775	99	0.81	ATL8C1 8410:6 41..19 3									
140912	ATU002 852	ATL8C4 0857:2 475..1 859	ATL8C4 0857:2 475..1 859	gap2	ATCEA4 C482_1	99	0.81	ATL8C4 0857:2 331..1 883									
140913	ATU002 853	ATL8C4 4275:3 72..60 9	ATL8C4 4275:3 72..60 9	gap2	ATCEA4 C453_1	99	0.81	ATL8C4 4275:5 25..60 9									
140914	ATU002 854	ATL8C4 2792:1 717..3 702	ATL8C4 2792:1 717..3 702	gap2	ATCEA4 C29308 1	99	0.81	ATL8C4 2792:1 717..3 493									
140915	ATU002 855	ATL8C1 7882:1 062..6 42	ATL8C1 7882:1 062..6 42	gap2	ATCEA4 C63_1	99	0.81	ATL8C1 7882:1 060..6 42									
140916	ATU002 856	ATL8C3 7750:4 13..11 72	ATL8C3 7750:4 13..11 72	gap2	ATCEA4 C69881 1	99	0.81	ATL8C3 7750:5 72..10 55									
140917	ATU002	ATL8C1	ATL8C1	gap2	ATCEA4	99, 99	0.81	ATL8C1									

140933	ATU002 873	ATL8C2 1667:2 125..1	gap2	ATCEA4 C916_1 , ATCEA4 S36288 , ATCEA4 C916_2	99, 98	ATL8C2 1667:1 760..3 1	0.80						n [Arabi dopsis thalia nal; (AL050 156) hypoth etical protei n [Homo sapien s]
140934	ATU002 874	ATL8C2 1657:2 755..1	gap2	ATCEA4 C28907 1, ATCEA4 C86946 1	99, 89	ATL8C2 1657:2 755..2 69	0.80						
140935	ATU002 875	ATL8C5 153:1. .1201	gap2	ATCEA4 C4699_1, ATCEA4 C4699_2, ATCEA4 C4472_1, ATCEA4 S27590	99, 98, 94, 85	ATL8C5 153:44 ..1012	0.80						
140936	ATU002 876	ATL8C4 9747:7 01..56 35	gap2	ATCEA4 C1531_1	99	ATL8C4 9747:1 073..5 353	0.80						
140937	ATU002	ATL8C1	gap2	ATCEA4	99	ATL8C1	0.80						

	877	1296:1 629..5 0		C44041 _1		1296:1 629..5 0						
140938	ATU002 878	ATL8C3 8546:1 987..3 34	gap2	ATCEA4 S14529 , ATCEA4 C28375 1	99, 98	ATL8C3 8546:1 987..3 34	0.80					
140939	ATU002 879	ATL8C2 0604:1 ..2557	gap2	ATCEA4 C739_1 , ATCEA4 C87382 1, ATCEA4 S36279 , ATCEA4 S2844	99, 97, 87, 82	ATL8C2 0604:6 ..2059	0.80					
140940	ATU002 880	ATL8C1 4076:8 656..1 27	gap2	ATCEA4 C2438_1 , ATCEA4 S30117	99, 96	ATL8C1 4076:8 656..1 27	0.80					
140941	ATU002 881	ATL8C2 435:32 ..1905	gap2	ATCEA4 C566_1 , ATCEA4 S36262 , ATCEA4 C26446 1	99, 84, 82	ATL8C2 435:25 1..176 0	0.80					
140942	ATU002 882	ATL8C4 3670:5 358..1 204	gap2	ATCEA4 C9782_1 , ATCEA4 C14463 1 1	99, 96	ATL8C4 3670:5 358..1 336	0.80					
140943	ATU002 883	ATL8C9 769:12 38..22 5	gap2	ATCEA4 C27024 1, ATCEA4	98, 82, 82, 82	ATL8C9 769:98 8..225	0.80	945393 48	100	1249	2.6e- 85	(AL035 539) putati ve

	906	2479:1 ..3248		C8009_		2479:1 ..3248														
140967	ATU002 907	ATL8C4 8050:1 ..1326	gap2	ATCEA4 C15613 1, ATCEA4 S27803 , ATCEA4 S1644, ATCEA4 S35852	99, 98, 97, 91	ATL8C4 8050:5 ..1326	0.79													
140968	ATU002 908	ATL8C1 9300:8 34..1	gap2	ATCEA4 C22076 1, ATCEA4 S26626	99, 98	ATL8C1 9300:8 21..29 3	0.79													
140969	ATU002 909	ATL8C1 2069:1 918..2 22	gap2	ATCEA4 S4781	99	ATL8C1 2069:1 918..2 64	0.79													
140970	ATU002 910	ATL8C2 7779:1 035..8	gap2	ATCEA4 S3780, ATCEA4 S9925	99, 92	ATL8C2 7779:1 014..8	0.79													
140971	ATU002 911	ATL8S1 0181:3 9..517	gap2	ATCEA4 C93632 1	99	ATL8S1 0181:1 85..39 9	0.79													
140972	ATU002 912	ATL8C5 53:1.. 1619	gap2	ATCEA4 S36380	99	ATL8C5 53:48. .1428	0.79													
140973	ATU002 913	ATL8C3 7813:1 09..98 1	gap2	ATCEA4 C26963 1, ATCEA4 C57008 1	99, 98	ATL8C3 7813:1 09..82 7	0.79													
140974	ATU002 914	ATL8C2 1581:1 080..3 70	gap2	ATCEA4 S4089, ATCEA4 C32830 1	99, 89	ATL8C2 1581:1 080..6 08	0.79													
140975	ATU002	ATL8C2	gap2	ATCEA4	99,	ATL8C2	0.79													

140983	ATU002 923	ATL8C2 6191:2 269..1	gap2	ATCEA4 S36250	99	ATL8C2 6191:2 255..4 26	0.79							[Oryza sativa]; SC01 (yeast homolo g) cytoch rome oxidas e defici ent 1 [Homo sapien s]
140984	ATU002 924	ATL8C3 6637:9 08..47 18	gap2	ATCEA4 C36234 1, ATCEA4 C33184 1, ATCEA4 S17059	98, 95, 95	ATL8C3 6637:1 114..4 718	0.79	529	100	g16522 17	1.5e- 48	(D9090 3) hypoth etical protei n [Synec hocyst is sp.]		
140985	ATU002 925	ATL8C2 919:18 75..1	gap2	ATCEA4 S5388, ATCEA4 C45253 2, ATCEA4 C45253 1, ATCEA4 S33933	99, 96, 94, 90	ATL8C2 919:18 75..11	0.79							
140986	ATU002 926	ATL8C3 2662:1 ..853	gap2	ATCEA4 C469_1 , ATCEA4 S4188	99, 98	ATL8C3 2662:1 34..85 3	0.79							

140987	ATU002 927	ATL8C6 591:11 56..19 0	gap2	ATCEA4 C9685_1	99	ATL8C6 591:10 05..19 0	0.79					
140988	ATU002 928	ATL8C1 8441:1 ..705	gap2	ATCEA4 C631_2 , ATCEA4 C631_1	99, 97	ATL8C1 8441:1 30..70 3	0.79					
140989	ATU002 929	ATL8C4 33:308 0..79	gap2	ATCEA4 C7661_1	99	ATL8C4 33:191 7..79	0.79					
140990	ATU002 930	ATL8C2 3555:1 ..556	gap2	ATCEA4 C5401_1	99	ATL8C2 3555:3 90..55 6	0.79					
140991	ATU002 931	ATL8C3 5082:1 ..2691	gap2	ATCEA4 S27015 , ATCEA4 C1358_1 , ATCEA4 S2834	99, 97 98, 97	ATL8C3 5082:2 45..24 99	0.79					
140992	ATU002 932	ATL8C4 78:649 ..4803	gap2	ATCEA4 S32199 , ATCEA4 S2431, ATCEA4 S2482	98, 85 96, 85	ATL8C4 78:865 ..4511	0.79	1631	100	g43712 85	1.8e- 142	(AC006 260) hypoth etical protein [Arabi dopsis thalia na]
140993	ATU002 933	ATL8C4 5231:3 8..787	gap2	ATCEA4 C1575_1 , ATCEA4 S28308 , ATCEA4 S18451	99, 97, 97, 94	ATL8C4 5231:8 5..208	0.79					
140994	ATU002 934	ATL8C1 1235:1	gap2	ATCEA4 C747_1	99	ATL8C1 1235:5	0.79					

141006	ATU002 946	ATL8C4 4502:1 281..3 686	gap2	ATCEA4 C62438 1, ATCEA4 C66027 _1	98, 92	ATL8C4 4502:1 281..3 686	0.78	g37765 59	100	1603	4.8e- 156	(AC005 388) Strong simila rity to gene F14J9. 26 [Arabi dopsis thalia na]
141007	ATU002 947	ATL8C4 4370:1 ..490	gap2	ATCEA4 C18580 1	99	ATL8C4 4370:3 8..490	0.78					
141008	ATU002 948	ATL8C3 8074:1 243..2 630	gap2	ATCEA4 S26556	98	ATL8C3 8074:1 243..2 477	0.78	g34027 10	100	550	5.3e- 58	(AC004 261) putati ve bzip protei n [Arabi dopsis thalia na]
141009	ATU002 949	ATL8C2 029:1. .749	gap2	ATCEA4 C874_1	99	ATL8C2 029:50 ..749	0.78					
141010	ATU002 950	ATL8C1 325:1. .3118	gap2	ATCEA4 C144_1 , ATCEA4 S36333 , ATCEA4 S36332	99, 98, 98	ATL8C1 325:45 ..3118	0.78					
141011	ATU002 951	ATL8C4 775:1. .2384	gap2	ATCEA4 C5880_1	98	ATL8C4 775:6. .2384	0.78	g48742 69	100	289	2.5e- 15	(AC007 354) T16B5. 7 [Arabi dopsis

141026	ATU002 966	ATL8C4 4899:1 172..3 441	gap2	ATCEA4 C2294_7, ATCEA4 S27191, ATCEA4 S22255	99, 98	ATL8C4 4899:1 832..3 303	0.77												
141027	ATU002 967	ATL8S3 0812:1 ..488	gap2	ATCEA4 S15599	99	ATL8S3 0812:3 64..48 8	0.77												
141028	ATU002 968	ATL8C3 1179:1 ..2383	gap2	ATCEA4 C2009_1	99	ATL8C3 1179:1 01..23 45	0.77												
141029	ATU002 969	ATL8C1 2155:9 0..861	gap2	ATCEA4 S34507	99	ATL8C1 2155:9 0..807	0.77												
141030	ATU002 970	ATL8C5 866:47 93..1	gap2	ATCEA4 S12456, ATCEA4 C10125_1, ATCEA4 C14423_8	99, 97 98, 97	ATL8C5 866:47 93..14	0.77												
141031	ATU002 971	ATL8C3 5117:2 018..1	gap2	ATCEA4 S26258, ATCEA4 C91561_1, ATCEA4 C3204_1	99, 91 98, 91	ATL8C3 5117:1 949..2 97	0.77												
141032	ATU002	ATL8C2	gap2	ATCEA4	99, 83	ATL8C2	0.77												

972	5315:9 67..37 0	C1361_1, ATCEA4 S23674		5315:9 17..47 5						
141033	ATU002 973	gap2	ATL8C2 747:1. .2065	ATL8C2 99, 98 747:63 5..206 5	0.77					
141034	ATU002 974	gap2	ATL8C2 377:20 89..88 1	ATL8C2 98 377:19 29..88 1	0.77	1342	100	g28084 38	1.3e- 136	(X7969 4) bg4 [Arabi dopsis thalia na]
141035	ATU002 975	gap2	ATL8C3 2223:3 707..1 762	ATL8C3 99, 2223:3 99, 470..2 89, 86 127	0.77					
141036	ATU002 976	gap2	ATL8C2 6575:5 4..175 5	ATL8C2 99 6575:5 4..113 1	0.77					
141037	ATU002 977	gap2	ATL8C4 8646:1 ..758	ATL8C4 99, 86 8646:2 05..62 2	0.77					
141038	ATU002 978	gap2	ATL8C4 0153:8 41..1	ATL8C4 99 0153:8 41..75	0.77					
141039	ATU002 979	gap2	ATL8C3 3947:3 41..58 38	ATL8C3 98, 95 3947:3 41..58 38	0.77	1325	100	g27087 50		(AC003 952) putati ve

141040	ATU002 980	ATL8C1 07:44. .1278	gap2	ATCEA4 S30391 , ATCEA4 S30392	98, 93	ATL8C1 07:164 ..1129	0.77	g63389 0	100	799			physic al impe nce protei n [Arabi dopsis thalia na]
141041	ATU002 981	ATL8C3 7720:1 265..1 33	gap2	ATCEA4 C11218 2, ATCEA4 C11218 1, ATCEA4 S13449	99, 87 98, 87	ATL8C3 7720:1 263..2 92	0.77						(S7292 6) glucos e and ribito l dehydr ogenas e homolo g [Horde um vulgar e]
141042	ATU002 982	ATL8C4 991:86 6..1	gap2	ATCEA4 C18581 1	99	ATL8C4 991:44 5..74	0.77						
141043	ATU002 983	ATL8C2 6740:5 9..144 0	gap2	ATCEA4 S6334, ATCEA4 C22727 _1	98, 91	ATL8C2 6740:3 36..14 40	0.77	g41389 12	100	1006	2.8e- 94	(AF059 487) expans in precu sor [Lycop ersico n]	

141044	ATU002 984	ATL8C2 4066:5 71..1	gap2	ATCEA4 S7361, ATCEA4 S8203	99, 82	ATL8C2 4066:5 14..62	0.77						escule ntum]
141045	ATU002 985	ATL8C4 1849:1 252..5 2	gap2	ATCEA4 S13830 , ATCEA4 S12910 , ATCEA4 C69125 1, ATCEA4 C34149 1, ATCEA4 S10027	99, 98, 93, 85, 82	ATL8C4 1849:1 204..4 55	0.77						
141046	ATU002 986	ATL8C2 6196:2 4..214 4	gap2	ATCEA4 S12244	99	ATL8C2 6196:2 144..2 4	0.77						
141047	ATU002 987	ATL8C2 7796:1 640..3 9	gap2	ATCEA4 S2801	99	ATL8C2 7796:1 473..3 9	0.77						
141048	ATU002 988	ATL8C6 828:44 9..295 7	gap2	ATCEA4 S11849	98	ATL8C6 828:44 9..277 0	0.77	g42205 41	100	1657	9.3e- 180	(AL035 356) Rab gerany lgeran yl transf erase like protei n [Arabi dopsis thalia na]	
141049	ATU002	ATL8C8	gap2	ATCEA4	99,	ATL8C8	0.77						

141050	989	980:1. .2399		C883_1 , ATCEA4 S22178 , ATCEA4 S33565	98, 94	980:17 8..217 8									
141051	ATU002 990	ATL8C1 6169:3 34..12 56	gap2	ATCEA4 S11364 , ATCEA4 S2388	99, 97	ATL8C1 6169:3 36..12 56	0.77								
141052	ATU002 991	ATL8C2 6425:1 ..1032	gap2	ATCEA4 C4419_1 , ATCEA4 S31927	99, 82	ATL8C2 6425:6 ..895	0.77								
141053	ATU002 992	ATL8C3 4705:2 17..69 2	gap2	ATCEA4 C75813 _1	99	ATL8C3 4705:2 17..69 2	0.77								
141054	ATU002 993	ATL8C4 5215:2 92..23 75	gap2	ATCEA4 S28751 , ATCEA4 S35077 , ATCEA4 C11660 9_1	98, 92, 90	ATL8C4 5215:3 70..20 02	0.77	g45860 36	100	782	5.6e- 81	(AC007 109) hypoth etical protein [Arabi dopsis thalia na]			
141055	ATU002 994	ATL8C1 3977:5 68..22 57	gap2	ATCEA4 S32139 , ATCEA4 S32106 , ATCEA4 C39032 _1, ATCEA4 C65592 1	98, 91, 87, 87	ATL8C1 3977:6 57..22 57	0.77	g45876 80	100	1630	1.2e- 170	(AC007 197) putati ve cytoch rome p450 [Arabi dopsis thalia na]			
141056	ATU002 995	ATL8C3	gap2	ATCEA4	99	ATL8C3	0.76								

141056	995	ATU002 996	ATL8C3 3598:8 26..1	gap2	C9305_1 ATCEA4 C2220_1, ATCEA4 S3697, ATCEA4 C2220_3, ATCEA4 C66363 ATCEA4 S4452	99, 88, 87, 82, 82	3746:1 25..16 31	0.76												
141057	ATU002 997	ATL8C2 4818:1 ..244	gap2	ATCEA4 C11642 4 1	99	ATL8C2 4818:5 4..150	0.76													
141058	ATU002 998	ATL8C4 665:95 ..1644	gap2	ATCEA4 C29453 1, ATCEA4 S11238	99, 92	ATL8C4 665:10 7..154 7	0.76													
141059	ATU002 999	ATL8C2 5016:2 705..2 28	gap2	ATCEA4 C1289_1, ATCEA4 S12462 , ATCEA4 S34257	99, 96, 89	ATL8C2 5016:2 445..5 06	0.76													
141060	ATU003 000	ATL8C5 0031:1 ..2369	gap2	ATCEA4 C5180_1, ATCEA4 S3024	99, 98	ATL8C5 0031:1 1..236 9	0.76													
141061	ATU003 001	ATL8C3 3342:1 511..1 01	gap2	ATCEA4 S29818	99	ATL8C3 3342:1 511..1 01	0.76													
141062	ATU003 002	ATL8C2 5475:1 622..8	gap2	ATCEA4 S14355 ,	99, 86	ATL8C2 5475:1 569..1	0.76													

141070	ATU003 010	ATL8C3 5714:1 646..1	gap2	ATCEA4 S36284	99	ATL8C3 5714:1 395..1 65	0.76				
141071	ATU003 011	ATL8C2 0377:4 80..24 3	gap2	ATCEA4 C64928 1	99	ATL8C2 0377:4 13..24 3	0.76				
141072	ATU003 012	ATL8C2 5534:5 18..1	gap2	ATCEA4 C2108 2	99	ATL8C2 5534:3 77..11	0.76				
141073	ATU003 013	ATL8C1 2379:1 484..9 05	gap2	ATCEA4 C24258 1	99	ATL8C1 2379:1 435..1 030	0.76				
141074	ATU003 014	ATL8S1 110:1. .564	gap2	ATCEA4 S2163, ATCEA4 C31812 1, ATCEA4 C1917 1, ATCEA4 S23919	99, 85, 85, 82	ATL8S1 110:36 8..129	0.76				
141075	ATU003 015	ATL8C8 104:73 8..347	gap2	ATCEA4 C1196 1	99	ATL8C8 104:69 6..636	0.76				
141076	ATU003 016	ATL8C3 8031:8 95..26 76	gap2	ATCEA4 C32299 1, ATCEA4 S31253	99, 90	ATL8C3 8031:8 95..26 76	0.76				
141077	ATU003 017	ATL8C4 7464:1 480..1	gap2	ATCEA4 C1791 1	99	ATL8C4 7464:1 438..2 07	0.76				
141078	ATU003 018	ATL8C4 9288:2 125..4 226	gap2	ATCEA4 C1433 1, ATCEA4 S31138	99, 96	ATL8C4 9288:2 345..4 226	0.76				
141079	ATU003 019	ATL8C3 0123:2	gap2	ATCEA4 S848	99	ATL8C3 0123:2	0.75				

		612..7 2				612..7 2												
141080	ATU003 020	ATL8C2 4394:8 67..1	gap2	ATCEA4 C1649_1	99	ATL8C2 4394:7 55..50	0.75											
141081	ATU003 021	ATL8C4 94:45. .5079	gap2	ATCEA4 S2296, ATCEA4 C11034 61	99, 90	ATL8C4 94:45. .5079	0.75											
141082	ATU003 022	ATL8S1 8303:3 72..69	gap2	ATCEA4 S13353 , ATCEA4 C18124 1	99, 99	ATL8S1 8303:2 08..69	0.75											
141083	ATU003 023	ATL8C1 4722:9 78..24 60	gap2	ATCEA4 C9735_1, ATCEA4 C6399_1	99, 98	ATL8C1 4722:9 79..24 19	0.75											
141084	ATU003 024	ATL8C1 4075:3 800..1 1112	gap2	ATCEA4 C14314 1, ATCEA4 C85198 1, ATCEA4 C35764 1, ATCEA4 S30774	98, 97, 96, 88	ATL8C1 4075:4 933..1 0939	0.75	g60675 1, g16193 00	100, 78	207, 184	1.1e- 12, 2.2e- 12					(L3493 4) RNA bindin g protei n [Droso phila melano gaster l; (X9526 9) LRR protei n [Lycop ersico n escule ntum]		
141085	ATU003 025	ATL8C2 1997:6	gap2	ATCEA4 C20237	99	ATL8C2 1997:5	0.75											

141097	ATU003 037	ATL8C3 5390:4 52..51 44	gap2	ATCEA4 C45801 2, ATCEA4 S1838, ATCEA4 C5417_1	98, 97, 95	ATL8C3 5390:4 52..48 22	0.75	g45104 01, g45104 07	100, 52	820, 292	3.7e- 65, 1.0e- 30	(AC006 587) putati ve genera l negati ve regula tor of transc riptio n [Arabi dopsis thalia na]; (AC006 587) unknow n protei n [Arabi dopsis thalia na]
141098	ATU003 038	ATL8C1 7422:1 ..907	gap2	ATCEA4 C59842 3, ATCEA4 C6389_1, ATCEA4 S24858 , ATCEA4 C59842 1	99, 97, 95, 93	ATL8C1 7422:4 8..907	0.75					
141099	ATU003 039	ATL8C1 5431:1 202..4 76	gap2	ATCEA4 S1461, ATCEA4 C892_1	99, 98	ATL8C1 5431:1 048..4 76	0.75					
141100	ATU003 040	ATL8C1 0077:4	gap2	ATCEA4 C497_1	99	ATL8C1 0077:4	0.75					

		ATU003	08..1			ATCEA4			08..11							
141101		ATU003 041	ATL8C3 0911:3 22..15 56	gap2		ATCEA4 C19138 _1	99		ATL8C3 0911:3 22..15 56	0.75						
141102		ATU003 042	ATL8C5 166:21 2..870	gap2		ATCEA4 C9632_1	99		ATL8C5 166:24 5..298	0.75						
141103		ATU003 043	ATL8C4 7121:3 243..2 977	gap2		ATCEA4 C373_1	99		ATL8C4 7121:3 243..3 184	0.75						
141104		ATU003 044	ATL8C9 667:61 0..45	gap2		ATCEA4 C29569 _1, ATCEA4 C29569 _2, ATCEA4 S9227	99, 93, 83		ATL8C9 667:61 0..335	0.75						
141105		ATU003 045	ATL8C2 4452:8 1..101 9	gap2		ATCEA4 C700_2 , ATCEA4 C700_1	99, 98		ATL8C2 4452:1 37..99 5	0.75						
141106		ATU003 046	ATL8C1 552:32 9..110 4	gap2		ATCEA4 S36330	99		ATL8C1 552:35 7..930	0.75						
141107		ATU003 047	ATL8C1 9398:1 24..11 17	gap2		ATCEA4 S1093, ATCEA4 S480	99, 88		ATL8C1 9398:2 53..11 17	0.74						
141108		ATU003 048	ATL8C3 3718:1 ..635	gap2		ATCEA4 C48867 _1, ATCEA4 S9108	99, 82		ATL8C3 3718:1 33..46 5	0.74						
141109		ATU003 049	ATL8C4 8555:1 46..68 1	gap2		ATCEA4 S1510, ATCEA4 C14706 _1	99, 97		ATL8C4 8555:1 46..62 5	0.74						

		9..211 5		ATCEA4 C3394_1, ATCEA4 S30161		2..242 1	g24672 72		3.4e- 82	No definition line found [Caenorhabditis elegans]; (Z99759) hypothetical protein [Schizosaccharomyces pombe]
141151	ATU003 091	ATL8C3 8428:1 151..1	gap2	ATCEA4 C12321 _1	99	ATL8C3 8428:1 034..2 33	0.73			
141152	ATU003 092	ATL8C4 8114:1 161..2 02	gap2	ATCEA4 S36236	99	ATL8C4 8114:1 160..2 02	0.73			
141153	ATU003 093	ATL8C4 7334:7 50..16 87	gap2	ATCEA4 C19960 _1, ATCEA4 C87358 _1	99, 97	ATL8C4 7334:7 54..16 87	0.73			
141154	ATU003 094	ATL8C3 8330:2 989..8 73	gap2	ATCEA4 C7325_1	99	ATL8C3 8330:2 989..8 73	0.73			
141155	ATU003 095	ATL8C1 3348:1 076..1 27	gap2	ATCEA4 S24395	99	ATL8C1 3348:1 076..1 72	0.73			
141156	ATU003	ATL8C4	gap2	ATCEA4	99,	ATL8C4	0.73			

141157	ATU003 097	3527:1 207..5 329	gap2	C573_1 , ATCEA4 S33104 , ATCEA4 S10383	96, 82	3527:1 305..5 075						
141158	ATU003 098	ATL8C1 3788:1 ..1134	gap2	ATCEA4 C1021_1, ATCEA4 S2989, ATCEA4 S3485	99, 96 97, 96	ATL8C1 3788:2 6..109 1	0.73					
141159	ATU003 099	ATL8C1 0001:1 234..1	gap2	ATCEA4 C17251 1, ATCEA4 C43153 1	99, 97	ATL8C1 0001:1 095..1 02	0.73					
141160	ATU003 100	ATL8C4 3879:2 104..6 0	gap2	ATCEA4 C27462 1, ATCEA4 C5889_1	99, 99	ATL8C4 3879:1 638..6 0	0.73					
141161	ATU003 101	ATL8C4 6843:2 25..12 92	gap2	ATCEA4 C18551 1_	99	ATL8C4 6843:2 25..12 92	0.73					
141162	ATU003 102	ATL8C1 4282:2 56..79 7	gap2	ATCEA4 C6806_2	99	ATL8C1 4282:2 56..78 2	0.73					
141163	ATU003 103	ATL8C1 9275:3 12..10 09	gap2	ATCEA4 S1813	99	ATL8C1 9275:3 12..10 09	0.73					
141164	ATU003 104	ATL8C1 3339:3 27..19 94	gap2	ATCEA4 S998, ATCEA4 S10406	99, 98	ATL8C1 3339:5 14..19 94	0.73					
		ATL8C5 823:52	gap2	ATCEA4 C77267	98, 93	ATL8C5 823:57	0.72, 0.98	977, 458	100, 60	94840 33,		(AJ133 753)

141165	ATU003 105	4..507 3		1, ATCEA4 C6803_2		2..334 6, ATL8C5 823:42 18..46 22		g17096 90				peptide methionine sulfoxide reductase [Arabidopsis thaliana]; PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET (O) REDUCTASE) [Brassicica napus]
141166	ATU003 106	ATL8C3 3408:5 38..14 1	gap2	ATCEA4 C6972_1	99	ATL8C3 3408:5 02..14 1	0.72					
141167	ATU003 107	ATL8C3 8561:2 838..1 286 ATL8C4 5994:4 920..9 6	gap2	ATCEA4 S13782 ATCEA4 C87114 1, ATCEA4 C28793 1, ATCEA4 S17442	99 99 99, 97, 83 97, 83	ATL8C3 8561:2 838..1 286 ATL8C4 5994:4 905..9 6	0.72					

141173	ATU003 113	ATL8C9 330:56 3..181 3	gap2	ATCEA4 S6254, ATCEA4 S5573, ATCEA4 S34964	99, 83, 82	ATL8C9 330:56 3..178 2	0.72					
141174	ATU003 114	ATL8C4 543:23 32..48 9	gap2	ATCEA4 C29273 1, ATCEA4 C21050 1, ATCEA4 S22565 , ATCEA4 S4305, ATCEA4 S24446 , ATCEA4 S22564	99, 97, 95, 90, 87, 83	ATL8C4 543:21 39..70 6	0.72					
141175	ATU003 115	ATL8C4 5477:4 40..88 0	gap2	ATCEA4 S2057	99	ATL8C4 5477:4 40..88 0	0.72					
141176	ATU003 116	ATL8C2 5174:8 6..307 6	gap2	ATCEA4 C411_1	99	ATL8C2 5174:8 8..282 7	0.72					
141177	ATU003 117	ATL8C4 1121:1 ..844	gap2	ATCEA4 C18913 1, ATCEA4 S1419	99, 93	ATL8C4 1121:7 9..836	0.72					
141178	ATU003 118	ATL8C4 560:95 ..3586	gap2	ATCEA4 C92219 1, ATCEA4 C5587_2, ATCEA4 S25022	99, 92	ATL8C4 560:95 ..3349	0.72					
141179	ATU003	ATL8C3	gap2	ATCEA4	99	ATL8C3	0.72					

141187	ATU003 127	ATL8C5 525:21 5..109 1	gap2	ATCEA4 C3984 1	99	ATL8C5 525:34 4..989	0.72					
141188	ATU003 128	ATL8C2 5817:4 09..15 14	gap2	ATCEA4 C30594 2	99	ATL8C2 5817:1 112..1 327	0.72					
141189	ATU003 129	ATL8C1 5813:2 160..2 8	gap2	ATCEA4 C47653 1	99	ATL8C1 5813:2 098..2 8	0.72					
141190	ATU003 130	ATL8C1 0837:3 194..3 97	gap2	ATCEA4 S29381 ATCEA4 C22267 1, ATCEA4 C3167 1, ATCEA4 S32656 ATCEA4 S26889	99, 99, 90, 87, 85	ATL8C1 0837:2 845..5 12	0.72					
141191	ATU003 131	ATL8C2 5305:6 37..1	gap2	ATCEA4 C15715 2	99	ATL8C2 5305:6 37..60	0.72					
141192	ATU003 132	ATL8C2 4173:1 876..1 24	gap2	ATCEA4 S25934 ATCEA4 C54611 1	99, 88	ATL8C2 4173:1 796..1 24	0.72					
141193	ATU003 133	ATL8C3 3891:6 02..1	gap2	ATCEA4 C15484 1	99	ATL8C3 3891:4 08..27 7	0.72					
141194	ATU003 134	ATL8C3 5450:1 368..8 42	gap2	ATCEA4 C11046 1, ATCEA4 S24511	99, 88, 83	ATL8C3 5450:1 244..1 045	0.72					

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155	141216	ATU003 156	8865:1 128..1 874	gap2	S36230 , ATCEA4 S3589, ATCEA4 C208_1 , ATCEA4 S12453	98, 93 97, 93	8865:1 128..1 866	0.71	g14831 77	100	1379	3.9e- 120	(D8659 8) antifr eze- like protei n (af70) [Picea abies]
			ATL8C3 6171:1 56..32 41	gap2	ATCEA4 S1069, ATCEA4 S31346 , ATCEA4 S34146 , ATCEA4 C5057_1	98, 94, 93, 92	ATL8C3 6171:4 43..31 83	0.71					
	141217	ATU003 157	ATL8C4 1806:1 189..5 210	gap2	ATCEA4 S5473, ATCEA4 S32073 , ATCEA4 C732_3 , ATCEA4 C732_2 , ATCEA4 S1120, ATCEA4 S13414	99, 98, 98, 93, 92, 83	ATL8C4 1806:1 330..5 011	0.71					
	141218	ATU003 158	ATL8C7 581:10 7..898	gap2	ATCEA4 S7200	99	ATL8C7 581:21 3..898	0.71					
	141219	ATU003 159	ATL8C4 8527:1 483..3 57	gap2	ATCEA4 S942	99	ATL8C4 8527:1 483..3 57	0.71					
	141220	ATU003 160	ATL8C1 4702:1	gap2	ATCEA4 C1650	99	ATL8C1 4702:4	0.71					

		87..86 5		1		27..84 8											
141221	ATU003 161	ATL8S1 1371:4 48..69	gap2	ATCEA4 C31000 1	99	ATL8S1 1371:4 48..69	0.71										
141222	ATU003 162	ATL8C4 2240:1 ..2105	gap2	ATCEA4 C11303 5_1, ATCEA4 C32116 1	99, 98	ATL8C4 2240:3 6..186 6	0.71										
141223	ATU003 163	ATL8C1 3450:3 966..1	gap2	ATCEA4 S25222 , ATCEA4 C12116 3_1	98, 90	ATL8C1 3450:3 966..2 4	0.71										(AL035 678) nucell in- like protei n [Arabi dopsis thalia na]; (AC004 793) Contai ns simila rity to [Arabi dopsis thalia na]
141224	ATU003 164	ATL8C3 6400:2 254..6 09	gap2	ATCEA4 C24606 1, ATCEA4 C9336- 1, ATCEA4 S2672, ATCEA4 S2563	99, 98, 97, 84	ATL8C3 6400:1 636..8 45	0.70										
141225	ATU003	ATL8C3	gap2	ATCEA4	99	ATL8C3	0.70										

141234	ATU003 174	ATL8C2 93:738 .1	gap2	C14379 2, ATCEA4 S8260, ATCEA4 C14379 1	99	ATL8C2 93:560 ..59	0.70										
141235	ATU003 175	ATL8C3 6995:1 475..1	gap2	ATCEA4 C1483 1, ATCEA4 S32872	99, 94	ATL8C3 6995:1 464..1 86	0.70										
141236	ATU003 176	ATL8C1 7316:1 934..2 67	gap2	ATCEA4 S10340	99	ATL8C1 7316:1 884..2 67	0.70										
141237	ATU003 177	ATL8C3 6170:2 300..5 1	gap2	ATCEA4 C49552 1, ATCEA4 S30102	99, 95	ATL8C3 6170:2 300..5 1	0.70										
141238	ATU003 178	ATL8C3 7120:1 327..3 14	gap2	ATCEA4 C32277 1	99	ATL8C3 7120:1 327..4 82	0.70										
141239	ATU003 179	ATL8S2 3827:6 75..1	gap2	ATCEA4 S33957	99	ATL8S2 3827:6 75..81	0.70										
141240	ATU003 180	ATL8C2 0354:9 2..980	gap2	ATCEA4 C191_1 , ATCEA4 C191_2 , ATCEA4 S33397	99, 93, 83	ATL8C2 0354:3 40..59 1	0.70										
141241	ATU003 181	ATL8C2 6596:1 255..1	gap2	ATCEA4 S36288 , ATCEA4 C916_2	99, 99, 99, 99, 95, 88	ATL8C2 6596:1 239..2 58	0.70										

141242	ATU003 182	ATL8C4 3490:1 40..11 62	gap2	ATCEA4 C916_1 ATCEA4 S2969, ATCEA4 S33983	99	ATL8C4 3490:1 41..97 9	0.70	945861 05	100	679	(AL049 638) putati ve protei n [Arabi dopsis thalia na]
141243	ATU003 183	ATL8C1 0533:5 42..19 52	gap2	ATCEA4 C6439_1	98	ATL8C1 0533:6 54..19 34	0.70				
141244	ATU003 184	ATL8C4 2607:3 134..1 9	gap2	ATCEA4 C28764_1	99	ATL8C4 2607:3 014..1 9	0.70				
141245	ATU003 185	ATL8C2 3741:4 501..1 097	gap2	ATCEA4 C12953 9_1, ATCEA4 S33744 ATCEA4 C12698 6_3, ATCEA4 S28167	98, 92, 90, 89	ATL8C2 3741:4 287..1 097	0.70	g39280 99	100	623	(AC005 770) unknow n protei n [Arabi dopsis thalia na]
141246	ATU003 186	ATL8C1 6945:7 004..5 43	gap2	ATCEA4 C1576_1, ATCEA4 C25677_1	99, 95	ATL8C1 6945:7 004..5 43	0.70				
141247	ATU003	ATL8C1	gap2	ATCEA4	99, 99	ATL8C1	0.70				

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141287	ATU003 227	ATL8C2 3335:7 053..9 670	gap2	ATCEA4 S12108 , ATCEA4 C11248 90, 1, ATCEA4 S10303 , ATCEA4 S28290 , ATCEA4 S7289, ATCEA4 S35319 , ATCEA4 S9508, ATCEA4 S9942	99, 96, 94, 94, 90, 89, 86, 82	ATL8C2 3335:9 646..7 053	0.67					
141288	ATU003 228	ATL8C3 8228:1 480..1 2	gap2	ATCEA4 C22283 1, ATCEA4 S24175	99, 84	ATL8C3 8228:1 480..1 2	0.67					
141289	ATU003 229	ATL8C4 7934:2 516..7 51	gap2	ATCEA4 S7506	99	ATL8C4 7934:2 516..7 51	0.67					
141290	ATU003 230	ATL8C1 7426:6 55..18 99	gap2	ATCEA4 C1143 1	99	ATL8C1 7426:1 541..1 839	0.67					
141291	ATU003 231	ATL8C1 5571:2 472..1 7	gap2	ATCEA4 C10164 1, ATCEA4 C57103 1, ATCEA4 C57103 2	99, 98, 93	ATL8C1 5571:2 368..1 7	0.67					
141292	ATU003	ATL8C3	gap2	ATCEA4	99	ATL8C3	0.67					

	232	4176:5 48..88 7		C10563 8_1		4176:6 99..79 9						
141293	ATU003 233	ATL8C3 2439:8 90..26 1	gap2	ATCEA4 C30403 1, ATCEA4 S33771	99, 93	ATL8C3 2439:8 90..26 1	0.67					
141294	ATU003 234	ATL8C2 5671:2 623..7 1	gap2	ATCEA4 C17903 _1	99	ATL8C2 5671:2 623..7 1	0.67					
141295	ATU003 235	ATL8C3 5699:3 304..1 228	gap2	ATCEA4 C39_1	99	ATL8C3 5699:3 304..1 436	0.67					
141296	ATU003 236	ATL8C4 7356:1 ..620	gap2	ATCEA4 C2698_1	99	ATL8C4 7356:1 35..62 0	0.67					
141297	ATU003 237	ATL8C1 9548:7 645..1 743	gap2	ATCEA4 C2099_1, ATCEA4 S17298 , ATCEA4 S34164 , ATCEA4 S34163 , ATCEA4 S36067 , ATCEA4 S17297 , ATCEA4 S11179	99, 98, 91, 91, 91, 89, 84	ATL8C1 9548:7 645..2 023	0.67					
141298	ATU003 238	ATL8C4 4367:3 6..935	gap2	ATCEA4 C87480 1	99	ATL8C4 4367:3 6..731	0.67					
141299	ATU003	ATL8C2	gap2	ATCEA4	99,	ATL8C2	0.67					

239	972:16 ..2761		S2891, ATCEA4 S2060, ATCEA4 S7851, ATCEA4 C12554 2 1	96, 95, 89	972:16 ..2576							
141300	ATU003 240	gap2	ATL8C3 3323:1 482..1	99 C1945 1	ATL8C3 3323:1 482..2 00	0.67						
141301	ATU003 241	gap2	ATL8C1 2207:2 86..55 84	98, 85 C30425 1, ATCEA4 S36305	ATL8C1 2207:1 045..5 584	0.67	100, 100	169, 415	1.0e- 15, 1.1e- 30	(U2953 5) C25H3. 4 gene product [Caeno rhabdi tis elegan s]; LIGATI N [Mus muscul us]		
141302	ATU003 242	gap2	ATL8C4 7099:1 357..1	99, 92, 87, 83	ATL8C4 7099:8 41..16 3	0.67						
141303	ATU003 243	gap2	ATL8C2 176:38 37..16 91	98 ATCEA4 S13008	ATL8C2 176:26 97..16 91	0.67	100	1592	4.8e- 163	(AC007 020) putati ve polyga		

141309	ATU003 249	ATL8C1 5714:1 ..760	gap2	ATCEA4 C11896 5 1, ATCEA4 C46696 1	99	ATL8C1 5714:2 43..36 7	0.67												
141310	ATU003 250	ATL8C4 9186:3 4..254 2	gap2	ATCEA4 C23878 1, ATCEA4 S12764 , ATCEA4 S12765	99, 98, 95	ATL8C4 9186:3 4..254 2	0.67												
141311	ATU003 251	ATL8C1 913:86 5..384	gap2	ATCEA4 S4596	99	ATL8C1 913:66 1..384	0.67												
141312	ATU003 252	ATL8S6 784:1. .571	gap2	ATCEA4 C240_1	99	ATL8S6 784:42 ..283	0.67												
141313	ATU003 253	ATL8C2 6231:1 ..902	gap2	ATCEA4 S4237	99	ATL8C2 6231:1 17..90 2	0.67												
141314	ATU003 254	ATL8C6 934:15 57..64 5	gap2	ATCEA4 C14116 1	99	ATL8C6 934:13 94..77 7	0.67												
141315	ATU003 255	ATL8C1 775:21 8..845	gap2	ATCEA4 C12422 1	99	ATL8C1 775:21 8..845	0.67												
141316	ATU003 256	ATL8C1 058:42 6..405 5	gap2	ATCEA4 C891_1	99	ATL8C1 058:77 6..400 4	0.67												
141317	ATU003 257	ATL8C4 9902:1 979..4 57	gap2	ATCEA4 C77218 1, ATCEA4 C15507	99, 97	ATL8C4 9902:1 838..4 57	0.67												

141327	ATU003 267	..2291		3, ATCEA4 C12838 1, ATCEA4 C8923 1, ATCEA4 S6888	97, 91	39..21 13						
			gap2	ATCEA4 C1980 1, ATCEA4 C1980 2, ATCEA4 S10080	99, 82	ATL8C1 7000:1 001..5 6	0.66					
141328	ATU003 268		gap2	ATCEA4 S11673 , ATCEA4 C11609 1 1	99, 96	ATL8C2 6744:1 75..10 11	0.66					
141329	ATU003 269		gap2	ATCEA4 S19921	99	ATL8S3 374:26 0..31	0.66					
141330	ATU003 270		gap2	ATCEA4 C23318 _1	99	ATL8C3 7829:4 83..16 57	0.66					
141331	ATU003 271		gap2	ATCEA4 C29732 1, ATCEA4 S33290 , ATCEA4 S34684	99, 89, 89	ATL8C2 4133:1 923..5 54	0.66					
141332	ATU003 272		gap2	ATCEA4 C12182 _1	98	ATL8C3 3702:1 798..1 90	0.66	949144 01	100	837	3.6e- 63	(AL050 352) hypoth etical protei n

141333	ATU003 273	ATL8C4 9034:1 452..1 85	gap2	ATCEA4 C39265 _1	99	ATL8C4 9034:1 452..1 85	0.66									[Arabi dopsis thalia na]
141334	ATU003 274	ATL8C1 2761:1 460..1	gap2	ATCEA4 C223_1	99	ATL8C1 2761:1 351..1 60	0.66									
141335	ATU003 275	ATL8C2 7815:1 245..1	gap2	ATCEA4 C1603_1	99	ATL8C2 7815:1 198..1 5	0.66									
141336	ATU003 276	ATL8C9 539:26 1..983	gap2	ATCEA4 C25204 _1, ATCEA4 S4217	99, 99	ATL8C9 539:26 4..581	0.66									
141337	ATU003 277	ATL8C1 4817:8 50..39 47	gap2	ATCEA4 C35283 _1	99	ATL8C1 4817:9 15..39 47	0.65									
141338	ATU003 278	ATL8C2 746:24 9..532 4	gap2	ATCEA4 C11691 _1, ATCEA4 S5101, ATCEA4 S35120 , ATCEA4 C23104 _1	98, 98, 90, 88	ATL8C2 746:11 03..30 11, ATL8C2 746:51 68..38 71	0.65, 0.67	100, 100	2439, 1051	3.3e- 242, 3.6e- 97						(AF077 409) Simila r to pectin esterase; T24M8. 6 [Arabi dopsis thalia na]; (AF077 409) No defini tion line

141339	ATU003 279	ATL8C2 0877:2 969..1 272	gap2	ATCEA4 C41215 1, ATCEA4 S12374 , ATCEA4 S4503	98, 82 96, 82	ATL8C2 0877:2 138..1 272	0.65	g11139 41	100	811	1.7e- 82	found [Arabi dopsis thalia na] (U4071 3) Pv42p [Phase olus vulgar is]
141340	ATU003 280	ATL8C1 4521:3 671..1 917	gap2	ATCEA4 C35_3, ATCEA4 C35_1, ATCEA4 C35_4, ATCEA4 S3053, ATCEA4 C35_2, ATCEA4 S22203	99, 98, 96, 95, 88, 82	ATL8C1 4521:3 640..1 917	0.65					
141341	ATU003 281	ATL8C2 6230:1 344..5 8	gap2	ATCEA4 C51456 _1	99	ATL8C2 6230:1 344..1 075	0.65					
141342	ATU003 282	ATL8C4 4126:7 1..807	gap2	ATCEA4 C32490 1	99	ATL8C4 4126:7 1..649	0.65					
141343	ATU003 283	ATL8C2 5078:1 ..981	gap2	ATCEA4 S2260	99	ATL8C2 5078:7 0..981	0.65					
141344	ATU003 284	ATL8C2 7437:1 759..1	gap2	ATCEA4 C62974 1, ATCEA4 S31638 , ATCEA4 C62974 3	98, 91 95, 91	ATL8C2 7437:1 658..1 53	0.65	g18853 10	100	624		(X9165 9) Endoxy logluc an transf erase (EXT) [Horde

141345	ATU003 285	ATL8C1 0201:2 95..23 43	gap2	ATCEA4 S27401	98		ATL8C1 0201:2 95..23 43	0.65	g43098 68	100	2533	um vulgar el (AC006 527) putati ve retrot ranspo son- like orf [Arabi dopsis thalia na]
141346	ATU003 286	ATL8C1 2698:8 81..46 5	gap2	ATCEA4 C434_4	99		ATL8C1 2698:8 81..69 0	0.65				
141347	ATU003 287	ATL8C1 986:11 47..15	gap2	ATCEA4 S8962	99		ATL8C1 986:11 47..12 7	0.65				
141348	ATU003 288	ATL8C9 93:262 ..4705	gap2	ATCEA4 C38737 1, ATCEA4 S6031, ATCEA4 C10181 4 1, ATCEA4 S3211, ATCEA4 S2569, ATCEA4 C47794 1	99, 94, 93, 92, 89, 84		ATL8C9 93:262 ..4397	0.65				
141349	ATU003 289	ATL8C1 8742:2 233..3 624	gap2	ATCEA4 C1573_8, ATCEA4 C44844	98, 89, 84, 82		ATL8C1 8742:2 273..3 616	0.65	g21305 21	100	1597	5.6e- 122 (U3156 5) revers ibly glycos

141350	ATU003 290	ATL8C3 6308:1 157..3 2	gap2	1, ATCEA4 S33961 , ATCEA4 S34172	98	ATL8C3 6308:1 139..3 25	0.65	g21296 36, g34829 14	100, 100	580, 244	8.1e- 56, 1.2e- 19	ylatab le polype ptide [Pisum sativu m]
141351	ATU003 291	ATL8C6 873:1. .2762	gap2	ATCEA4 C24476 1, ATCEA4 S1806, ATCEA4 S1355	99, 93, 93	ATL8C6 873:45 0..276 2	0.65					
141352	ATU003 292	ATL8C1 8401:2 305..1 328	gap2	ATCEA4 C18170 1, ATCEA4 S16035	99, 98	ATL8C1 8401:2 290..1 370	0.65					
141353	ATU003 293	ATL8C3 7392:1 47..14 76	gap2	ATCEA4 C16529 1, ATCEA4 C15693	99, 96, 84	ATL8C3 7392:3 17..14 76	0.65					

141354	ATU003 294	ATL8C3 2566:3 482..1	gap2	0 1, ATCEA4 S17706	99, 96, 96, 91, 88, 84, 83	ATL8C3 2566:3 412..2 29	0.65									
141355	ATU003 295	ATL8C2 622:92 5..158 8	gap2	ATCEA4 C29428 1, ATCEA4 S6105	99, 95	ATL8C2 622:10 48..15 88	0.64									
141356	ATU003 296	ATL8C4 9542:4 76..1	gap2	ATCEA4 C13546 8 1, ATCEA4 C93077 1	99, 88	ATL8C4 9542:3 22..16	0.64									
141357	ATU003 297	ATL8C2 6895:8 97..12 70	gap2	ATCEA4 C78148 2, ATCEA4 C78148 1	99, 99	ATL8C2 6895:1 225..1 145	0.64									
141358	ATU003 298	ATL8C2 4785:1 ..1816	gap2	ATCEA4 C9 1, ATCEA4 S21281	99, 86, 86, 84	ATL8C2 4785:1 05..18 16	0.64									

141359	ATU003 299	ATL8S2 5893:6 4..420	gap2	ATCEA4 S19689 , ATCEA4 S21280	99, 95	ATL8S2 5893:2 53..18 2	0.64										
141360	ATU003 300	ATL8C7 286:94 ..818	gap2	ATCEA4 C22198 1	99	ATL8C7 286:21 4..569	0.64										
141361	ATU003 301	ATL8C3 3913:2 539..1 16	gap2	ATCEA4 C9731 1	99	ATL8C3 3913:2 539..1 16	0.64										
141362	ATU003 302	ATL8C2 5498:1 ..718	gap2	ATCEA4 C26339 1	99	ATL8C2 5498:1 38..53 3	0.64										
141363	ATU003 303	ATL8C2 0259:6 45..99 6	gap2	ATCEA4 S3414	99	ATL8C2 0259:6 58..92 2	0.64										
141364	ATU003 304	ATL8C4 8309:1 117..1 01	gap2	ATCEA4 C1447 1	99	ATL8C4 8309:1 111..1 01	0.64										
141365	ATU003 305	ATL8C1 8391:5 31..74 6	gap2	ATCEA4 C11690 0_1	99	ATL8C1 8391:5 57..72 5	0.64										
141366	ATU003 306	ATL8C4 0101:3 28..13 53	gap2	ATCEA4 C32444 1, ATCEA4 S11499	99, 99	ATL8C4 0101:3 28..13 53	0.64										
141367	ATU003 307	ATL8C1 6044:1 ..701	gap2	ATCEA4 C141_1 , ATCEA4 S36082 ,	99, 98, 96, 93, 90,	ATL8C1 6044:2 73..45 3	0.64										

141368	ATU003 308	ATL8C4 6222:2 251..6 07	gap2	ATCEA4 S33797 , ATCEA4 S13836 , ATCEA4 C141_4 , ATCEA4 S35606 , ATCEA4 S35972 , ATCEA4 C141_7 , ATCEA4 S23546	90, 85, 83	ATL8C4 6222:2 251..6 07	0.64	944172 87	100	1837	6.9e- 175	(AC007 019) unknown protein [Arabidopsis thaliana]
141369	ATU003 309	ATL8C7 72:484 7..155	gap2	ATCEA4 S8764, ATCEA4 C19982 1, ATCEA4 S34275 , ATCEA4 C19982 2	99, 98, 96, 96	ATL8C7 72:478 3..314	0.64					
141370	ATU003 310	ATL8C5 0038:1 418..1	gap2	ATCEA4 C1173_1	99	ATL8C5 0038:1 134..7 5	0.64					

141371	ATU003 311	ATL8C4 1745:1 ..2783	gap2	ATCEA4 C921_1	99	ATL8C4 1745:5 2..278 3	0.64					
141372	ATU003 312	ATL8C2 9249:1 938..9 41	gap2	ATCEA4 S30004 , ATCEA4 S844	99, 96	ATL8C2 9249:1 938..9 41	0.64					
141373	ATU003 313	ATL8C1 4854:6 87..1	gap2	ATCEA4 C48992 _1	99	ATL8C1 4854:6 33..15 6	0.64					
141374	ATU003 314	ATL8C2 3679:1 ..1162	gap2	ATCEA4 C5790_1, ATCEA4 C23316_1	99, 93	ATL8C2 3679:9 5..101 3	0.64					
141375	ATU003 315	ATL8C2 7750:1 24..17 86	gap2	ATCEA4 C1754_1	99	ATL8C2 7750:1 24..14 80	0.64					
141376	ATU003 316	ATL8C4 8695:4 270..7 38	gap2	ATCEA4 C10236 1_1, ATCEA4 S28037 , ATCEA4 S25267	98, 97, 90	ATL8C4 8695:3 351..7 38	0.64	g45860 58, g24941 40	100, 98	529, 197	5.4e- 39, 6.2e- 07	(AC007 020) unknown protein [Arabi dopsis thalia na]; (AC003 002) R29515 1 [Homo sapien s]
141377	ATU003 317	ATL8C1 7129:2 207..1	gap2	ATCEA4 C1510_1, ATCEA4	99, 99	ATL8C1 7129:2 207..1 09	0.63					

141378	ATU003 318	ATL8C1 2015:1 007..1	gap2	S14091 ATCEA4 S27047 , ATCEA4 S13778 , ATCEA4 S31305 , ATCEA4 S35092	99, 99, 89, 88	ATL8C1 2015:1 007..5 5	0.63								
141379	ATU003 319	ATL8C1 9402:3 08..10 75	gap2	ATCEA4 S11968 , ATCEA4 C45225 1, ATCEA4 S11969	99, 96, 91	ATL8C1 9402:4 42..86 0	0.63								
141380	ATU003 320	ATL8C2 3707:9 29..1	gap2	ATCEA4 S36362	99	ATL8C2 3707:8 85..10 4	0.63								
141381	ATU003 321	ATL8C2 6167:2 032..1	gap2	ATCEA4 S13333 , ATCEA4 S35938 , ATCEA4 C7499_1, ATCEA4 C77767 1	99, 97, 90, 84	ATL8C2 6167:2 014..6 5	0.63								
141382	ATU003 322	ATL8C4 8579:2 428..1 374	gap2	ATCEA4 C9789_1	98	ATL8C4 8579:2 373..1 374	0.63	g32506 79	100	766	3.7e- 78	(AL024 486) putati ve protei n [Arabi dopsis			

141413	ATU003 353	ATL8C3 1790:7 241..3 755	gap2	ATCEA4 S26063 ' ATCEA4 S20118	99, 98, 94, 92, 92, 82	ATL8C3 1790:6 953..4 008	0.62									
141414	ATU003 354	ATL8S2 3272:4 13..80	gap2	ATCEA4 C866_1 ' ATCEA4 C866 2	99, 86	ATL8S2 3272:4 11..82	0.62									
141415	ATU003 355	ATL8S1 5336:8 1..491	gap2	ATCEA4 C1178_1	99	ATL8S1 5336:8 1..341	0.62									
141416	ATU003 356	ATL8C1 8996:1 877..1	gap2	ATCEA4 S1621, ATCEA4 C18378 1	99, 95	ATL8C1 8996:1 780..1 65	0.62									
141417	ATU003 357	ATL8C3 2556:5 18..1	gap2	ATCEA4 C49252 _1	99	ATL8C3 2556:5 13..12 7	0.62									
141418	ATU003 358	ATL8C2 7736:1 594..2 457	gap2	ATCEA4 S14056	99	ATL8C2 7736:1 691..2 457	0.62									
141419	ATU003 359	ATL8C3 6272:6 40..14	gap2	ATCEA4 S12431	99	ATL8C3 6272:6 40..13	0.62									

141437	ATU003 377	ATL8C1 9533:2 995..2 394	gap2	ATCEA4 C1811_1, ATCEA4 S29995	99, 98	ATL8C1 9533:2 864..2 530	0.61					
141438	ATU003 378	ATL8C4 0269:1 76..13 23	gap2	ATCEA4 C50470_1, ATCEA4 S32981	99, 97	ATL8C4 0269:1 79..12 35	0.61					
141439	ATU003 379	ATL8C3 3898:2 52..38 19	gap2	ATCEA4 C4600_2, ATCEA4 C4600_1, ATCEA4 S27051 , ATCEA4 C11981 5_1, ATCEA4 S11470	99, 97, 96, 92, 90	ATL8C3 3898:2 62..38 19	0.61					
141440	ATU003 380	ATL8C2 1232:1 19..51 00	gap2	ATCEA4 C14720_1_	98	ATL8C2 1232:1 19..51 00	0.61	g10013 79	100	558	1.2e- 47	(D6400 6) aspart ate beta- semial dehyde dehydr ogenes e [Synec hocyst is sp.]
141441	ATU003 381	ATL8C3 5545:8 0..957	gap2	ATCEA4 C11760 0_1	99	ATL8C3 5545:8 0..442	0.61					
141442	ATU003 382	ATL8C2 5438:2 02..79	gap2	ATCEA4 S7967	99	ATL8C2 5438:6 54..79	0.61					

141443	ATU003 383	7	ATL8C2 8245:6 71..96 7	gap2	ATCEA4 S3939	99	ATL8C2 8245:7 59..93 8	0.61												
141444	ATU003 384		ATL8C1 9096:1 70..13 18	gap2	ATCEA4 S2297, ATCEA4 S32272	99, 90	ATL8C1 9096:1 70..11 92	0.61												
141445	ATU003 385		ATL8C3 6839:6 1..284 6	gap2	ATCEA4 C70753 1, ATCEA4 S30468 , ATCEA4 S33249	98, 90 86, 85	ATL8C3 6839:7 28..22 59	0.61		100	g45672 81	1697	2.2e-134	(AC006841) unknown protein [Arabidopsis thaliana].						
141446	ATU003 386		ATL8C3 3221:8 77..12 35	gap2	ATCEA4 C49877 _1	99	ATL8C3 3221:9 39..12 33	0.61												
141447	ATU003 387		ATL8C3 4888:1 353..4 2	gap2	ATCEA4 S1478, ATCEA4 C31245 1	99, 98	ATL8C3 4888:1 326..4 2	0.61												
141448	ATU003 388		ATL8C4 6686:1 ..1653	gap2	ATCEA4 C439_1	99	ATL8C4 6686:6 48..12 91	0.61												
141449	ATU003 389		ATL8C2 5127:1 384..5 4	gap2	ATCEA4 S5615	99	ATL8C2 5127:1 369..5 4	0.61												
141450	ATU003 390		ATL8C1 5889:8 24..1	gap2	ATCEA4 C1063_2, ATCEA4 C1063_6	99, 94	ATL8C1 5889:7 73..59	0.61												
141451	ATU003 391		ATL8C3 2740:1	gap2	ATCEA4 S710	99	ATL8C3 2740:1	0.61												

		12..20 74	gap2	ATCEA4 S1960	99	12..20 74	0.60											
141452	ATU003 392	ATL8C4 8518:9 16..48 1	gap2	ATCEA4 S1960	99	ATL8C4 8518:8 70..55 5	0.60											
141453	ATU003 393	ATL8C2 6102:6 75..10 1	gap2	ATCEA4 C1510 1	99	ATL8C2 6102:6 73..10 4	0.60											
141454	ATU003 394	ATL8C3 3535:3 231..2 02	gap2	ATCEA4 S439, ATCEA4 C15470 1, ATCEA4 C14155 1, ATCEA4 C18540 1	99, 98, 97, 96	ATL8C3 3535:3 125..2 02	0.60											
141455	ATU003 395	ATL8C3 9534:2 295..1 232	gap2	ATCEA4 C29675 1 1	99	ATL8C3 9534:2 165..1 395	0.60											
141456	ATU003 396	ATL8C2 4286:4 189..1 722	gap2	ATCEA4 C7039 2, ATCEA4 C47888 1	99, 98	ATL8C2 4286:4 041..2 006	0.60											
141457	ATU003 397	ATL8C5 339:16 27..48 60	gap2	ATCEA4 C12154 7 1, ATCEA4 S1920, ATCEA4 C6815 1, ATCEA4 S1166, ATCEA4 S26371	99, 99, 98, 95, 89	ATL8C5 339:16 52..48 60	0.60											
141458	ATU003	ATL8C5	gap2	ATCEA4	99	ATL8C5	0.60											

141468	ATU003 408	875..1	gap2	ATCEA4 C32445 1, ATCEA4 C20476 1	99, 92	862..7 5	0.60	g11892 6	100	586	1.4e- 60	DESSIC ATION- RELATE D PROTEI N CLONE PCC13- 62 PRECUR SOR [Crate rostig ma planta gineum]
141469	ATU003 409	ATL8C8 752:11 21..1	gap2	ATCEA4 C52058 1, ATCEA4 S26496	98, 85	ATL8C1 7499:8 96..23 29	0.60					
141470	ATU003 410	ATL8C3 1420:1 346..1 961	gap2	ATCEA4 C6056 1	99	ATL8C3 1420:1 386..1 961	0.59					
141471	ATU003 411	ATL8C3 63:1.. 3335	gap2	ATCEA4 C12568 2 1, ATCEA4 S31260 , ATCEA4 S27573 , ATCEA4 S32205	99, 92, 88, 86, 86	ATL8C3 63:68. .3005	0.59					

[illegible]

141497	ATU003 437	ATL8C2 5794:1 069..1	gap2	2, ATCEA4 S5459	99, 93 95, 93	ATL8C2 5794:1 069..2 88	0.58												
141498	ATU003 438	ATL8C1 7519:2 166..5 51	gap2	ATCEA4 S824	99	ATL8C1 7519:1 889..5 51	0.58												
141499	ATU003 439	ATL8C2 3649:2 033..3 3	gap2	ATCEA4 S6437	99	ATL8C2 3649:2 033..3 3	0.58												
141500	ATU003 440	ATL8C2 896:16 9..100 7	gap2	ATCEA4 S3061, ATCEA4 C364_1 , ATCEA4 S33781 , ATCEA4 C20508 _1, ATCEA4 S6001	99, 91, 91, 82, 82	ATL8C2 896:20 8..938	0.58												
141501	ATU003 441	ATL8C3 0594:1 ..2494	gap2	ATCEA4 S999, ATCEA4 C68003 _1, ATCEA4 S25413	99, 92, 92	ATL8C3 0594:3 9..226 6	0.58												
141502	ATU003 442	ATL8C2 9317:4 84..1	gap2	ATCEA4 C61938 _1	99	ATL8C2 9317:4 42..73	0.57												
141503	ATU003	ATL8C2	gap2	ATCEA4	99	ATL8C2	0.57												

141504	443	ATU003 444	2469:3 105..1 493	gap2	C1704_1	98, 96	2469:3 052..1 743	0.57	g42061 95	100	642	2.3e- 46	(AF071 527) hypo- thetical protein [Arabi- dopsis thaliana]
141505	ATU003 445	ATL8C1 155:21 15..47	ATL8C9 775:96 3..165 0	gap2	ATCEA4 C47768 1, ATCEA4 C74835 1	99	ATL8C9 775:11 41..15 05	0.57					
141506	ATU003 446	ATL8C2 327:12 03..78 7	ATL8C2 327:11 71..10 66	gap2	ATCEA4 S15175	99	ATL8C2 327:11 71..10 66	0.57					
141507	ATU003 447	ATL8C6 730:1. .603	ATL8C6 730:32 1..363	gap2	ATCEA4 S36319	99	ATL8C6 730:32 1..363	0.57					
141508	ATU003 448	ATL8C1 976:96 6..106	ATL8C1 976:96 6..106	gap2	ATCEA4 C3424_1, ATCEA4 C3424_2	99, 97	ATL8C1 976:96 6..127	0.57					
141509	ATU003 449	ATL8C4 6740:6 66..13 14	ATL8C4 6740:8 04..13 14	gap2	ATCEA4 S14179 , ATCEA4 S2797	99, 88	ATL8C4 6740:8 04..13 14	0.57					
141510	ATU003 450	ATL8C3 0701:1 ..1820	ATL8C3 0701:1 ..1820	gap2	ATCEA4 C1565_1	99	ATL8C3 0701:3 5..169 7	0.57					
141511	ATU003 451	ATL8C2 1806:1 ..1056	ATL8C2 1806:1 ..1056	gap2	ATCEA4 C644_1	99	ATL8C2 1806:5 73..96 2	0.57					
141512	ATU003	ATL8C9	ATL8C9	gap2	ATCEA4	99,	ATL8C9	0.57					

141513	452	650:99 0..1		S1278, ATCEA4 C12942 1, ATCEA4 S33815 , ATCEA4 S6514, ATCEA4 S33927 , ATCEA4 S32881 ATCEA4 C71889 1 _	98, 95, 95, 94, 91	650:45 0..724					
141514	ATU003 453	ATL8C3 3857:1 311..1 68	gap2	ATCEA4 C71889 1 _	99	ATL8C3 3857:1 147..1 68	0.57				
141515	ATU003 454	ATL8C1 9292:1 27..32 41	gap2	ATCEA4 C47696 1, ATCEA4 C31131 1, ATCEA4 S7629, ATCEA4 S11331	99, 97, 89, 82	ATL8C1 9292:1 27..32 41	0.57				
141516	ATU003 455	ATL8C4 6453:1 43..71 3	gap2	ATCEA4 S1225	99	ATL8C4 6453:6 02..71 3	0.57				
141517	ATU003 456	ATL8C3 4756:6 22..20 04	gap2	ATCEA4 C16730 1 _	99	ATL8C3 4756:8 60..20 04	0.57				
141518	ATU003 457	ATL8C2 6283:5 84..21 8	gap2	ATCEA4 S1769	99	ATL8C2 6283:3 14..21 8	0.57				
141519	ATU003 458	ATL8C6 016:1. .623	gap2	ATCEA4 C3942 1, ATCEA4	99, 84	ATL8C6 016:58 ..599	0.57				

141527	ATU003 467	2967:5 81..10 7	gap2	C903_1 , ATCEA4 S22145	2967:5 10..11 4						
141528	ATU003 468	ATL8C2 796:13 76..13 4	gap2	ATCEA4 C66699 1, ATCEA4 S25004	ATL8C2 796:77 7..134	0.56					
141529	ATU003 469	ATL8C2 826:19 88..1	gap2	ATCEA4 C31984 1, ATCEA4 C79697 1	ATL8C2 826:16 62..78	0.56					
141530	ATU003 470	ATL8C3 4876:8 87..28 40	gap2	ATCEA4 C47478 1, ATCEA4 S2658	ATL8C3 4876:1 252..2 840	0.56					
141531	ATU003 471	ATL8C5 180:43 7..108 8	gap2	ATCEA4 S7187	ATL8C5 180:43 7..108 8	0.56					
141532	ATU003 472	ATL8C4 637:15 77..27 9	gap2	ATCEA4 S2267	ATL8C4 637:15 77..27 9	0.56					
141533	ATU003 473	ATL8C2 6476:1 016..1 265	gap2	ATCEA4 C2803 2, ATCEA4 C4210 1	ATL8C2 6476:1 016..1 265	0.56					
141534	ATU003 474	ATL8C2 9080:5 34..10 04	gap2	ATCEA4 S36314	ATL8C2 9080:5 60..96 8	0.56					
141535	ATU003 475	ATL8C1 2977:1 ..328	gap2	ATCEA4 C1776 1	ATL8C1 2977:2 23..32 8	0.56					
141536	ATU003 476	ATL8C3 4684:2	gap2	ATCEA4 C8272	ATL8C3 4684:2	0.56					

	484	7789:5 373..2 2	S1967			7789:5 373..2 2									(AF096 372) No defini- tion line found [Arabi [Arabi dopsis thalia na]; (AL031 018) putati ve fizzy-rele d protein [Arabi dopsis thalia na]
141545	ATU003 485	ATL8C4 4497:2 239..3 610	gap2	ATCEA4 C66562 _1	99	ATL8C4 4497:2 239..3 610	0.55								
141546	ATU003 486	ATL8C1 7376:1 437..2 19	gap2	ATCEA4 S36276	99	ATL8C1 7376:1 414..4 02	0.55								
141547	ATU003 487	ATL8C1 3527:1 69..47 42	gap2	ATCEA4 C22298 _1	98	ATL8C1 3527:3 45..45 43	0.55	g36953 97, g32928 16	100, 67	1498, 595	1.1e- 124, 2.6e- 47				
141548	ATU003 488	ATL8C1 0567:1 249..1 849	gap2	ATCEA4 C68562 _2, ATCEA4 C68562 _1	99, 96	ATL8C1 0567:1 276..1 774	0.55								
141549	ATU003 489	ATL8C1 4422:8 538..1	gap2	ATCEA4 C19071 _2,	98, 97, 93	ATL8C1 4422:9 085..1	0.55	g43357 53, g45393	100, 73	441, 1236	3.2e- 31, 3.5e-				(AC006 284) unknown

		1913		ATCEA4 C71853 1, ATCEA4 S15671		1913		1913		94		116	n protei n [Arabi dopsis thalia na]; (AL035 526) putati ve protei n [Arabi dopsis thalia na]
141550	ATU003 490	ATL8C1 4503:1 44..99 3	gap2	ATCEA4 C1872_1	99	ATL8C1 4503:1 44..96 4	0.55						
141551	ATU003 491	ATL8C1 9505:3 444..2 171	gap2	ATCEA4 S30411 , ATCEA4 S27439	99, 95	ATL8C1 9505:3 444..2 699	0.55						
141552	ATU003 492	ATL8C3 9176:1 847..5 4	gap2	ATCEA4 S30557 , ATCEA4 C69144 1, ATCEA4 S35230	99, 89 98, 89	ATL8C3 9176:1 784..6 24	0.55						
141553	ATU003 493	ATL8C4 4716:1 ..3676	gap2	ATCEA4 C84301 1, ATCEA4 C60907 1, ATCEA4 C13814 1, ATCEA4 C13120	99, 97, 95, 92, 90	ATL8C4 4716:2 42..36 60	0.55						

534	7300:1 ..738	S5391		7300:1 28..738		0.52	g40380 66, g47739 10, g37859 84	100, 58, 34	122, 102, 1144	0.013, 0.0010 , 6.7e- 108	(AC005 897) hypoth etical protei n [Arabi dopsis thalia na]; (AF147 259) No defi nition line found [Arabi dopsis thalia na]; (AC005 560) putati ve revers e transc riptas e [Arabi dopsis thalia na]
141595	ATU003 535	ATCEA4 S253	gap2	ATL8C2 2405:5 199..1	98	ATL8C2 2405:4 288..1 214					
141596	ATU003 536	ATCEA4 C77421 1, ATCEA4 C12105 1, ATCEA4 S22778	gap2	ATL8C5 400:43 94..20 56	98, 98, 97	ATL8C5 400:39 19..20 56	g41917 74	100	1130	2.6e- 123	(AC005 917) putati ve beta- 1,3- endogl ucanas

141597	ATU003 537	ATL8C2 8486:1 ..843	gap2	ATCEA4 C8507_1	99	ATL8C2 8486:1 ..843	0.51						e [Arabi dopsis thalia nal]
141598	ATU003 538	ATL8C9 479:14 85..20 2	gap2	ATCEA4 S15070 , ATCEA4 S36361 , ATCEA4 C1801_3	99, 95 96, 95	ATL8C9 479:14 68..44 9	0.51						
141599	ATU003 539	ATL8C4 8703:1 ..122	gap2	ATCEA4 C20471_1	99	ATL8C4 8703:5 3..122	0.51						
141600	ATU003 540	ATL8C2 6029:1 ..832	gap2	ATCEA4 C30921_1	99	ATL8C2 6029:8 5..832	0.51						
141601	ATU003 541	ATL8C2 0885:1 423..9 10	gap2	ATCEA4 S36301	99	ATL8C2 0885:1 361..1 116	0.51						
141602	ATU003 542	ATL8C4 7250:8 53..30 4	gap2	ATCEA4 C1356_1, ATCEA4 S26213 , ATCEA4 S25047 , ATCEA4 S33584	99, 97, 85, 85	ATL8C4 7250:6 90..50 5	0.51						
141603	ATU003 543	ATL8C2 1652:1 00..48 4	gap2	ATCEA4 C9366_1, ATCEA4 C10090_1	99, 97	ATL8C2 1652:1 22..47 8	0.51						

141614	553	565:58 ..986	gap2	S31364	99	565:58 ..986	0.50						
	ATU003 554	ATL8C1 4454:8 1..102 1	gap2	ATCEA4 S535	99	ATL8C1 4454:8 1..850	0.50						
141615	ATU003 555	ATL8C2 7563:1 ..308	gap2	ATCEA4 C500_1 , ATCEA4 C500_4 , ATCEA4 S24699	99, 99, 84	ATL8C2 7563:8 ..251	0.50						
141616	ATU003 556	ATL8C1 6634:1 24..17 39	gap2	ATCEA4 C8904_1 , ATCEA4 S30227 , ATCEA4 S6991	99, 99, 98	ATL8C1 6634:7 26..12 32	0.50						
141617	ATU003 557	ATL8C4 5914:1 ..601	gap2	ATCEA4 C1916_1 , ATCEA4 S34599 , ATCEA4 S14740 , ATCEA4 C1916_2	99, 98, 97, 86	ATL8C4 5914:3 1..280	0.50						
141618	ATU003 558	ATL8C1 3656:7 48..23 65	gap2	ATCEA4 C19139 1, ATCEA4 S1285	99, 98	ATL8C1 3656:9 86..23 65	0.50						
141619	ATU003 559	ATL8C3 6732:6 60..28	gap2	ATCEA4 C15344 1	99	ATL8C3 6732:4 99..28	0.50						
141620	ATU003 560	ATL8C3 2702:3	gap2	ATCEA4 S34333	98	ATL8C3 2702:3	0.50	g45394 44,	100, 40	634, 114	1.4e- 65,	(AL049 523)	

141621	ATU003 561	296..1					296..1 1	g30804 27	0.70	hypothetical protein [Arabidopsis thaliana]; (AL022604) putative protein [Arabidopsis thaliana]
141622	ATU003 562	ATL8C1 9829:1 214..2 67	gap2	ATCEA4 C4971_1	99	ATL8C1 9829:1 214..2 67	0.50			
141623	ATU003 563	ATL8C1 9035:2 099..1 90	gap2	ATCEA4 S11309 , ATCEA4 S11310	99, 86	ATL8C1 9035:2 099..6 42	0.50			
141624	ATU003 564	ATL8C2 7838:1 ..370	gap2	ATCEA4 C99731 _1	99	ATL8C2 7838:1 33..30 1	0.49			
141625	ATU003 565	ATL8C2 6746:1 ..592	gap2	ATCEA4 C1173_1	99	ATL8C2 6746:4 7..570	0.49			
141626	ATU003 566	ATL8C4 7145:1 242..7 75	gap2	ATCEA4 S14045	99	ATL8C4 7145:1 053..7 75	0.49			
141627	ATU003 567	ATL8C1 2590:1 ..422	gap2	ATCEA4 C5416_2, ATCEA4 C5416_3,	99, 87 98, 87 22..21 0	ATL8C1 2590:4 22..21 0	0.49			

141632	ATU003 572	ATL8C3 5688:1 42..21 35	gap2	ATCEA4 S23936 , ATCEA4 S6694	99, 96	ATL8C3 5688:1 50..18 77	0.49					
141633	ATU003 573	ATL8C3 6936:1 132..2 81	gap2	ATCEA4 S2814	99	ATL8C3 6936:6 22..28 1	0.49					
141634	ATU003 574	ATL8C2 3518:2 33..79 4	gap2	ATCEA4 S8328	99	ATL8C2 3518:2 84..68 3	0.49					
141635	ATU003 575	ATL8C2 2514:1 ..990	gap2	ATCEA4 C6688 1, ATCEA4 S29706	99, 99	ATL8C2 2514:1 58..75 4	0.49					
141636	ATU003 576	ATL8C4 5625:1 372..2 308	gap2	ATCEA4 C4223 1, ATCEA4 S33219 , ATCEA4 C6089 1	99, 94, 93	ATL8C4 5625:2 125..1 485	0.49					
141637	ATU003 577	ATL8C3 7899:1 244..2 92	gap2	ATCEA4 C48282 1	99	ATL8C3 7899:1 221..2 92	0.49					
141638	ATU003 578	ATL8C2 777:43 78..31 61	gap2	ATCEA4 C3101 1, ATCEA4 C13509 7 1, ATCEA4 S6854	99, 98, 83	ATL8C2 777:43 24..33 99	0.49					
141639	ATU003 579	ATL8C4 8852:7 68..1	gap2	ATCEA4 C50086 1	99	ATL8C4 8852:7 68..28	0.49					
141640	ATU003 580	ATL8C1 3786:1	gap2	ATCEA4 S3653	99	ATL8C1 3786:5	0.49					

		03..69 1				84..69 1												
141641	ATU003 581	ATL8C4 8280:1 18..26 82	gap2	ATCEA4 C33241 _1	99	ATL8C4 8280:1 18..26 60	0.48											
141642	ATU003 582	ATL8C4 704:35 9..1	gap2	ATCEA4 C45829 _1	99	ATL8C4 704:32 0..33	0.48											
141643	ATU003 583	ATL8C1 650:71 53..30 84	gap2	ATCEA4 S25356 , ATCEA4 C20774 _1	98, 97	ATL8C1 650:71 53..30 97	0.48	g48951 95, g43253 67	100, 66	163, 139	1.7e- 06, 5.9e- 12	(AC007 661) putati ve mitoch ondria l carrie r family protei n [Arabi dopsis thalia na]; (AF128 396) contai ns simila rity to Nicoti ana tabacu m B- type cyclin (GB:D5 0737) [Arabi dopsis thalia na]						
141644	ATU003	ATL8S1	gap2	ATCEA4	99, 93	ATL8S1	0.48											

	594	893:84 ..310		C7461_1		893:29 6..85												
141655	ATU003 595	ATL8C4 4609:9 28..20	gap2	ATCEA4 S2762	99	ATL8C4 4609:4 96..20	0.47											
141656	ATU003 596	ATL8C3 9374:8 27..35	gap2	ATCEA4 C48807 1	99	ATL8C3 9374:4 17..35	0.47											
141657	ATU003 597	ATL8C1 8172:1 ..591	gap2	ATCEA4 C14305 1	99	ATL8C1 8172:1 93..44 1	0.47											
141658	ATU003 598	ATL8C3 2610:3 21..34 95	gap2	ATCEA4 S860	99	ATL8C3 2610:3 21..34 95	0.47											
141659	ATU003 599	ATL8C2 4242:2 561..7 40	gap2	ATCEA4 S14344 , ATCEA4 C1665_1	99, 98	ATL8C2 4242:2 381..1 008	0.47											
141660	ATU003 600	ATL8C3 1573:1 ..396	gap2	ATCEA4 S16201	99	ATL8C3 1573:1 55..26 5	0.47											
141661	ATU003 601	ATL8C3 1478:7 04..16 5	gap2	ATCEA4 S7198	99	ATL8C3 1478:6 55..16 5	0.47											
141662	ATU003 602	ATL8S2 312:1. .447	gap2	ATCEA4 C17146 1	99	ATL8S2 312:13 9..447	0.47											
141663	ATU003 603	ATL8C3 1043:7 15..15 18	gap2	ATCEA4 C763_1 , ATCEA4 S11337	99, 82	ATL8C3 1043:9 02..14 57	0.46											
141664	ATU003 604	ATL8C3 3085:7 88..1	gap2	ATCEA4 C996_1 , ATCEA4 S12533	99, 87, 85	ATL8C3 3085:4 37..15 7	0.46											

	8		ATCEA4 S12260 , ATCEA4 S36024 , ATCEA4 S12651		81							
141675	ATU003 615	ATL8C2 8695:1 137..1	gap2		99, 84 ATL8C2 8695:1 137..2 56	0.46						
141676	ATU003 616	ATL8C2 2280:1 13..50 99	gap2		99, 96 ATL8C2 2280:1 13..50 99	0.46						
141677	ATU003 617	ATL8C1 0000:1 578..5 3	gap2		98 ATL8C1 0000:1 578..1 94	0.46	g38343 19	100	1348			(AC005 679) Simila r to [Arabi dopsis thalia na]
141678	ATU003 618	ATL8C2 6564:7 4..122 4	gap2		99, 95 ATL8C2 6564:7 4..110 7	0.46						
141679	ATU003 619	ATL8C2 0169:1 ..489	gap2		99 ATL8C2 0169:4 4..489	0.46						
141680	ATU003 620	ATL8C1 0631:1 72..16 41	gap2		99 ATL8C1 0631:1 72..16 41	0.46						
141681	ATU003 621	ATL8C4 8460:8 96..12	gap2		99, 89 ATL8C4 8460:7 07..30	0.46						

		0		ATCEA4 C771_2 , ATCEA4 S31451		6								
141682	ATU003 622	ATL8C2 9262:1 022..1 c	gap2	ATCEA4 C743_1 , ATCEA4 C743_2	99, 82	ATL8C2 9262:9 46..19 0	0.46							
141683	ATU003 623	ATL8C4 7027:1 431..4 1	gap2	ATCEA4 S29853	99	ATL8C4 7027:1 431..4 1	0.46							
141684	ATU003 624	ATL8C3 6133:3 596..4	gap2	ATCEA4 S3342, ATCEA4 C5252_ 1, ATCEA4 S3727, ATCEA4 S6379	99, 92, 85, 82	ATL8C3 6133:3 596..4	0.45							
141685	ATU003 625	ATL8C3 7098:1 200..2 87	gap2	ATCEA4 C1139_ 1	99	ATL8C3 7098:5 41..28 7	0.45							
141686	ATU003 626	ATL8C2 8815:1 ..524	gap2	ATCEA4 C1951_ 3, ATCEA4 C1951_ 1	99, 99	ATL8C2 8815:2 2..467	0.45							
141687	ATU003 627	ATL8C1 237:30 79..10 31	gap2	ATCEA4 S27401	98	ATL8C1 237:30 79..10 31	0.45	g43098 68	100	2562	7.8e- 205	(AC006 527) putati ve retrot ranspo son- like orf [Arabi dopsis		

141694	ATU003 634	ATL8C4 4707:2 572..5 0	gap2	ATCEA4 S3219	98	ATL8C4 4707:2 572..2 04	0.45	g28275 61	100	1976	2.1e- 195	(AL021 635) predic ted protei n [Arabi dopsis thalia na]
141695	ATU003 635	ATL8C2 6508:1 ..2210	gap2	ATCEA4 S2357, ATCEA4 C22442 1, ATCEA4 S2063, ATCEA4 S35091 , ATCEA4 C20239 1, ATCEA4 S2174	99, 96, 95, 94, 89, 86	ATL8C2 6508:8 3..221 0	0.44					
141696	ATU003 636	ATL8C1 9955:1 055..5 8	gap2	ATCEA4 S27033 , ATCEA4 C49605 1	99, 97	ATL8C1 9955:1 005..5 8	0.44					
141697	ATU003 637	ATL8C1 3485:1 ..2158	gap2	ATCEA4 S10910	98	ATL8C1 3485:7 3..215 8	0.44	g32490 67	100	552	1.6e- 54	(AC004 473) T13D8. 7 [Arabi dopsis thalia na]
141698	ATU003 638	ATL8C4 5844:1 585..5 31	gap2	ATCEA4 C4564 1, ATCEA4 S26331	99, 88 94, 88	ATL8C4 5844:1 539..8 01	0.44					

141713	ATU003 653	ATL8C2 8237:1 019..1	gap2	ATCEA4 C63633 1, ATCEA4 C49945 1	99, 92	ATL8C2 8237:1 013..4 9	0.43					
141714	ATU003 654	ATL8C4 0532:1 076..1	gap2	ATCEA4 C11239 _1	99	ATL8C4 0532:1 076..6 9	0.43					
141715	ATU003 655	ATL8C2 968:10 04..27 12	gap2	ATCEA4 C27063 _1	99	ATL8C2 968:12 56..27 12	0.43					
141716	ATU003 656	ATL8C2 3199:9 82..11	gap2	ATCEA4 S2963, ATCEA4 C34372 2, ATCEA4 S6253	99, 96, 87	ATL8C2 3199:8 23..11	0.43					
141717	ATU003 657	ATL8S1 1728:5 69..17 0	gap2	ATCEA4 C10006 4_1	99	ATL8S1 1728:4 54..31 8	0.42					
141718	ATU003 658	ATL8C1 525:65 ..666	gap2	ATCEA4 C77862 1	99	ATL8C1 525:84 ..666	0.42					
141719	ATU003 659	ATL8C3 5573:1 207..1	gap2	ATCEA4 S4911	99	ATL8C3 5573:1 207..7 14	0.42					
141720	ATU003 660	ATL8C1 354:25 70..31 85	gap2	ATCEA4 C7636 _1	99	ATL8C1 354:25 86..31 85	0.42					
141721	ATU003 661	ATL8C1 6967:6 197..7 6	gap2	ATCEA4 C1167 _1, ATCEA4 C1167 _2, ATCEA4 S6578,	98, 96, 96, 91	ATL8C1 6967:6 197..7 6	0.42	g36418 38	100	390	1.2e- 42	(AL023 094) putati ve protei n (fragm ent)

		3..169 7		ATCEA4 C4069_1		53..16 97						
141730	ATU003 670	ATL8C3 8439:1 ..688	gap2	ATCEA4 C773_1 ATCEA4 S9795	99, 88	ATL8C3 8439:7 6..223	0.41					
141731	ATU003 671	ATL8C4 3595:1 172..5	gap2	ATCEA4 S74	98	ATL8C4 3595:1 043..1 66	0.41	100	g32128 60	475	(AC004 005) hypoth etical protein [Arabi dopsis thalia na]	
141732	ATU003 672	ATL8C1 0029:4 086..3 239	gap2	ATCEA4 C11803 9_1	99	ATL8C1 0029:4 026..3 596	0.41					
141733	ATU003 673	ATL8S1 5958:1 ..335	gap2	ATCEA4 C1529_1	99	ATL8S1 5958:1 14..29 9	0.41					
141734	ATU003 674	ATL8C9 04:273 ..1443	gap2	ATCEA4 S26902 ATCEA4 C24613 1, ATCEA4 S33558	99, 92	ATL8C9 04:523 ..1143	0.41					
141735	ATU003 675	ATL8C2 0960:1 33..77 4	gap2	ATCEA4 C58023 _1	99	ATL8C2 0960:1 33..75 0	0.41					
141736	ATU003 676	ATL8C3 3680:1 ..791	gap2	ATCEA4 C387_1	99	ATL8C3 3680:7 5..743	0.41					
141737	ATU003 677	ATL8C4 2304:5	gap2	ATCEA4 C11010	99, 92	ATL8C4 2304:1	0.40					

141948	ATU003 888	ATL8C1 3022:2 699..2 137	gap2	ATCEA4 S22010 , ATCEA4 S26460 , ATCEA4 S26459 , ATCEA4 S21505	99, 96, 87, 83						
141949	ATU003 889	ATL8C1 6358:9 66..12 76	gap2	ATCEA4 C9370_2, ATCEA4 C9370_1	99, 96						
141950	ATU003 890	ATL8C8 693:26 52..22 09	gap2	ATCEA4 S30225	99						
141951	ATU003 891	ATL8C4 186:39 4..824	gap2	ATCEA4 S29766	99						
141952	ATU003 892	ATL8C1 845:21 71..15 7	gap2	ATCEA4 S27408 , ATCEA4 C267 1	99, 89						
141953	ATU003 893	ATL8S1 5747:2 62..1	gap2	ATCEA4 C1292_1	99						
141954	ATU003 894	ATL8C8 669:10 95..69 6	gap2	ATCEA4 C10104 _1	99						
141955	ATU003 895	ATL8C4 1851:1 ..183	gap2	ATCEA4 S10007	99						
141956	ATU003 896	ATL8C1 6430:6 16..86 4	gap2	ATCEA4 C615_1	99						
141957	ATU003	ATL8S1	gap2	ATCEA4	99, 92						

141989	ATU003 929	96..15 01	gap2	ATCEA4 S36353	99														TINY [Arabi dopsis thalia na]
141990	ATU003 930	ATL8C1 6988:7 75..10 99	gap2	ATCEA4 C10926 1, ATCEA4 C10926 2	99, 85														
141991	ATU003 931	ATL8C2 0365:5 76..83 6	gap2	ATCEA4 C11554 9_1	99														
141992	ATU003 932	ATL8C8 83:105 2..150 2	gap2	ATCEA4 S11890	99														
141993	ATU003 933	ATL8C3 8330:8 80..65 7	gap2	ATCEA4 S1369	99														
141994	ATU003 934	ATL8C1 3059:1 401..3 097	gap2	ATCEA4 S5191, ATCEA4 C35158 1	99, 98														
141995	ATU003 935	ATL8C3 0963:8 919..6 184	gap2	ATCEA4 S4067, ATCEA4 C31724 1, ATCEA4 S33711 , ATCEA4 C79691 _1	98, 97, 91, 90														(U9321 5) maize transp oson MuDR mudrA protei n isolog [Arabi dopsis thalia

142090	ATU004 030	88..25 07	gap2	ATCEA4 C8330_1, ATCEA4 C8330_4	99, 99													putative retrotransposon-like orf [Arabidopsis thaliana]
142091	ATU004 031	ATL8C2 8635:2 84..89 0	gap2	ATCEA4 S6736	99													
142092	ATU004 032	ATL8S1 5441:5 95..28 3	gap2	ATCEA4 S22066	99													
142093	ATU004 033	ATL8C4 5560:1 577..1 163	gap2	ATCEA4 C33493_1	99													
142094	ATU004 034	ATL8C8 670:12 7..139 9	gap2	ATCEA4 C15369_1, ATCEA4 S33023	98, 89													(AC004238) putative zinc-finger protein [Arabidopsis thaliana]
142095	ATU004 035	ATL8C9 071:24 2..840	gap2	ATCEA4 C1359_2,	99, 98, 92													

142096	ATU004 036	ATL8C1 7558:1 27..73 6	gap2	ATCEA4 S7591, ATCEA4 S2987	99, 83														
142097	ATU004 037	ATL8C8 487:38 3..1	gap2	ATCEA4 C6356_5, ATCEA4 C6356_3, ATCEA4 C6356_2, ATCEA4 C6356_1, ATCEA4 S35803 , ATCEA4 S17542 , ATCEA4 S33966	99, 99, 99, 97, 92, 91, 84														
142098	ATU004 038	ATL8C4 5553:5 83..95 5	gap2	ATCEA4 S12852	99														
142099	ATU004 039	ATL8C8 482:11 20..60	gap2	ATCEA4 S2513, ATCEA4 C24167 1	99, 87														
142100	ATU004 040	ATL8C8 481:17 36..1	gap2	ATCEA4 C28477 1, ATCEA4 C98707 1	99, 89														

142101	ATU004 041	ATL8C1 3158:1 28..12 41	gap2	ATCEA4 C19921 _1	98				948352 39	100	679	2.6e- 71	(AL049 862) putati ve DNA-3- methyl adenin e glycos idase [Arabi dopsis thalia na]
142102	ATU004 042	ATL8S1 5281:3 71..11 2	gap2	ATCEA4 S4655	99								
142103	ATU004 043	ATL8C2 8779:5 91..13 51	gap2	ATCEA4 C20462 _1	99								
142104	ATU004 044	ATL8C3 3863:1 ..612	gap2	ATCEA4 S30441 , ATCEA4 S12632	99, 91								
142105	ATU004 045	ATL8S3 0840:2 28..1	gap2	ATCEA4 C365_1	99								
142106	ATU004 046	ATL8C3 5183:1 ..1610	gap2	ATCEA4 C896_1	99								
142107	ATU004 047	ATL8C2 365:73 8..146 3	gap2	ATCEA4 S765	99								
142108	ATU004 048	ATL8C2 364:31 97..35 73	gap2	ATCEA4 S11973	99								
142109	ATU004 049	ATL8C5 663:1. .258	gap2	ATCEA4 C11855 3 1,	99, 85								

		046		ATCEA4 S29205 , ATCEA4 S33225 , ATCEA4 C51227 2															zinc finger protein isololog [Arabi dopsis thaliana]
142137	ATU004 077	ATL8C7 897:1. .427	gap2	ATCEA4 S26397	99														
142138	ATU004 078	ATL8C4 5362:2 90..1	gap2	ATCEA4 S329	99														
142139	ATU004 079	ATL8C4 1404:4 95..1	gap2	ATCEA4 S30370	99														
142140	ATU004 080	ATL8C3 4630:1 ..489	gap2	ATCEA4 C51309 1, ATCEA4 S6102	99, 84														
142141	ATU004 081	ATL8C3 4729:2 43..1	gap2	ATCEA4 C12770 1	99														
142142	ATU004 082	ATL8C7 591:1. .667	gap2	ATCEA4 C458_1	99														
142143	ATU004 083	ATL8C1 874:71 1..950	gap2	ATCEA4 S32968	99														
142144	ATU004 084	ATL8C3 4807:3 029..3 390	gap2	ATCEA4 C36994 _1	99														
142145	ATU004 085	ATL8C7 476:76 5..111 5	gap2	ATCEA4 C5490_1	99														
142146	ATU004 086	ATL8C3 8986:1 59..88 4	gap2	ATCEA4 C1268_5, ATCEA4	99, 88														

142158	ATU004 098	ATL8C6 94:386 ..1	gap2	ATCEA4 S33606 , ATCEA4 C773_1 , ATCEA4 S15401	99, 99, 97							dopsis thalia na]
142159	ATU004 099	ATL8C3 1907:2 69..44 8	gap2	ATCEA4 S2005	99							
142160	ATU004 100	ATL8C7 78:441 6..425 8	gap2	ATCEA4 C82345 _1	99							
142161	ATU004 101	ATL8C2 0877:3 543..4 023	gap2	ATCEA4 C3528 _1	99							
142162	ATU004 102	ATL8C3 8283:1 ..542	gap2	ATCEA4 C36163 _1	99							
142163	ATU004 103	ATL8C3 5127:7 82..47 9	gap2	ATCEA4 S12129	99							
142164	ATU004 104	ATL8C3 7827:2 01..1	gap2	ATCEA4 S14123	99							
142165	ATU004 105	ATL8C3 7812:1 8..628	gap2	ATCEA4 C26639 _3	99							
142166	ATU004 106	ATL8C7 74:556 5..516 4	gap2	ATCEA4 S27193	99							
142167	ATU004 107	ATL8C1 8704:1 058..6 79	gap2	ATCEA4 S12170	99							

142177	116 ATU004 117	4495:1 06..1 ATL8C6 501:70 ..881	gap2	C32494 1 ATCEA4 C77309 _1	98				g44328 18	100	643	4.9e- 41	(AC006 593) putati ve ethyle ne respon sive elemen t bindin g protei n [Arabi dopsis thalia na]
142178	ATU004 118	ATL8S1 4493:1 ..266	gap2	ATCEA4 S682	99								
142179	ATU004 119	ATL8C3 5874:6 65..95 6	gap2	ATCEA4 S26855 , ATCEA4 S26858	99, 87								
142180	ATU004 120	ATL8C3 7799:1 577..1	gap2	ATCEA4 C430_1	99								
142181	ATU004 121	ATL8C2 3957:9 61..12 55	gap2	ATCEA4 C30135 _1	99								
142182	ATU004 122	ATL8C7 681:1. .273	gap2	ATCEA4 S11087	99								
142183	ATU004 123	ATL8C3 5928:5 74..10 64	gap2	ATCEA4 S29855 , ATCEA4 C6742_8	99, 93, 91, 85								

142206	ATU004 146	ATL8C1 2229:1 176..1 390	gap2	ATCEA4 C1858_1, ATCEA4 C1858_2	99, 83												
142207	ATU004 147	ATL8C3 6633:3 802..4 186	gap2	ATCEA4 C21136_1, ATCEA4 S21487	99, 83												
142208	ATU004 148	ATL8S2 4074:4 22..59 1	gap2	ATCEA4 C983_1, ATCEA4 S31953	99, 94												
142209	ATU004 149	ATL8C3 6685:1 ..1092	gap2	ATCEA4 C19190_1, ATCEA4 C14620_1	99, 97												
142210	ATU004 150	ATL8C5 634:1. .776	gap2	ATCEA4 S24889, ATCEA4 C47494_1, ATCEA4 C47494_2, ATCEA4 S34756	99, 99, 97, 85												
142211	ATU004 151	ATL8C4 1235:2 24..82 4	gap2	ATCEA4 C11064_1	99												
142212	ATU004 152	ATL8C2 8408:1 ..532	gap2	ATCEA4 S14122, ATCEA4 S33086, ATCEA4	99, 89, 82												

142213	ATU004 153	ATL8C3 6746:2 641..2 804	gap2	C27091 1	99														
142214	ATU004 154	ATL8C5 457:19 1..207 2	gap2	ATCEA4 C551_1 , ATCEA4 S24352	99, 83														
142215	ATU004 155	ATL8S2 0283:3 01..41 9	gap2	ATCEA4 C4904_1	99														
142216	ATU004 156	ATL8C7 525:12 61..89 2	gap2	ATCEA4 S11953	99														
142217	ATU004 157	ATL8C4 1222:7 33..10 94	gap2	ATCEA4 C34397_1	99														
142218	ATU004 158	ATL8C4 1217:2 52..39 5	gap2	ATCEA4 S197	99														
142219	ATU004 159	ATL8C3 7722:9 20..30 3	gap2	ATCEA4 S36274	99														
142220	ATU004 160	ATL8C1 4470:5 29..95 6	gap2	ATCEA4 S12214 , ATCEA4 S3577	99, 83														
142221	ATU004 161	ATL8C1 3248:6 02..81 2	gap2	ATCEA4 C1483_1	99														
142222	ATU004 162	ATL8C5 359:22 49..25 36	gap2	ATCEA4 C9372_1	99														

142242	181	8449:1 ..230		S33287 , ATCEA4 S26588															
	ATU004 182	ATL8C7 677:1. .232	gap2	ATCEA4 C9335_1	99														
142243	ATU004 183	ATL8C3 7498:2 701..3 196	gap2	ATCEA4 C5544_4, ATCEA4 C5544_1, ATCEA4 C5544_3, ATCEA4 S33428	99, 97, 91, 86														
142244	ATU004 184	ATL8C2 8430:7 01..26 2	gap2	ATCEA4 S30135	99														
142245	ATU004 185	ATL8C3 7600:4 51..64 4	gap2	ATCEA4 C7378_1	99														
142246	ATU004 186	ATL8C5 0061:5 38..13 26	gap2	ATCEA4 S286, ATCEA4 C3644_1	99, 94														
142247	ATU004 187	ATL8C7 456:71 8..112 8	gap2	ATCEA4 S1939	99														
142248	ATU004 188	ATL8C4 111:23 71..27 37	gap2	ATCEA4 S12733	99														
142249	ATU004 189	ATL8C4 4999:5 0..226	gap2	ATCEA4 S26163	99														
142250	ATU004 190	ATL8C3 7656:3	gap2	ATCEA4 S26141	99														

142275	ATU004 215	ATL8C2 7294:1 809..2 272	gap2	S4534 ATCEA4 C11751 7_1	99														
142276	ATU004 216	ATL8C4 9786:1 ..225	gap2	ATCEA4 C33505 1	99														
142277	ATU004 217	ATL8C2 57:114 3..83	gap2	ATCEA4 S33541 , ATCEA4 C86085 1, ATCEA4 S23330 , ATCEA4 S25168	99, 92, 92, 85														
142278	ATU004 218	ATL8C2 8345:5 46..90 0	gap2	ATCEA4 S1640	99														
142279	ATU004 219	ATL8C2 8323:1 028..5 92	gap2	ATCEA4 S15143	99														
142280	ATU004 220	ATL8C3 4926:2 73..57 3	gap2	ATCEA4 C14035 1_	99														
142281	ATU004 221	ATL8C2 2067:1 661..1 412	gap2	ATCEA4 C8752_1	99														
142282	ATU004 222	ATL8C7 224:16 0..706	gap2	ATCEA4 C26368 1	99														
142283	ATU004 223	ATL8C3 8193:1 239..7 85	gap2	ATCEA4 C23596 _1	99														
142284	ATU004 224	ATL8C2 5541:5	gap2	ATCEA4 S30418	99														

142316	ATU004 256	68 ATL8C3 8867:1 300..9 66	gap2	ATCEA4 C48149 1, ATCEA4 S33842	99, 93															
142317	ATU004 257	ATL8C2 8209:4 27..59 0	gap2	ATCEA4 S1452	99															
142318	ATU004 258	ATL8C4 9021:1 496..1 602	gap2	ATCEA4 C10094 9_1	99															
142319	ATU004 259	ATL8C4 8957:5 95..10 17	gap2	ATCEA4 C10170 0_2, ATCEA4 S24928	99, 99															
142320	ATU004 260	ATL8C1 6759:1 204..2 596	gap2	ATCEA4 S5872, ATCEA4 C11435 2, ATCEA4 C11435 1	99, 98, 98, 98															
142321	ATU004 261	ATL8C3 8571:1 121..5 28	gap2	ATCEA4 C1880_ 1, ATCEA4 S33059, ATCEA4 S28488, ATCEA4 S28329, ATCEA4 C1880_ 4	99, 98, 97, 91, 89															
142322	ATU004 262	ATL8C4 8390:1	gap2	ATCEA4 S30670	99															

142333	ATU004 273	ATL8C4 8365:1 ..212	gap2	S30116 , ATCEA4 S32234 , ATCEA4 S35446 , ATCEA4 S27139								610, gb N38 459, gb T45 174, gb R30 481 and gb N64 971 come from this gene. [Arabi dopsis thalia na]
142334	ATU004 274	ATL8C1 2149:9 46..49 7	gap2	ATCEA4 C12433 0_1, ATCEA4 S33391 , ATCEA4 S29224 , ATCEA4 S29229 ATCEA4 S33392 , ATCEA4 C2218 1, ATCEA4 S36051	99, 99, 92, 88							
142335	ATU004 275	ATL8C1 4885:7 24..31 7	gap2	ATCEA4 C95603 1 ATCEA4 S36051	99							
142336	ATU004 276	ATL8C3 7455:1 070..6 39	gap2	ATCEA4 S719	99							

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142344	ATU004 284	ATL8C3 4721:7 29..37 0	gap2	ATCEA4 C756_1	99							
142345	ATU004 285	ATL8C7 032:64 0..112 9	gap2	ATCEA4 S26092	99							
142346	ATU004 286	ATL8C4 8047:1 636..3 69	gap2	ATCEA4 S15944 , ATCEA4 C14344 2_1, ATCEA4 S26112 , ATCEA4 S5105	99, 94, 93, 87							
142347	ATU004 287	ATL8C3 7432:1 769..2 186	gap2	ATCEA4 S14559	99							
142348	ATU004 288	ATL8C2 4013:2 91..1	gap2	ATCEA4 C32733 1, ATCEA4 S31265	99, 95							
142349	ATU004 289	ATL8C3 7430:3 04..1	gap2	ATCEA4 C75132 1	99							
142350	ATU004 290	ATL8C1 3353:7 09..32 9	gap2	ATCEA4 C856_1	99							
142351	ATU004 291	ATL8C4 9605:3 26..1	gap2	ATCEA4 C23839 1	99							
142352	ATU004 292	ATL8C3 3341:2 27..79 0	gap2	ATCEA4 C24492 1, ATCEA4	99, 84							

142394	333	7285:1 094..2 89		C6331_1							35	661) hypothetical protein [Arabidopsis thaliana]
142395	ATU004 334	ATL8C2 7947:2 722..3 004	gap2	ATCEA4 S13762	99							
142396	ATU004 335	ATL8C3 7308:7 56..17 8	gap2	ATCEA4 C40068 _1	99							
142397	ATU004 336	ATL8C4 7214:2 076..2 74	gap2	ATCEA4 C12829 _1, ATCEA4 S9211	99, 97							
142398	ATU004 337	ATL8C4 4544:1 035..1 54	gap2	ATCEA4 C1421_1	99							
142399	ATU004 338	ATL8C3 5877:1 778..1 518	gap2	ATCEA4 C1808_1, ATCEA4 C1808_5, ATCEA4 S28866 , ATCEA4 S28252	99, 99, 97, 82							
142400	ATU004 339	ATL8C2 7909:1 ..353	gap2	ATCEA4 S14671	99							
142401	ATU004 340	ATL8C4 712:24 94..20 51	gap2	ATCEA4 S14969 , ATCEA4	99, 82							

142474	ATU004 414	ATL8C4 528:1. .509	gap2	ATCEA4 S28267 , ATCEA4 C12013 5 1	99, 84														
142475	ATU004 415	ATL8C4 8000:2 63..71 2	gap2	ATCEA4 C23681 _1	99														
142476	ATU004 416	ATL8C1 8044:1 877..1 561	gap2	ATCEA4 S11420	99														
142477	ATU004 417	ATL8C3 7121:3 87..1	gap2	ATCEA4 C26351 1	99														
142478	ATU004 418	ATL8S1 1772:1 ..253	gap2	ATCEA4 S12725	99														
142479	ATU004 419	ATL8S1 1729:3 52..55 7	gap2	ATCEA4 S30407	99														
142480	ATU004 420	ATL8C2 0465:1 29..56 5	gap2	ATCEA4 C33762 _1	99														
142481	ATU004 421	ATL8C4 028:75 3..619	gap2	ATCEA4 S11670	99														
142482	ATU004 422	ATL8C3 3894:8 99..13 36	gap2	ATCEA4 S3452, ATCEA4 S31042 , ATCEA4 C4851_1, ATCEA4 S24059 , ATCEA4 C30193	99, 98, 96, 89, 82														

142513	ATU004 453	ATL8C4 3749:1 70..39 8	gap2	ATCEA4 C4561_1, ATCEA4 S34675, ATCEA4 S15807, ATCEA4 C4808_1																
142514	ATU004 454	ATL8S1 0237:5 74..1	gap2	ATCEA4 S34053, ATCEA4 C1789_1, ATCEA4 S13632, ATCEA4 S19535	99, 98, 94, 87															
142515	ATU004 455	ATL8C2 034:1. .479	gap2	ATCEA4 S14212	99															
142516	ATU004 456	ATL8C4 4984:4 030..3 500	gap2	ATCEA4 S2369, ATCEA4 S30160	99, 95															
142517	ATU004 457	ATL8C1 801:80 6..448	gap2	ATCEA4 S13878	99															

142559	ATU004 499	644	ATL8C4 7782:3 81..73	gap2	ATCEA4 S6232, ATCEA4 C64501 1	99														
142560	ATU004 500		ATL8C2 3631:2 244..1 475	gap2	ATCEA4 S36386 , ATCEA4 S4966, ATCEA4 S22418	99, 87, 86														
142561	ATU004 501		ATL8S2 1853:3 36..52 4	gap2	ATCEA4 S32184	99														
142562	ATU004 502		ATL8C6 122:16 86..14 34	gap2	ATCEA4 S1671	99														
142563	ATU004 503		ATL8S2 2833:5 21..27 9	gap2	ATCEA4 S35151	99														
142564	ATU004 504		ATL8C1 2405:3 99..12 9	gap2	ATCEA4 C19388 1, ATCEA4 S4125	99, 92														
142565	ATU004 505		ATL8C3 0820:1 699..1 042	gap2	ATCEA4 S5007	99														
142566	ATU004 506		ATL8C2 4981:5 09..83 9	gap2	ATCEA4 C1239- 1, ATCEA4 S24691	99, 94														
142567	ATU004 507		ATL8C4 775:29 47..26	gap2	ATCEA4 S33297	99														

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[illegible]

142862	ATU004 802	ATL8C1 958:13 27..50 5	gap2	ATCEA4 C14427 _1	98	ATL8C1 958:12 13..55 4	0.96	g29110 66	99	501	4.5e- 39	(AL021 960) adreno- doxin- like protei n [Arabi dopsis thalia na]
142863	ATU004 803	ATL8C1 002:45 ..778	gap2	ATCEA4 S34321 , ATCEA4 C63806 3, ATCEA4 S35961 , ATCEA4 S25337 , ATCEA4 S25617	98, 88, 87, 87, 84	ATL8C1 002:22 7..368	0.96	g42636 98	99	97	3.2e- 07	(AC006 223) unknow n protei n [Arabi dopsis thalia na]
142864	ATU004 804	ATL8C2 7169:6 85..25	gap2	ATCEA4 C11579 2_1	98	ATL8C2 7169:6 85..18 1	0.95	g39281 00	99	310	1.9e- 28	(AC005 770) putati ve protea se inhibi tor [Arabi dopsis thalia na]
142865	ATU004 805	ATL8C7 679:1. .3328	gap2	ATCEA4 C5494_2, ATCEA4 C2190_1, ATCEA4 C91464	98, 98, 94, 93, 89, 87, 85	ATL8C7 679:20 18..26 44	0.91	g21296 59, g35823 28	99, 60	404, 633	1.8e- 29, 5.1e- 60	oleosi n, isofo r m 21K - Arabi dopsi s thalia

142866	ATU004 806	ATL8C1 0958:1 83..11 99	gap2	ATCEA4 C11252 01, ATCEA4 S4314, ATCEA4 S17185 , ATCEA4 S12002	98, 82 82, 82	ATL8C1 0958:2 21..97 8	0.90	g45444 34	99	505	4.4e- 47	na [Arabi dopsis thalia na]; (AC005 496) hypoth etical protei n [Arabi dopsis thalia na]
142867	ATU004 807	ATL8S2 7328:1 08..58 9	gap2	ATCEA4 C18110 1, ATCEA4 S31268	98, 83	ATL8S2 7328:1 42..53 3	0.89	g25074 21	99	427	2.6e- 40	PROTEI N TRANSL ATION FACTOR SUI1 HOMOLO G [Arabi dopsis thalia na]
142868	ATU004 808	ATL8C2 0787:1 229..1	gap2	ATCEA4 C9180- 1, ATCEA4	98, 94, 91, 86	ATL8C2 0787:1 139..7 0	0.88	g11731 87	99	619	1.4e- 55	40S RIBOSO MAL. PROTEI

142869	ATU004 809	ATL8C1 8933:1 707..2 8	gap2	C9180_2, ATCEA4 S33986 , ATCEA4 S9233 ATCEA4 C9996_1	98	ATL8C1 8933:1 665..4 11	0.87	g39279 16	99	375	1.2e- 28	N S23 (S12) [Fragaria x ananas]
142870	ATU004 810	ATL8C7 840:12 4..799	gap2	ATCEA4 C1701_1, ATCEA4 S9968	98, 98	ATL8C7 840:32 2..456	0.87	g29976 84	99	374	5.2e- 33	(AJ130887) glycine-rich protein 2 [Fagus sylvatica]
142871	ATU004 811	ATL8C1 5908:1 018..5	gap2	ATCEA4 C1223_2, ATCEA4 S34255	98, 95	ATL8C1 5908:9 44..92	0.87	g25585 18	99	270	8.0e- 29	(AJ001901) Ubiquitin-like protein [Cicer arietinum]
142872	ATU004 812	ATL8C2 1766:2 664..1 754	gap2	ATCEA4 C20094 1, ATCEA4 C20094	98, 96, 94, 88	ATL8C2 1766:2 573..1 897	0.87	g38855 11	99	443	5.9e- 32	(AF084200) similarity to PSI-K

142873	ATU004 813	ATL8C5 54:600 ..1	gap2	ATCEA4 S13839 , ATCEA4 S35518 , ATCEA4 S9072	98	ATL8C5 54:600 ..245	0.85	g45859 22	99	300	2.1e- 26	(AC007 211) putati ve glucan endo- 1,3- beta- D- glucos idase precu sor [Arabi dopsis thalia na]	subuni t of photos ystem I from barley [Medic ago sativa]
142874	ATU004 814	ATL8C4 6907:1 23..54 23	gap2	ATCEA4 S16109 , ATCEA4 C787_5 , ATCEA4 S8498, ATCEA4 C787_6 , ATCEA4 C787_1	98, 95, 84, 83, 82	ATL8C4 6907:1 23..54 23	0.85	g13507 20	99	493	3.2e- 31	60S RIBOSO MAL PROTEI N L32 []	
142875	ATU004 815	ATL8C5 107:41 70..1	gap2	ATCEA4 C29729 1, ATCEA4 C28722	98, 96, 96, 95	ATL8C5 107:38 48..18 9	0.85	g16522 17, g26493 45	99, 59	204, 762	1.4e- 15, 4.4e- 66	(D9090 3) hypoth etical protei	

142876	ATU004 816	ATL8C4 13:534 2..103 3	gap2	ATCEA4 S12380 , ATCEA4 C24459 _1	98, 94 96, 88	ATL8C4 13:534 2..116 6	0.85	g43357 25	99	241	4.9e- 22	n [Synec hocyst is sp.]; (AE001 019) trypto phan syntha se, subuni t beta (trpB- 1) [Archa eoglob us fulgid us]
142877	ATU004 817	ATL8C6 446:31 8..991	gap2	ATCEA4 S10687	98	ATL8C6 446:32 3..674	0.84	g22447 09	99	178	5.1e- 15	(AC006 248) hypoth etical protei n [Arabi dopsis thalia na]
142878	ATU004 818	ATL8C4 6623:3 118..5 477	gap2	ATCEA4 S10657 , ATCEA4 C14364 6_1	98, 94	ATL8C4 6623:3 353..5 053	0.83	g46153 2	99	474	9.5e- 47	(AB005 295) HY5 [Arabi dopsis thalia na] ADP- RIBOSY LATION FACTOR [Histo plasma capsul atum]

142879	ATU004 819	ATL8C1 1378:1 429..5 20	gap2	ATCEA4 C27727 _1	98	ATL8C1 1378:1 266..5 30	0.83	g44068 01	99	375	3.2e- 38	(AC006 304) unknown protein [Arabi dopsis thalia na]
142880	ATU004 820	ATL8C3 8035:2 83..14 38	gap2	ATCEA4 C45119 _1	98	ATL8C3 8035:3 07..13 80	0.82	g43097 57	99	247	3.1e- 11	(AC006 217) hypoth etical protein [Arabi dopsis thalia na]
142881	ATU004 821	ATL8C6 905:14 47..63 9	gap2	ATCEA4 C17556 _1, ATCEA4 C17556 _2	98, 85	ATL8C6 905:14 22..82 9	0.82	g38603 08	99	142	5.8e- 11	(AJ012 681) hypoth etical protein [Cicer arieti num]
142882	ATU004 822	ATL8C5 28:51. .1399	gap2	ATCEA4 C21835 _1	98	ATL8C5 28:51. .1064	0.81	g40281 55, g13562 6	99, 39	300, 82	7.8e- 25, 0.0015	(AF083 221) YDR140 w homolo g [Fugu rubrip es]; TRANSC RIPTIO N INITIA TION FACTOR TFIID-

142883	ATU004 823	ATL8C1 0366:1 598..3 382	gap2	ATCEA4 C37465 1, ATCEA4 S29989	98, 96	ATL8C1 0366:2 563..3 382	0.81	g45673 11	99	279			1 (TATA- BOX FACTOR 1) (TATA SEQUEN CE- BINDIN G PROTEI N 1) (TBP- 1) [Arabi dopsis thalia na]
142884	ATU004 824	ATL8C5 0159:9 37..27	gap2	ATCEA4 C20781 1, ATCEA4 S33522 , ATCEA4 S32633	98, 97, 95	ATL8C5 0159:9 17..13 5	0.81	g13620 09	99	549	2.3e- 42	ubiqui tin- like protei n 7 - Arabid opsis thalia na []	
142885	ATU004 825	ATL8C6 563:10 2..565	gap2	ATCEA4 S2846	98	ATL8C6 563:46 3..189	0.81	g48039 25	99	117	0.91	(AC006 264) hypoth etical protei n [Arabi	

142886	ATU004 826	ATL8C2 0964:1 ..2033	gap2	ATCEA4 C7530_1, ATCEA4 S14809	98, 96	ATL8C2 0964:1 05..20 26	0.80	g10855 13	99	131	1.7e- 07	hnRNP X protei n - mouse (fragm ent) []
142887	ATU004 827	ATL8C3 5735:1 111..4 780	gap2	ATCEA4 C647_3	98	ATL8C3 5735:1 111..4 583	0.79	g28524 49, g33675 77	99, 41	964, 178	1.6e- 81, 6.9e- 10	(D8820 7) protei n kinase [Arabi dopsis thalia nal; (AL031 135) putati ve protei n [Arabi dopsis thalia nal]
142888	ATU004 828	ATL8C4 5021:2 446..9 05	gap2	ATCEA4 S1353	98	ATL8C4 5021:2 446..9 05	0.79	g17308 43	99	88	0.0012	HYPOTH ETICAL 17.1 KD PROTEI N IN SIP3- MRPL30 INTERG ENIC REGION [Sacch aromyc es cerevi

142889	ATU004 829	ATL8C3 6232:8 69..21 17	gap2	ATCEA4 C13296 91, ATCEA4 S30740 , ATCEA4 C52883 1	98, 94 96, 94	ATL8C3 6232:9 42..19 41	0.77	949143 38	99	763	2.2e- 81	siae] (AC005 489) F14N23 .24 [Arabi dopsis thalia na]
142890	ATU004 830	ATL8C4 4148:5 14..16 38	gap2	ATCEA4 C934_2 , ATCEA4 C934_1 , ATCEA4 S24405 , ATCEA4 C27863 1	98, 87, 84, 82	ATL8C4 4148:5 58..15 50	0.75	911732 21	99	533	1.1e- 50	40S RIBOSO MAL PROTEI N S11- BETA [Arabi dopsis thalia na]
142891	ATU004 831	ATL8C1 7732:5 58..38 19	gap2	ATCEA4 C28600 1, ATCEA4 S12067 , ATCEA4 C86900 1	98, 94 96, 94	ATL8C1 7732:6 81..38 19	0.74	940975 73	99	506	3.1e- 30	(U6491 7) GMFP7 [Glyci ne max]
142892	ATU004 832	ATL8C4 2254:4 934..2 664	gap2	ATCEA4 S1449	98	ATL8C4 2254:3 250..2 664	0.73	938595 91, 944163 07	99, 72	772, 99	1.1e- 69, 0.0035	(AF104 919) No defini tion line found [Arabi dopsis thalia na]; (AF105 716) hypoth

142893	ATU004 833	ATL8C1 3481:6 16..26 82	gap2	ATCEA4 C33213 1, ATCEA4 C33213 2, ATCEA4 C21839 2	98, 82 97, 82	ATL8C1 3481:6 29..26 82	0.73	g31282 03	99	640	2.3e- 63	etical protei n [Zea mays]
142894	ATU004 834	ATL8C4 7704:1 19..10 20	gap2	ATCEA4 C11115 9_1	98	ATL8C4 7704:1 24..74 8	0.72	g21911 65	99	273	1.1e- 24	(AF007 270) A_IG00 2P16.1 4 gene produc t [Arabi dopsis thalia na]
142895	ATU004 835	ATL8C1 2065:5 038..6 692	gap2	ATCEA4 S11186 , ATCEA4 C64793 1, ATCEA4 S35598	98, 94 97, 94	ATL8C1 2065:5 111..6 451	0.72	g45672 03	99	602	7.6e- 55	(AC007 168) putati ve beta- hydrox yacyl- ACP dehydr atase [Arabi dopsis thalia na]
142896	ATU004 836	ATL8C1 5155:1 196..1	gap2	ATCEA4 C7687 - 1, ATCEA4 S35179	98, 95, 95, 92 95, 92	ATL8C1 5155:7 09..16 0	0.68	g16519 34	99	185	8.4e- 17	(D9090 1) hypoth etical protei

142897	ATU004 837	ATL8C2 9528:9 4..143 1	gap2	ATCEA4 C7687_2, ATCEA4 S32006 ATCEA4 C59679 _1	98	ATL8C2 9528:1 52..12 62	0.68	g37383 29	99	647	1.5e- 59	n [Synec hocyst is sp.] (AC005 170) unknow n protei n [Arabi dopsis thalia nal
142898	ATU004 838	ATL8C1 7087:3 45..29 85	gap2	ATCEA4 C2202_1, ATCEA4 C330_1 ATCEA4 S15428 ATCEA4 C2202_2, ATCEA4 C30240 1, ATCEA4 S1319	98, 98, 95, 94, 83, 82	ATL8C1 7087:3 47..28 75	0.67	g38603 15	99	427	6.6e- 40	(AJ012 684) 40S riboso mal protei n S19 [Cicer arieti num]
142899	ATU004 839	ATL8C4 8019:5 56..15 06	gap2	ATCEA4 C14034 1, ATCEA4 C14034 2, ATCEA4 S16340	98, 97, 82	ATL8C4 8019:6 06..13 26	0.66	g39144 42	99	602	8.8e- 42	PHOTOS YSTEM I ON CENTRE SUBUNI T VI PRECUR SOR (LIGHT _

142900	ATU004 840	ATL8C1 7161:1 317..6 64	gap2	ATCEA4 C75917 _1	98	ATL8C1 7161:1 289..8 59	0.66	g14208 87	99	106	1.4e- 06	HARVESTING COMPLEX XII KDP PROTEIN (PSI-H) [Brassicarapa] (U34334) non-specific lipid transfer- like protein [Phaeolusvulgaris]
142901	ATU004 841	ATL8C1 4500:6 274..2 457	gap2	ATCEA4 S2573, ATCEA4 C1960_2, ATCEA4 S25955	98, 87, 82	ATL8C1 4500:6 274..2 457	0.63	g48039 30	99	813	1.5e- 71	(AC006264) cyclophilin (CYP2) [Arabidopsis thaliana]
142902	ATU004 842	ATL8C3 5247:2 65..94 3	gap2	ATCEA4 C11641 _1	98	ATL8C3 5247:5 31..91 2	0.63	g32128 64	99	291	3.5e- 13	(AC004005) unknown protein [Arabidopsis thaliana]

		4..1		, ATCEA4 S13027 , ATCEA4 C793_2 , ATCEA4 S9788	83, 83	3..220						calmod ulin TaCaM2 -1 [Triti cum aestiv um]
142907	ATU004 847	ATL8C2 4627:5 131..8 122	gap2	ATCEA4 C4138_2, ATCEA4 S10683 , ATCEA4 S19315 , ATCEA4 S19316 , ATCEA4 S16996	98, 97, 87, 85, 82	ATL8C2 4627:5 294..8 058	0.48	g31525 86	99	161	5.0e- 10	(AC002 986) YUP8H1 2R.28 [Arabi dopsis thalia na]
142908	ATU004 848	ATL8C3 2057:1 147..2 381	gap2	ATCEA4 C88250 1, ATCEA4 C90164 _1	98, 89	ATL8C3 2057:1 147..2 119	0.45	g33230 63	99	153	3.5e- 15	(AE001 247) polype ptide deform ylase (def) [Trepo nema pallid um]
142909	ATU004 849	ATL8C3 5879:6 17..1	gap2	ATCEA4 C59792 _1	98	ATL8C3 5879:5 58..45 2	0.45	g48039 22	99	265	3.3e- 21	(AC006 264) putati ve auxin- induce d protei n [Arabi dopsis]

142910	ATU004 850	ATL8C1 3134:5 433..3 105	gap2	ATCEA4 S7760	98		ATL8C1 3134:5 433..3 105	0.43	g46512 04	99	266	2.7e- 23	thalia na] (AB026 262) ring finger protei n [Cicer arieti num]
142911	ATU004 851	ATL8C4 8177:1 544..5 11	gap2	ATCEA4 C77084 _1	98				g46804 89	99	384	9.7e- 35	(AF119 222) hypoth etical protei n [Oryza sativa]
142912	ATU004 852	ATL8C2 2796:5 33..11 93	gap2	ATCEA4 C13519 9_1	98				g45805 21	99	397	2.5e- 33	(AF036 304) scarec row- like 7 [Arabi dopsis thalia na]
142913	ATU004 853	ATL8C2 058:20 1..646	gap2	ATCEA4 C15836 1, ATCEA4 S7974	98, 90				g39351 67	99	516	5.6e- 50	(AC004 557) F17L21 .10 [Arabi dopsis thalia na]
142914	ATU004 854	ATL8C4 2631:1 121..5 44	gap2	ATCEA4 C23450 _1	98				g18715 77	99	375	2.0e- 35	(Y1155 3) putati ve 21kD protei n

142915	ATU004 855	ATL8C2 5341:5 92..26	gap2	ATCEA4 S10570	98					99	144	1.9e- 09	(AF134 155) RING finger protei n [Arabi dopsis thalia na]	precu sor [Medic ago sativa]
142916	ATU004 856	ATL8C1 7082:1 105..1 423	gap2	ATCEA4 S29699	98					99	291	0.95	(AF124 226) pollen - specif ic protei n BAN102 [Brass ica rapa]	
142917	ATU004 857	ATL8C1 6596:1 294..1 979	gap2	ATCEA4 C31168 1, ATCEA4 S32705	98, 84					99	758	6.4e- 67	(AC006 260) putati ve 60S riboso mal protei n L12 [Arabi dopsis thalia na]	
142918	ATU004 858	ATL8C3 4656:4 3..637	gap2	ATCEA4 C51254 1	98					99	257	3.9e- 18	(X7716 2) ferred oxin- thiore	

142919	ATU004 859	ATL8C4 7018:1 ..626	gap2	ATCEA4 C5895_1, ATCEA4 S20116	98, 95					99	332	3.6e-20	doxin reductase SU A [Spina cia olerac ea] (AC006 919) putati ve transc riptio nal acativ ator CBF1 [Arabi dopsis thalia na]
142920	ATU004 860	ATL8C1 1734:6 66..14 87	gap2	ATCEA4 C5078_1	98					99	364	2.7e-31	(AC002 561) hypoth etical protei n [Arabi dopsis thalia na]
142921	ATU004 861	ATL8C2 0772:4 8..158 0	gap2	ATCEA4 C51489_1	98					99	112	3.9e-08	MACROP HAGE MIGRAT ION INHIBI TORY FACTOR (MIF) [Gallu s gallus l]
142922	ATU004	ATL8C7	gap2	ATCEA4	98					99	347	4.7e-	(M7585

142923	862	047:14 99..92 6	gap2	C12158 9_1	98					3	99	751	3.6e- 52	6) PVPR3 [Phase olus vulgar is]
	ATU004 863	ATL8C2 3741:1 114..2 379	gap2	ATCEA4 C43744 _1						g29210 94				(AF018 174) thiore doxin- f [Brass ica napus]
142924	ATU004 864	ATL8C1 3105:2 002..2 592	gap2	ATCEA4 C34624 _1	98					g11753 95	99	230	4.0e- 12	HYPOTH ETICAL 14.1 KD PROTEI N C31A2. 02 IN CHROMO SOME I [Schiz osacch aromyc es pombe]
142925	ATU004 865	ATL8C3 5583:8 92..16 9	gap2	ATCEA4 S2546	98					g40493 51	99	1032	1.6e- 67	(AI034 567) noduli n-like protei n [Arabi dopsis thalia na]
142926	ATU004 866	ATL8C1 7741:1 669..1 021	gap2	ATCEA4 S98	98					g41851 33	99	349	5.6e- 28	(AC005 724) putati ve zinc finger

142927	ATU004 867	ATL8C1 4729:1 669..1	gap2	ATCEA4 C37234 2, ATCEA4 S34435 , ATCEA4 C37234 _1	98, 90 97, 90					g11463 1	99	553	4.0e- 44	proteins [Arabidopsis thaliana] ATP SYNTHASE B CHAIN (SUBUNIT I) [Nicotiana tabacum]
142928	ATU004 868	ATL8C1 9702:1 0..560	gap2	ATCEA4 S32167	98					g17629 47	99	372	1.1e- 36	(U66270) ORF; able to induce HR-like lesions [Nicotiana tabacum]
142929	ATU004 869	ATL8C2 4229:1 499..6 45	gap2	ATCEA4 C63254 1, ATCEA4 C63254 _2	98, 95	ATL8C2 4229:1 365..9 15	0.98			g28426 62	98	96	3.5e- 06	DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.0 KD POLYPEPTIDE (ABC10-ALPHA) (RPB7.

142930	ATU004 870	ATL8C4 8465:3 288..1 925	gap2	ATCEA4 C27156 _1	98	ATL8C4 8465:3 225..2 047	0.80	g46886 61	98	104	0.90	0)
												(METAL LOTHIO NEIN-I GENE TRANSC RIPTIO N ACTIVA TOR) []
												(AL031 581) /predi ction= (metho d:; /predi ction= (metho d:; /match =(desc :; /match =(desc : [Dróso phila melano gaster]
142931	ATU004 871	ATL8C4 5633:1 24..29 03	gap2	ATCEA4 C59297 _1	98	ATL8C4 5633:1 24..29 03	0.63	g38614 02	98	142	3.7e- 08	(AJ235 273) 50S RIBOSO MAL PROTEI N L33 (rpmG) [Ricke ttsia prowaz ekii]
142932	ATU004	ATL8C4	gap2	ATCEA4	98,	ATL8C4	0.54	g47419	98	1228	7.7e-	(AF134

872	6264:1 482...3 24			C2812_1, ATCEA4 S33951 , ATCEA4 C2812_4, ATCEA4 S10674 , ATCEA4 C2812_3, ATCEA4 S28592 , ATCEA4 S10121 , ATCEA4 S10152	93, 92, 91, 88, 84, 84, 82	6264:1 144...5 10	40			120	120) lhca2 protei n [Arabi dopsis thalia na]	
142933	ATU004 873	gap2	ATL8C3 7638:1 422...1	ATCEA4 C15657 _1	98	ATL8C3 7638:1 120...1 3	0.51	947603 44	98	171	4.3e- 06	(AL049 769) mitoch ondria l 60s riboso mal protei n l10 precu sor [Schiz osacch aromyc es pombe]
142934	ATU004 874	gap2	ATL8C4 8975:1 834...1	ATCEA4 C12923 _1, ATCEA4 C49084 _1	98, 96	ATL8C4 8975:1 758...8	0.50	945067 17	98	113	4.9e- 08	riboso mal protei n S29 [Homo sapien s]

142935	ATU004 875	ATL8S1 483:15 6..552	gap2	ATCEA4 C10925 _1	98	ATL8S1 483:22 2..333	0.42	942622 38	98	221	0.34	(AC006 200) unknown protein [Arabi dopsis thalia na]
142936	ATU004 876	ATL8C3 2554:4 33..11 31	gap2	ATCEA4 C24250 2, ATCEA4 S28301	98, 85			g17105 49	98	242	2.4e- 21	60S RIBOSO MAL PROTEI N L39 []
142937	ATU004 877	ATL8C1 4793:4 165..5 104	gap2	ATCEA4 S6516, ATCEA4 C3075_ 1, ATCEA4 S5768	98, 95, 91			g28299 8	98	118	1.2e- 05	hypoth etical protein n 44 (psbI 3', region) - barley chloro plast [Horde um vulgar e]
142938	ATU004 878	ATL8C5 89:313 ..880	gap2	ATCEA4 C1976_ 3, ATCEA4 S34322 , ATCEA4 S34324 , ATCEA4 S30134	98, 92, 91, 88			g45394 28	98	199	0.049	(AL049 171) putati ve protein [Arabi dopsis thalia na]
142939	ATU004 879	ATL8C1 4822:5 48..1	gap2	ATCEA4 C40309 1	98			g13343 66	98	133	2.6e- 08	(X0244 1) gtag start

142940	ATU004 880	ATL8C4 8876:8 76..1	gap2	ATCEA4 S10957	98	ATL8C4 8876:8 76..37	0.90	g35229 54	97	773	2.5e- 41	[Nicot iana tabacu m] (AC004 411) IAA20 [Arabi dopsis thalia na]
142941	ATU004 881	ATL8C1 2079:2 454..8 97	gap2	ATCEA4 S560	98	ATL8C1 2079:2 432..8 97	0.81	g15865 51	97	967	1.8e- 107	CCAAT- bindin g factor :SUBUN IT=B [Brass ica napus]
142942	ATU004 882	ATL8C2 831:33 93..29 2	gap2	ATCEA4 S10920	98	ATL8C2 831:33 73..29 2	0.50	g44688 04	97	953	2.6e- 96	(AL035 601) putati ve protei n [Arabi dopsis thalia na]
142943	ATU004 883	ATL8C1 1402:4 29..18 98	gap2	ATCEA4 S29868 , ATCEA4 C11613 4 1, ATCEA4 S29869	98, 90, 88	ATL8C1 1402:4 80..16 20	0.84	g39351 76	96	857	3.9e- 82	(AC004 557) F17L21 .19 [Arabi dopsis thalia na]
142944	ATU004 884	ATL8C4 9462:1 06..15 07	gap2	ATCEA4 C3707- 1	98	ATL8C4 9462:6 63..13 29	0.73	g42637 11	96	819	8.8e- 79	(AC006 223) putati ve CCR4- associ

142945	ATU004 885	ATL8C2 0866:3 591..2 418	gap2	ATCEA4 C3156_ 9	98	ATL8C2 0866:3 556..2 418	0.60	g29795 53	96	774	3.7e- 78	ated transc riptio n factor [Arabi dopsis thalia na] (AC003 680) hypoth etical protei n [Arabi dopsis thalia na]
142946	ATU004 886	ATL8C2 0060:1 265..1	gap2	ATCEA4 S14799 , ATCEA4 C7047_ 1, ATCEA4 S5548	98, 98, 92	ATL8C2 0060:1 148..1 48	0.50	g21271 92, g36459 80	96, 95	261, 141		riboki nase (EC 2.7.1. 15) - Bacill us subtil is [Bacil lus subtil is]; (AL031 581) /predi ction= (metho d:; /predi ction= (metho d:; /match =(desc :;

142950	ATU004 890	ATL8C1 3130:4 63..29 37	gap2	ATCEA4 S6157	98	ATL8C1 3130:4 63..28 50	0.71	g46619 0	95	526	9.2e- 52	depend ent phosph ofruct o-1- kinase [Arabi dopsis thalia na]
142951	ATU004 891	ATL8C1 888:34 16..1	gap2	ATCEA4 S1307, ATCEA4 C51288 1, ATCEA4 C12760 7_1	98, 90, 88	ATL8C1 888:30 14..34	0.71	g46461 99	95	2806	8.1e- 286	(AC007 230) EST gb T22 166 comes from this gene. [Arabi dopsis thalia

142952	ATU004 892	ATL8C8 04:1.. 3611	gap2	ATCEA4 C13455 9_1, ATCEA4 C22424 _1	98, 96	ATL8C8 04:46. .2518	0.59	g29247 85	95	3303	0.0	na] (AC002 334) simila r to diseas e resist ance protei n [Arabi dopsis thalia na]
142953	ATU004 893	ATL8C3 6937:2 000...3 651	gap2	ATCEA4 C22561 _1	98			g39138 75	95	369	5.2e- 34	HYPA PROTEI N [Clost ridium perfri ngens]
142954	ATU004 894	ATL8C4 9674:1 577...3 949	gap2	ATCEA4 C84453 1, ATCEA4 S4821, ATCEA4 C42752 _1	98, 91 96, 91	ATL8C4 9674:1 577...3 556	0.90	g12968 05	94	864	1.3e- 64	(X9092 9) C- termin al peptid ase of the D1 protei n [Horde um vulgar el]
142955	ATU004 895	ATL8C4 7635:1 ..1504	gap2	ATCEA4 S1774, ATCEA4 C12070 4_1	98, 93	ATL8C4 7635:9 1..150 4	0.83	g44068 18	94	484	9.9e- 51	(AC006 201) putati ve transc riptio n factor -like protei

142956	ATU004 896	ATL8C1 3464:1 ..8006	gap2	ATCEA4 S30525 , ATCEA4 C37540 _1	98, 96	ATL8C1 3464:5 5..758 9	0.78	g33954 32, g21044 46	94, 39	1529, 1036	2.0e- 120, 1.2e- 78	n [Arabi dopsis thalia na]
142957	ATU004 897	ATL8C4 5104:4 529..1 07	gap2	ATCEA4 S32007 , ATCEA4 S4859	98, 98	ATL8C4 5104:4 382..1 07	0.65	g48877 60, g38595 97	94, 71	362, 112	2.1e- 42, 3.2e- 08	n [Arabi dopsis thalia na]; (AC004 683) unknown n protei n [Arabi dopsis thalia na]; (Z9539 6) WD- repeat protei n [Schiz osacch aromyc es pombel] (AC006 533) putati ve ARI,RI NG finger protei n [Arabi dopsis thalia na]; (AF104 919) No defini tion line found

142958	ATU004 898	ATL8C1 1405:2 335..1	gap2	ATCEA4 S27128 , ATCEA4 S33759	98, 90	ATL8C1 1405:1 157..9 7	0.63	g45103 48	94	878	6.6e- 92	[Arabi dopsis thalia na] (AC006 921) unknown n protei n [Arabi dopsis thalia na]
142959	ATU004 899	ATL8C3 2040:1 ..6298	gap2	ATCEA4 S968	98			g45875 84	94	4081	0.0	(AC007 232) unknown n protei n [Arabi dopsis thalia na]
142960	ATU004 900	ATL8C2 5837:3 303..1 511	gap2	ATCEA4 C854_1 , ATCEA4 C854_2	98, 91	ATL8C2 5837:2 257..1 789	0.92	g33416 81	93	677	1.9e- 54	(AC003 672) small GTP- bindin g protei n [Arabi dopsis thalia na]
142961	ATU004 901	ATL8C1 2016:1 ..4163	gap2	ATCEA4 C76382 1, ATCEA4 C93057 1, ATCEA4 C5222_1,	98, 98, 98, 94, 83	ATL8C1 2016:3 89..35 39	0.91	g18389 84	93	877	2.1e- 71	(X9564 2) serine C- palmit oyltra nsfera se [Mus

142962	ATU004 902	ATL8C2 3347:2 528..1	gap2	ATCEA4 S7944, ATCEA4 S1843	98, 82	ATL8C2 3347:2 363..3 76	0.88	g11435 11	93	1147	2.2e- 103	(Z4707 6) Ser/Th r protei n phosph atase homolo gous to PPX [Malus domest ica]
142963	ATU004 903	ATL8C1 5588:1 ..1013	gap2	ATCEA4 C30010 1, ATCEA4 C70681 1, ATCEA4 S17708	98, 97, 85			g44572 21	93	103	8.3e- 06	(AF127 797) putati ve bZIP DNA- bindin g protei n [Capsi cum chinene se]
142964	ATU004 904	ATL8C1 7646:5 309..1 799	gap2	ATCEA4 S3013, ATCEA4 S1764, ATCEA4 S2055	98, 96, 83			g44671 24	93	916	5.5e- 98	(AL035 538) hypoth etical protei n [Arabi dopsis thalia na]
142965	ATU004 905	ATL8C4 9140:2 192..1	gap2	ATCEA4 C12129 9 1,	98, 98, 92	ATL8C4 9140:1 455..1	0.97	g30435 29, g22449	92, 37	120, 147	2.4e- 15, 3.4e-	(AJ002 204) polyam

142966	ATU004 906	ATL8C1 650:1. .1569	gap2	ATCEA4 C1881- 1, ATCEA4 S8154	98, 86	ATL8C1 650:4. .1407	0.86	g44270 03	92	1047	2.9e- 87	(AF127 664) NBD- like protei n [Arabi dopsis thalia nal]
142967	ATU004 907	ATL8C4 9728:1 ..5834	gap2	ATCEA4 S11380	98	ATL8C4 9728:1 16..58 34	0.77	g24355 17	92	629	5.6e- 61	(AF024 504) contai ns simila rity to peptid ase family A1 [Arabi

142968	ATU004 908	ATL8C4 8543:1 186..1	gap2	ATCEA4 S36290 , ATCEA4 C924_2	98, 93	ATL8C4 8543:6 76..40	0.59	g58591 7	92	482	4.8e- 36	DNA- DIRECT ED RNA POLYME RASE II 19 KD POLYPE PTIDE (RNA POLYME RASE II SUBUNI T 5) [Arabi dopsis thalia na]
142969	ATU004 909	ATL8C1 5378:9 73..1	gap2	ATCEA4 S30368 , ATCEA4 S2886, ATCEA4 C30805 _1	98, 94, 90			947339 93	92	346	6.4e- 44	(AC007 188) unknow n protei n [Arabi dopsis thalia na]
142970	ATU004 910	ATL8C4 1620:1 ..1528	gap2	ATCEA4 S29597	98	ATL8C4 1620:1 70..15 28	0.88	g33675 21	91	406	5.9e- 43	(AC004 392) Simila r to gb U08 285 membra ne- associ ated salt- induci ble

142971	ATU004 911	ATL8C3 4202:4 84..26 17	gap2	ATCEA4 C26488 1, ATCEA4 S461, ATCEA4 C26488 4, ATCEA4 S4559	98, 97, 95, 83	ATL8C3 4202:5 41..25 49	0.78	g39803 78	91	1864	1.1e- 172	protei n from Nicoti ana tabacu m. ESTs gb T44 131 and gb T04 378 come from this gene. [Arabi dopsis thalia na]
142972	ATU004 912	ATL8C3 6951:3 73..29 18	gap2	ATCEA4 C25397 1, ATCEA4 S29558 , ATCEA4 S3125	98, 94, 93	ATL8C3 6951:4 17..27 73	0.77	g45259 3	91	1333	4.6e- 126	(D2181 4) ORF [Liliu m longif lorum]
142973	ATU004 913	ATL8C9 043:48 11..42	gap2	ATCEA4 S27401	98	ATL8C9 043:16 97..42	0.74	g43097 67	91	3557		(AC006 217) putati ve Athila

142974	ATU004 914	ATL8C4 2805:1 60..13 26	gap2	ATCEA4 C28184 _1	98				g38057 63	91	591	1.8e- 68	(AC005 693) hypoth etical protei n [Arabi dopsis thalia na]
142975	ATU004 915	ATL8C4 2851:1 19..26 63	gap2	ATCEA4 C2886 _1, ATCEA4 C36515 _1	98, 94	ATL8C4 2851:1 24..26 63	0.98		g38505 83	90	1562	1.1e- 118	(AC005 278) Contai ns simila rity to transc riptio n initia tion factor IIE, alpha subuni t gb X63 468 from Homo sapien s. [Arabi dopsis thalia na]

142976	ATU004 916	ATL8C2 2299:3 698..1	gap2	ATCEA4 S4150	98	ATL8C2 2299:3 668..2 4	0.71	g26538 85	90	2830	6.8e- 303	na] (AF027 408) phosph olipas e D- gamma; PLD- gamma [Arabi dopsis thalia na]
142977	ATU004 917	ATL8C1 6063:2 499..6 55	gap2	ATCEA4 C82201 1, ATCEA4 C26141 1, ATCEA4 C29081 1	98, 98, 93	ATL8C1 6063:2 497..7 67	0.71	g11711 61	90	1110	1.2e- 113	(U4147 2) pectat e lyase homolo g [Medic ago sativa]
142978	ATU004 918	ATL8C6 691:31 70..87 1	gap2	ATCEA4 C3626 1, ATCEA4 C6760 1, ATCEA4 S20968 , ATCEA4 C22766 1, ATCEA4 S35843	98, 98, 91, 89, 82	ATL8C6 691:26 97..11 63	0.71	g31281 68	90	1213	1.5e- 133	(AC004 521) putati ve carbox yl- termin al peptid ase [Arabi dopsis thalia na]
142979	ATU004 919	ATL8C1 5512:1 ..1509	gap2	ATCEA4 S1861	98	ATL8C1 5512:3 37..10 20	0.58	g44671 52	90	1789	4.1e- 183	(AL035 540) putati ve protei n [Arabi

142980	ATU004 920	ATL8C4 4915:1 493..1	gap2	ATCEA4 C22331 _1	98	ATL8C4 4915:1 493..9	0.95	g40975 47	89	316	7.5e- 06	dopsis thalia na] (U6490 6) ATFP3 [Arabi dopsis thalia na]
142981	ATU004 921	ATL8C2 7607:4 17..35 98	gap2	ATCEA4 C8200_ 2, ATCEA4 S366, ATCEA4 S30847 , ATCEA4 C4359_ 1	98, 97, 95, 94	ATL8C2 7607:4 17..34 21	0.89	g28277 11	89	3857		(Al021 684) oxoglu tarate dehydr ogenas e - like protei n [Arabi dopsis thalia na]
142982	ATU004 922	ATL8C3 2907:6 51..33 86	gap2	ATCEA4 C19623 _1	98	ATL8C3 2907:6 51..32 47	0.77	g45672 46	89	665	2.1e- 45	(AC007 070) unknow n protei n [Arabi dopsis thalia na]
142983	ATU004 923	ATL8C2 5118:2 444..6 19	gap2	ATCEA4 S879, ATCEA4 S34076 , ATCEA4 C59541 _1	98, 92, 89	ATL8C2 5118:2 290..7 50	0.74	g19030 34	89	1083	3.6e- 115	(X9462 5) amp- bindin g protei n [Brass ica napus]

142984	ATU004 924	ATL8C2 7166:2 371..5 6	gap2	ATCEA4 C12732 1, ATCEA4 C74963 1, ATCEA4 C75030 1_	98, 97 98, 97	ATL8C2 7166:1 745..5 6	0.57	g44552 42	89	259	4.7e- 25	(AL035 523) gerany lgeran ylated protei n ATGP4 [Arabi dopsis thalia na]
142985	ATU004 925	ATL8C4 3694:1 298..2 59	gap2	ATCEA4 S3023	98			g48503 83	89	1493		(AC007 357) Contai ns simila rity to []
142986	ATU004 926	ATL8C1 5062:1 113..1 27	gap2	ATCEA4 C827_1 , ATCEA4 S15604 , ATCEA4 S874, ATCEA4 C827_2 , ATCEA4 C827_3 , ATCEA4 S10106	98, 97, 96, 91, 84, 82			g11700 89	89	805	9.8e- 84	GLUTAT HIONE S- TRANSF ERASE ERD13 (CLASS PHI) [Arabi dopsis thalia na]
142987	ATU004 927	ATL8C2 3825:1 ..1302	gap2	ATCEA4 S14427 , ATCEA4 C28239 1_	98, 96	ATL8C2 3825:2 50..90 7	0.74	g33090 82	88	575	2.7e- 48	(AF076 251) calcin eurin B-like protei n 1 [Arabi dopsis thalia

142988	ATU004 928	ATL8C2 4360:3 466..3 93	gap2	ATCEA4 S4576, ATCEA4 S32251	98, 89	ATL8C2 4360:3 136..7 68	0.55	g48951 79	88	884	4.4e- 80	na] (AC007 661) hypoth etical protei n [Arabi dopsis thalia na]
142989	ATU004 929	ATL8C3 834:1. .644	gap2	ATCEA4 C50660 _1	98			g32984 41	88	419	1.2e- 44	(AB010 879) chloro plast riboso mal protei n L10 [Nicot iana tabacu m]
142990	ATU004 930	ATL8C4 36:1.. 2472	gap2	ATCEA4 C1940_ 1, ATCEA4 S15092 , ATCEA4 S7618, ATCEA4 S31281	98, 98, 88, 87	ATL8C4 36:157 ..2198	0.94	g36390 89	87	3527	0.0	(AF090 445) phosph olipas e D1 [Brass ica olerac ea var. capita tal]
142991	ATU004 931	ATL8C2 7004:3 26..29 66	gap2	ATCEA4 S2743, ATCEA4 S14785 , ATCEA4 S14786	98, 92, 89	ATL8C2 7004:3 26..29 18	0.88	g39140 84	87	509	9.4e- 35	MUTS2 PROTEI N [Bacil lus subtil is]
142992	ATU004 932	ATL8C3 0421:1	gap2	ATCEA4 S27411	98	ATL8C3 0421:1	0.80	g30212 76	87	1237	7.5e- 129	(AL022 347)

142993	ATU004 933	ATL8C2 5196:2 993..1	gap2	ATCEA4 S987, ATCEA4 S2700, ATCEA4 S307	98, 95 98, 95	ATL8C2 5196:2 560..1 06	0.70	g10448 0	87	363	9.2e- 24	serine /threo nine kinase - like protei n [Arabi dopsis thalia nal]
142994	ATU004 934	ATL8C4 4758:1 746..4 17	gap2	ATCEA4 C7416_1	98	ATL8C4 4758:1 675..4 17	0.66	g33353 53	87	1549	4.0e- 154	(AC004 512) Simila r to cytoch rome P450 gbIX90 458 from A. thalia na. [Arabi dopsis thalia nal]
142995	ATU004 935	ATL8C1 5628:5 625..1 94	gap2	ATCEA4 C34297 1, ATCEA4 C26567 1, ATCEA4 C34297	98, 95, 91, 85	ATL8C1 5628:5 210..1 94	0.57	g42042 65, g22448 06	87, 69	672, 131	7.8e- 77, 4.5e- 12	(AC005 223) 45643 [Arabi dopsis thalia nal]; (Z9733

142996	ATU004 936	ATL8C1 9820:3 522..1 73	gap2	ATCEA4 C13194 1_1, ATCEA4 S2994	98, 98	ATL8C1 9820:2 796..3 47	0.97	g42204 74	86	1926	9.1e- 192	(AC006 069) putati ve myosin heavy chain [Arabi dopsis thalia na]
142997	ATU004 937	ATL8C4 4645:1 42..17 53	gap2	ATCEA4 S4920	98	ATL8C4 4645:1 42..17 36	0.90	g36872 52	86	2297	1.7e- 226	(AC005 169) hypoth etical protei n, 3' partia l [Arabi dopsis thalia na]
142998	ATU004 938	ATL8C1 300:31 28..36 0	gap2	ATCEA4 S4598	98	ATL8C1 300:22 13..64 6	0.88	g49143 68	86	1799	3.9e- 163	(AC007 584) hypoth etical protei n simila r to T18A10 .3 [Arabi dopsis thalia

142999	ATU004 939	ATL8C2 1000:1 595..1	gap2	ATCEA4 C34789 _1	98	ATL8C2 1000:1 484..2 7	0.82	g45394 27	86	727	1.2e- 62	na] (AL049 171) putati ve protei n [Arabi dopsis thalia na]
143000	ATU004 940	ATL8C2 7989:9 08..8	gap2	ATCEA4 C3804_2, ATCEA4 S270, ATCEA4 C3804_1	98, 91, 91	ATL8C2 7989:7 96..13 8	0.99	g24672 74	85	211		(Z9975 9) rna bindin g protei n [Schiz osacch aromyc es pombe]
143001	ATU004 941	ATL8C1 6492:9 42..1	gap2	ATCEA4 S13877	98	ATL8C1 6492:5 95..47	0.96	g45672 57	85	420	3.3e- 30	(AC007 070) hypoth etical protei n [Arabi dopsis thalia na]
143002	ATU004 942	ATL8C1 7347:1 ..2082	gap2	ATCEA4 S7499, ATCEA4 C53702 _1, ATCEA4 C226_1	98, 87 96, 87	ATL8C1 7347:1 28..17 90	0.83	g32420 77	85	1855	1.1e- 201	(AJ003 119) protei n phosph atase 2C [Arabi dopsis thalia na]
143003	ATU004	ATL8C2	gap2	ATCEA4	98, 97	ATL8C2	0.81	g10762	85	598	4.0e-	ATAF2

143004	943	6491:1 6..138 8	gap2	C71246 1, ATCEA4 C12028 8_1	98, 96	ATL8C3 6640:1 628..3 3	0.77	944688 13	85	495	6.9e- 48	protei n - Arabid opsis thalia na [] (AL035 601) putati ve protei n [Arabi dopsis thalia na]
143005	ATU004 945	ATL8C3 6365:2 170..1	gap2	ATCEA4 C3599_1, ATCEA4 S34502 , ATCEA4 S31391	98, 89 89, 89	ATL8C4 6365:2 091..2 35	0.60	911744 70	85	1831	2.7e- 195	OLIGOS ACCHAR YL TRANSF ERASE STT3 SUBUNI T HOMOLO G (B5) (INTEG RAL MEMBRA NE PROTEI N 1) [Mus muscul us]
143006	ATU004 946	ATL8C3 4057:1 13..16 97	gap2	ATCEA4 C52762 1, ATCEA4 S7230	98, 86	ATL8C3 4057:1 13..80 5	0.53	928424 91	85	1000	3.3e- 77	(AL021 749) putati ve protei n [Arabi dopsis thalia na]

143007	ATU004 947	ATL8C4 4219:1 ..2534	gap2	ATCEA4 C3169_1	98	ATL8C4 4219:4 8..163 0	0.48	g33353 67	85	123	2.4e- 06	(AC003 028) unknown protein [Arabi dopsis thalia na]
143008	ATU004 948	ATL8C5 308:44 9..312 0	gap2	ATCEA4 C10864 7_1, ATCEA4 S18203	98, 85			g35823 28	85	841	5.3e- 72	(AC005 496) hypoth etical protein [Arabi dopsis thalia na]
143009	ATU004 949	ATL8C3 4974:2 951..2 20	gap2	ATCEA4 S25815 , ATCEA4 S15710 , ATCEA4 C17169 _1	98, 85 91, 85	ATL8C3 4974:2 680..4 40	0.94	g17093 58	84	821	3.2e- 66	NUCLEO SIDE- TRIPHO SPHATA SE (NUCLE OSIDE TRIPHO SPHATE PHOSPH OHYDRO LASE) (NTPAS E) [Pisum sativu m]
143010	ATU004 950	ATL8C5 0054:1 027..1	gap2	ATCEA4 C36717 1, ATCEA4 C2200_1	98, 97	ATL8C5 0054:7 66..23	0.91	g63389 0	84	786	6.2e- 84	(S7292 6) glucos e and ribito l dehydr ogenas

143011	ATU004 951	ATL8C3 7382:1 360..1	gap2	ATCEA4 C3495_1	98	ATL8C3 7382:1 360..1 06	0.84	g29822 93	84	104		e homolog [Hordeum vulgare]
143012	ATU004 952	ATL8C3 8957:1 ..1234	gap2	ATCEA4 S34308 , ATCEA4 C31720_1	98, 88	ATL8C3 8957:1 49..11 96	0.77	g45673 10	84	739	9.4e- 63	(AC005 956) unknown protein [Arabis dopsis thaliana]
143013	ATU004 953	ATL8C4 9444:4 98..1	gap2	ATCEA4 C29160_1, ATCEA4 S16456	98, 86			g19463 74	84	92	3.6e- 10	(U9321 5) myb-like protein isolated [Arabis dopsis thaliana]
143014	ATU004 954	ATL8C4 5782:1 247..1	gap2	ATCEA4 C47932_2, ATCEA4 C47932_3, ATCEA4 C47932	98, 96, 95, 92, 86, 86, 84	ATL8C4 5782:1 127..2 11	0.99	g11705 55	83	601	1.8e- 61	MYO- INOSITOL 4-O- METHYL TRANSFERASE [Mesembryanthemum]

143015	ATU004 955	ATL8C1 918:22 39..78 2	gap2	ATCEA4 C4304_1, ATCEA4 S26836, ATCEA4 S7906, ATCEA4 S31242	98, 97	ATL8C1 918:20 30..10 26	0.91	g44903 32	83	598	3.0e- 58	(AL035 656) putati ve protei n [Arabi dopsis thalia na]
143016	ATU004 956	ATL8C1 3096:1 ..1429	gap2	ATCEA4 C70486 _1	98	ATL8C1 3096:1 23..12 51	0.87	g38222 25	83	241	7.9e- 26	(AF079 183) RING- H2 finger protei n RHG1a [Arabi dopsis thalia na]
143017	ATU004 957	ATL8C4 9416:1 449..1	gap2	ATCEA4 C4534_1	98	ATL8C4 9416:9 04..28 5	0.83	g29147 06	83	388	7.6e- 43	(AC003 974) putati ve homeob ox protei n [Arabi dopsis thalia na]

143018	ATU004 958	ATL8C2 4347:1 47..57 62	gap2	ATCEA4 C75789 1, ATCEA4 S12771 , ATCEA4 S34378 , ATCEA4 C10475 7_1, ATCEA4 C5324_1, ATCEA4 S11172	98, 97, 94, 93, 93, 90	ATL8C2 4347:5 647..4 926, ATL8C2 4347:1 47..41 63	0.81, 0.79	g45040 85	83	1082	2.7e- 114	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens]
143019	ATU004 959	ATL8C2 3359:2 883..8 1	gap2	ATCEA4 S4551, ATCEA4 C13376 0_1, ATCEA4 S8633, ATCEA4 C18918 _1	98, 97, 90, 82	ATL8C2 3359:2 786..8 1	0.73	g31842 81	83	1443	4.1e- 69	(AC004136) putative cytochrome P450 [Arabis dopsis thaliana]
143020	ATU004 960	ATL8C3 0963:1 ..6161	gap2	ATCEA4 C14046 1, ATCEA4 S32185 , ATCEA4 C30093 _1	98, 96, 92	ATL8C3 0963:4 8..616 1	0.69	g45389 29	83	539	1.1e- 46	(AL049483) putative nucleic acid binding protein [Arabis dopsis thaliana]
143021	ATU004 961	ATL8C2 0849:8 008..1	gap2	ATCEA4 S32643	98, 84	ATL8C2 0849:8 008..6	0.68	g48681 20	83	460	4.5e- 30	(AF116556) putative

143022	ATU004 962	ATL8C4 4740:1 ..895	gap2	ATCEA4 S242	98	ATL8C4 4740:4 67..64 8	0.62	g30985 71	83	1000	2.9e- 100	ve transc riptio n factor [Arabi dopsis thalia na]
143023	ATU004 963	ATL8C3 872:18 2..163 5	gap2	ATCEA4 C12362 1, ATCEA4 S7939, ATCEA4 S30037	98, 97, 93	ATL8C3 872:29 9..152 0	0.60	g30045 51	83	365	1.6e- 34	(AF049 028) BURP domain contai ning protei n [Brass ica napus] (AC003 673) hypoth etical protei n [Arabi dopsis thalia na]
143024	ATU004 964	ATL8C1 0312:1 ..1511	gap2	ATCEA4 S7193	98	ATL8C1 0312:4 06..13 11	0.52	g38058 54	83	1602		(AL031 986) putati ve protei n [Arabi dopsis thalia na]
143025	ATU004 965	ATL8C4 6579:3 457..1	gap2	ATCEA4 S12669	98	ATL8C4 6579:3 457..6 4	0.46	g46894 54	83	3907	0.0	(AC006 267) putati ve polypr

143026	ATU004 966	ATL8C3 2413:1 ..5485	gap2	ATCEA4 C743_2 , ATCEA4 S27401 , ATCEA4 C743_1	98, 96, 84					g43097 67, g30470 63	83, 76	2887, 173	1.4e- 264, 6.8e- 07	(AC006 217) putati ve Athila retroee lement ORF1 protei n [Arabi dopsis thalia na]; (AF058 825) No defini tion line found [Arabi dopsis thalia na]
143027	ATU004 967	ATL8C1 0836:1 502..3 57	gap2	ATCEA4 S7588	98	ATL8C1 0836:1 122..4 20	0.95			g22449 08	82	1003	7.2e- 93	(Z9733 9) hypoth etical protei n [Arabi dopsis thalia na]
143028	ATU004 968	ATL8C1 6524:7 09..1	gap2	ATCEA4 C32399 1, ATCEA4 S2166	98, 95	ATL8C1 6524:5 38..25 7	0.86			g23448 97	82	711	1.2e- 53	(AC002 388) unknow n protei

143029	ATU004 969	ATL8C3 0532:1 ..1579	gap2	ATCEA4 C18389 2, ATCEA4 S30964	98, 92	ATL8C3 0532:3 0..690	0.82	g19463 72	82	127	2.3e- 11	n [Arabi dopsis thalia na] (U9321 5) yeast hypoth etical protei n YDB1_S CHPO_ isolog [Arabi dopsis thalia na]
143030	ATU004 970	ATL8C2 7299:1 ..1338	gap2	ATCEA4 S4960	98	ATL8C2 7299:7 2..133 8	0.80	g45393 03	82	1128		(AL049 480) putati ve protei n [Arabi dopsis thalia na]
143031	ATU004 971	ATL8C1 5506:4 785..4 31	gap2	ATCEA4 C63944 1, ATCEA4 S31113 , ATCEA4 S32417	98, 91, 87	ATL8C1 5506:4 540..4 58	0.77	g22449 90, g41159 18	82, 69	3891, 139	3.8e- 284, 0.52	(Z9734 0) simila rity to LIM homeob ox protei n - Caenor habdit is [Arabi dopsis thalia na];

143032	ATU004 972	ATL8C4 6058:1 984..4 44	gap2	ATCEA4 S781, ATCEA4 C767_1	98, 82	ATL8C4 6058:1 807..6 09	0.77	g24996 08	82	1368	9.8e- 142	(AF118 222) simila r to nascen t polype ptide associ ated comple x alpha chain [Arabi dopsis thalia na]
143033	ATU004 973	ATL8C1 635:20 87..1	gap2	ATCEA4 C30703 1, ATCEA4 C10579 3_1	98, 95	ATL8C1 635:18 76..12 2	0.73	g44552 93	82	301	3.0e- 26	(AL035 528) putati ve protei n [Arabi dopsis thalia na]

143034	ATU004 974	ATL8C3 6760:1 ..1973	gap2	ATCEA4 S26195 , ATCEA4 C10789 _1	98, 96	ATL8C3 6760:5 61..14 16	0.73	g28326 77	82	1003	1.4e- 93	na] (AL021 712) hypoeth etical proteins [Arabi dopsis thalia na]
143035	ATU004 975	ATL8C1 0655:1 65..10 74	gap2	ATCEA4 S2551, ATCEA4 S36159	98, 97	ATL8C1 0655:1 82..99 4	0.69	g31579 36	82	239		(AC002 131) Contai ns simila rity to NFATc3 gb U28 807 from Mus muscul us. [Arabi dopsis thalia na]
143036	ATU004 976	ATL8C4 3269:7 585..1 090	gap2	ATCEA4 S26314 , ATCEA4 C19022 _1, ATCEA4 C635_1	98, 85 98, 85	ATL8C4 3269:7 080..2 131	0.67	g32528 07, g45453 04	82, 54	737, 177	7.5e- 79, 3.0e- 12	(AC004 705) hypoeth etical proteins [Arabi dopsis thalia na]; (AF126 488) nuclea r inhibi tor of

143037	ATU004 977	ATL8C1 5850:1 073..1	gap2	ATCEA4 S6614, ATCEA4 C41430 _1	98, 96	ATL8C1 5850:1 021..5 9	0.66	g17070 10	82	1132	2.4e- 113	phosphatase-1 [Homo sapiens]
143038	ATU004 978	ATL8C3 6953:1 551..7 5	gap2	ATCEA4 C11517 _1	98	ATL8C3 6953:1 523..2 29	0.53	g44540 31	82	271	1.1e- 27	(Al035394) putative protein [Arabis dopsis thaliana]
143039	ATU004 979	ATL8C3 9257:1 34..13 56	gap2	ATCEA4 C5695_1	98	ATL8C3 9257:3 66..13 21	0.45	g42635 26	82	124	5.8e- 06	(AC004044) hypothetical protein [Arabis dopsis thaliana]
143040	ATU004 980	ATL8C4 9535:1 ..1677	gap2	ATCEA4 C7645_1, ATCEA4 C53147	98, 98			g48836 03	82	1171	1.1e- 120	(AC006922) putative xylogl

143041	ATU004 981	ATL8C1 879:16 22..33 8	gap2	ATCEA4 C22845 1, ATCEA4 C10414 8_1	98, 95	ATL8C1 879:15 62..50 1	0.99	g68190 8	81	696	3.4e- 57	(D3171 3) cp31 [Arabi dopsis thalia na]	ucan endo- transg lycosy lase [Arabi dopsis thalia na]
143042	ATU004 982	ATL8C1 5818:1 ..961	gap2	ATCEA4 C1586 1	98	ATL8C1 5818:6 2..640	0.91	g27603 62	81	429	3.4e- 35	(AF016 511) 15.9 kDa subuni t of RNA polyme rase II [Arabi dopsis thalia na]	ucan endo- transg lycosy lase [Arabi dopsis thalia na]
143043	ATU004 983	ATL8C3 7190:1 841..8 74	gap2	ATCEA4 S27235	98	ATL8C3 7190:1 592..9 48	0.89	g30687 05	81	827		(AF049 236) unknown [Arabi dopsis thalia na]	ucan endo- transg lycosy lase [Arabi dopsis thalia na]
143044	ATU004 984	ATL8C2 9316:1 ..1633	gap2	ATCEA4 C10203 9_1, ATCEA4 C16763 1	98, 95	ATL8C2 9316:8 3..133 4	0.85	g43357 49	81	1134	1.0e- 122	(AC006 284) unknown protei n [Arabi dopsis thalia na]	ucan endo- transg lycosy lase [Arabi dopsis thalia na]

143045	ATU004 985	ATL8C1 0845:1 ..5427	gap2	ATCEA4 S11508	98	ATL8C1 0845:2 55..53 61	0.75	g42042 72, g24941 31	81, 60	1581, 3664	1.6e- 156, 0.0	dopsis thalia na] (AC005 223) Hypoth etical protei n [Arabi dopsis thalia na]; (AC002 376) Strong simila rity to Lycop rsicon aldeh de oxidas e (gb U8 2559). [Arabi dopsis thalia na]
143046	ATU004 986	ATL8C2 1784:8 22..25 10	gap2	ATCEA4 C991_1	98	ATL8C2 1784:8 70..24 36	0.72	g13463 88	81	1452	1.1e- 90	KNOTTE D-LIKE HOMEOP OX PROTEI N 4 [Arabi dopsis thalia na]
143047	ATU004 987	ATL8C1 6470:9 9..254 4	gap2	ATCEA4 C37238 _1	98	ATL8C1 6470:1 58..12 24,	0.53, 0.49	g48502 85, g26668 9	81, 77	132, 99	5.3e- 12, 0.076	(AL049 876) putati ve

143048	ATU004 988	ATL8C1 7379:6 60...29 96	gap2	ATCEA4 S13912	98	ATL8C1 6470:2 093...1 693		g46626 42	81	1273	5.0e- 99	prote n [Arabi dopsis thalia na]; P24 OLEOSI N ISOFOR M B (P91) [Glyci ne max] (AC006 429) hypoth etical protei n [Arabi dopsis thalia na]
143049	ATU004 989	ATL8C4 9476:1 510...1 86	gap2	ATCEA4 S13591	98	ATL8C4 9476:1 233...1 86	0.96	g22448 35	80	946	1.5e- 104	(Z9733 7) protei n kinase homolo g [Arabi dopsis thalia na]
143050	ATU004 990	ATL8C3 4758:2 491...1 374	gap2	ATCEA4 S29684	98	ATL8C3 4758:2 491...2 015	0.94	g33955 92	80	126	2.5e- 06	(AL031 179) hypoth etical protei n [Schiz osacch aromyc

143051	ATU004 991	ATL8C7 419:1. .515	gap2	ATCEA4 C729_1 , ATCEA4 S31717	98, 83	ATL8C7 419:13 3..430	0.88	g22449 31	80	468	1.9e- 46	es pombel] (Z9733 9) hypoth etical protei n [Arabi dopsis thalia na]
143052	ATU004 992	ATL8C8 569:19 36..33 05	gap2	ATCEA4 C4200_ 1, ATCEA4 S6162	98, 93	ATL8C8 569:24 72..32 70	0.76	g30687 05	80	199	9.8e- 11	(AF049 236) unknow n [Arabi dopsis thalia na]
143053	ATU004 993	ATL8C1 1184:4 36..28 48	gap2	ATCEA4 C15266 1, ATCEA4 C51528 1, ATCEA4 C59493 1, ATCEA4 S27940 , ATCEA4 S12019	98, 98, 96, 88, 83	ATL8C1 1184:6 51..27 32	0.73	g36000 52	80	888	9.1e- 83	(AF080 120) contai ns simila rity to glycos yl hydrol ases family 9 (Pfam: glycos yl hyd ro5.hm m, score: 88.03) [Arabi dopsis thalia na]
143054	ATU004	ATL8C3	gap2	ATCEA4	98	ATL8C3	0.56	g22752	80	488	2.0e-	(AC002

143055	ATU004 995	ATL8C1 6263:2 148..1	gap2	ATCEA4 C19286 _2	98	ATL8C1 6263:2 148..5 2	0.54	g41602 80	80	1000	2.2e- 104	(AJ006 224) purple acid phosph atase [Ipomo ea batata s]	337) unknown protein [Arabi dopsis thalia na]
143056	ATU004 996	ATL8C4 3226:2 279..4 909	gap2	ATCEA4 C12766 1, ATCEA4 S5209	98, 96			g36680 91	80	236	2.7e- 22	(AC004 667) hypoth etical protein [Arabi dopsis thalia na]	51
143057	ATU004 997	ATL8C4 776:27 8..199 9	gap2	ATCEA4 S464	98	ATL8C4 776:29 6..172 7	0.86	g41917 79	79	1053	3.6e- 91	(AC005 917) putati ve reca protein [Arabi dopsis thalia na]	
143058	ATU004 998	ATL8C4 6917:1 ..1475	gap2	ATCEA4 S29533	98	ATL8C4 6917:1 03..14 75	0.85	g46662 87	79	734	4.8e- 80	(D8576 4) cytoso lic monode	

143059	ATU004 999	ATL8C3 3859:1 405..6 71	gap2	ATCEA4 C77853 _1	98	ATL8C3 3859:1 353..7 29	0.80	g48357 58	79	1066		hydroa scorba te reduct ase [Oryza sativa]
143060	ATU005 000	ATL8C3 8118:9 75..22 40	gap2	ATCEA4 C18241 _1	98	ATL8C3 8118:2 081..1 926	0.79	g48952 60	79	410	4.5e- 36	(AC007 658) thiore doxin- like protei n [Arabi dopsis thalia na]
143061	ATU005 001	ATL8C3 2080:1 ..5355	gap2	ATCEA4 S12836 , ATCEA4 S12839	98, 94	ATL8C3 2080:4 53..53 55	0.57	g47411 96	79	2573	3.8e- 225	(AL049 746) ABC- type transp ort- like protei n [Arabi

143062	ATU005 002	ATL8C2 8101:4 37..11 80	gap2	ATCEA4 C67921 _1	98					g42205 24	79	189	2.9e- 19	dopsis thalia na]
143063	ATU005 003	ATL8C3 2529:3 8..604	gap2	ATCEA4 C82710 _1	98	ATL8C3 2529:7 8..507	0.99	g97429 4	78	276	1.6e- 29	(U3130 9) LP6 [Pinus taeda]		
143064	ATU005 004	ATL8C1 1368:1 ..696	gap2	ATCEA4 C64057 _1, ATCEA4 S32919	98, 88	ATL8C1 1368:9 5..555	0.98	g40975 49	78	369	3.1e- 26	(U6490 7) ATFP4 [Arabi dopsis thalia na]		
143065	ATU005 005	ATL8C4 2728:1 488..2 04	gap2	ATCEA4 C96381 _1, ATCEA4 S31153 , ATCEA4 C29018 _1	98, 84 88, 84	ATL8C4 2728:1 280..3 38	0.97	g41551 28	78	150	2.2e- 07	(AE001 491) putati ve 3- HYDROX YACID DEHYDR OGENAS E [Helic obacte r pylori J99]		
143066	ATU005 006	ATL8C2 097:11 79..28 1	gap2	ATCEA4 C11852 9.1, ATCEA4 C30815 _1	98, 84	ATL8C2 097:11 76..42 5	0.73	g26699 1	78	127	0.29	SPLICI NG FACTOR , ARGINI NE/SER		

143067	ATU005 007	ATL8C2 2353:5 967..2 416	gap2	ATCEA4 S30293 , ATCEA4 S10883 , ATCEA4 C5338_1	98, 96 97, 96	ATL8C2 2353:5 909..2 416	0.48	g28656 23	78	1182	3.7e- 117	INE- RICH 2 (SPLIC ING FACTOR SC35) (SC- 35) (SPLIC ING COMPON ENT, 35 KD) (PR264 PROTEI N) [Gallu s gallus]
143068	ATU005 008	ATL8C1 4194:1 251..3 53	gap2	ATCEA4 C156_7 , ATCEA4 C74359 _1	98, 95	ATL8C1 4194:1 165..5 12	0.46	g22534 42	78	189	3.9e- 07	(AF007 784) LTCOR1 1 [Lavata era thurin giaca]

143069	ATU005 009	ATL8C3 8048:1 211..6 49	gap2	ATCEA4 C23252 _1	98				g42396 92	78	924	3.1e- 92	(AJ132 745) hypoth etical protein [Arabi dopsis thalia na]
143070	ATU005 010	ATL8C2 857:25 00..1	gap2	ATCEA4 S1735, ATCEA4 S31091	98, 97	ATL8C2 857:24 78..15 6	0.98		g41063 95	77	2119	3.0e- 235	(AF073 744) raffin ose syntha se [Cucum is sativu s]
143071	ATU005 011	ATL8C1 5896:2 058..1	gap2	ATCEA4 C11699 _1, ATCEA4 S32009 , ATCEA4 C74184 _1, ATCEA4 S24358 , ATCEA4 C22468 _1	98, 95, 92, 89, 83	ATL8C1 5896:1 965..8 7	0.87		g48503 85	77	1240	1.5e- 112	(AC007 357) EST gb T22 808 comes from this gene. [Arabi dopsis thalia na]
143072	ATU005 012	ATL8C4 5507:1 335..3 508	gap2	ATCEA4 C61487 _1	98	ATL8C4 5507:1 335..3 038	0.86		g42205 14	77	833	5.0e- 76	(AL035 356) putati ve protein [Arabi dopsis thalia na]

143073	ATU005 013	ATL8C4 8109:2 691..1	gap2	ATCEA4 S36311	98		ATL8C4 8109:2 684..4 98	0.81	g39158 14	77	1403	3.2e- 130	PP1/PP 2A PHOSPH ATASES PLEIOT ROPIC REGULA TOR. PRL2 [Arabi dopsis thalia na]
143074	ATU005 014	ATL8C3 8500:2 574..1 71	gap2	ATCEA4 C43521 1, ATCEA4 S33182 , ATCEA4 C33172 1, ATCEA4 C74774 1, ATCEA4 C54781 1, ATCEA4 S28602	98, 97, 97, 96, 93, 82		ATL8C3 8500:2 227..4 61	0.70	g37863 24	77	861	8.1e- 81	(AB015 139) chloro phylla oxygen ase [Chlam ydomon as reinha rdtii]
143075	ATU005 015	ATL8C9 567:19 31..25 1	gap2	ATCEA4 S3987, ATCEA4 C12627 81, ATCEA4 C18045 1	98, 92, 89		ATL8C9 567:17 00..86 8	0.40	g21440 98, g45072 01	77, 63	384, 110	7.8e- 43, 2.2e- 09	SC2 - rat [Rattus sp.]; steroid-5- alpha- reductase, alpha polypeptide 1 (3-oxo-5

143076	ATU005 016	ATL8C4 16:269 5..474	gap2	ATCEA4 C28657 1, ATCEA4 C14102 1_	98, 98					g19463 55	77	1545	1.1e- 155	(U9321 5) maize transp oson MuDR mudrA protei n isolog [Arabi dopsis thalia na]	alpha- steroi d delta 4- dehydr ogenas e alpha 1) [Homo sapien s]
143077	ATU005 017	ATL8C3 4688:1 475..1	gap2	ATCEA4 C2978_1, ATCEA4 C92318 1_	98, 96	ATL8C3 4688:1 466..1 62	0.96			g16532 45	76	208	2.6e- 13	(D9091 2) hypoth etical protei n [Synec hocyst is sp.]	(D9091 2) hypoth etical protei n [Synec hocyst is sp.]
143078	ATU005 018	ATL8C3 296:35 28..16 8	gap2	ATCEA4 C6475_1, ATCEA4 C96948 1, ATCEA4 S20250	98, 92 94, 92	ATL8C3 296:32 81..13 55	0.95			g45593 53, g45593 51	76, 33	1627, 655	1.6e- 69, 6.2e- 90	(AC006 585) putati ve extrag enic suppre ssor	(AC006 585) putati ve extrag enic suppre ssor

143079	ATU005 019	ATL8C2 3787:1 ..2539	gap2	ATCEA4 S3420, ATCEA4 S29654 , ATCEA4 S34676 , ATCEA4 S31423 , ATCEA4 C15106 9_1	98, 95, 91, 90, 89	ATL8C2 3787:4 8..242 6	0.94	g17070 32	76	1285	1.2e- 124	protein [Arabis dopsis thaliana] ; (AC006 585) hypoth etical protein [Arabis dopsis thaliana] (U8044 5) coded for by C. elegans cDNA yk13g5 .3; coded for by C. elegans cDNA yk21g6 .3; coded for by C. elegans cDNA CEMSE1 8F; coded for by C. elegans cDNA yk126b
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143080	ATU005 020	ATL8C3 0770:3 452..5 83	gap2	ATCEA4 S983, ATCEA4 S31993	98, 94	ATL8C3 0770:3 095..8 58	0.76	g44540 11	76	1994	7.0e- 171	AL035 (396) putati ve protei n [Arabi dopsis thalia na]	1.3; coded for by C. elegan s cDNA yk65h8 .3; coded for by C. elegan s cDNA yk65h8 []
143081	ATU005 021	ATL8C1 479:14 24..32 3	gap2	ATCEA4 C12825 2, ATCEA4 C12825 3, ATCEA4 S13247	98, 95, 88	ATL8C1 479:14 18..32 8	0.72	g34200 55	76	659	2.7e- 49	(AC004 680) cyclop hilin [Arabi dopsis thalia na]	
143082	ATU005 022	ATL8S2 5698:5 03..1	gap2	ATCEA4 S34298 , ATCEA4 C115_2 , ATCEA4 S2594, ATCEA4 S13614	98, 98, 95, 90	ATL8S2 5698:4 12..14 5	0.64	g10766 78	76	287	3.4e- 32	ubiqui tin / riboso mal protei n S27a - potato (fragm ent) []	

143083	ATU005 023	ATL8C3 8903:3 082..2 9	gap2	ATCEA4 C32479 1, ATCEA4 S14608 , ATCEA4 C80058 1, ATCEA4 S33098	98, 97, 97, 95	ATL8C3 8903:3 012..1 93	0.61	g18144 01	76	851	1.5e- 79	(U8488 8) phospho glucosyl mutase [Mesembryanthemum crystallinum]
143084	ATU005 024	ATL8C4 5099:6 76..17 49	gap2	ATCEA4 S1527, ATCEA4 S34028 , ATCEA4 S648, ATCEA4 C13839 1 1	98, 95, 93, 92	ATL8C4 5099:7 87..16 96	0.55	g38941 91	76	681	9.2e- 49	(AC005 662) unknown protein [Arabidopsis thaliana]
143085	ATU005 025	ATL8C1 5953:2 370..4 48	gap2	ATCEA4 C11816 3_1	98	ATL8C1 5953:2 370..7 39	0.53	g43357 64	76	1339	4.1e- 149	(AC006 284) putative WRKY DNA- binding protein [Arabidopsis thaliana]
143086	ATU005 026	ATL8S1 6095:1 ..510	gap2	ATCEA4 S5492, ATCEA4 C21462 _1	98, 95			g37694 72	76	277	3.4e- 28	(AF064 732) putative phospholipase A2 [Dianthus caryophyllus]

143087	ATU005 027	ATL8C4 4492:1 054..2 819	gap2	ATCEA4 C27399 _1	98					g17233 78	76	221	1.8e- 22	HYPOTH ETICAL 28.1 KD PROTEI N IN CARA- YCF30 INTERG ENIC REGION (ORF23 8) [Porph yra purpur ea]
143088	ATU005 028	ATL8C2 1350:9 69..1	gap2	ATCEA4 C229_1 , ATCEA4 C229_2	98, 95	ATL8C2 1350:7 28..31 8	0.99			g22857 92	75	523	4.6e- 55	(AB004 568) cyanas e [Arabi dopsis thalia na]
143089	ATU005 029	ATL8C4 820:45 89..13 27	gap2	ATCEA4 C81705 _1, ATCEA4 C6295 _1	98, 98	ATL8C4 820:43 93..24 92	0.94			g46783 62	75	803	1.2e- 79	(AL049 659) protei n kinase -like protei n [Arabi dopsis thalia na]
143090	ATU005 030	ATL8C1 5645:1 ..495	gap2	ATCEA4 C11623 9_1	98	ATL8C1 5645:1 45..26 0	0.92			g44552 35	75	218	0.0092	(AL035 523) PROTEI N TRANSP ORT

143091	ATU005 031	ATL8C3 122:1. .1058	gap2	ATCEA4 C24919 1, ATCEA4 C11790 0_1	98, 86	ATL8C3 122:76 ..963	0.89	g18711 76	75	723	4.0e- 35	(U9043 9) unknown protein [Arabi dopsis thalia na]
143092	ATU005 032	ATL8C4 9936:1 ..918	gap2	ATCEA4 C39322 1_1	98	ATL8C4 9936:3 65..90 6	0.78	g37383 24	75	641	5.3e- 55	(AC005 170) GMP syntha se- like protein [Arabi dopsis thalia na]
143093	ATU005 033	ATL8C9 30:1.. 1534	gap2	ATCEA4 C9727_1	98	ATL8C9 30:216 ..1431	0.76	g30470 85	75	1211	2.9e- 78	(AF058 914) No defini tion line found [Arabi dopsis thalia na]
143094	ATU005 034	ATL8C1 4239:1	gap2	ATCEA4 S14007	98	ATL8C1 4239:2	0.74	g11761 26	75	190	4.5e- 07	HYPOTH ETICAL

143095	ATU005 035	ATL8C4 5069:8 15..1	gap2	ATCEA4 C21833 _1	98					05..16 73									35.8 KD PROTEI N IN EBGC- UXAA INTERG ENIC REGION [Esche richia coli]
143096	ATU005 036	ATL8C1 2605:1 428..4 065	gap2	ATCEA4 S740, ATCEA4 S1246	98, 98														(AC006 283) unknow n protei n [Arabi dopsis thalia na]
143097	ATU005 037	ATL8C3 6842:2 173..1	gap2	ATCEA4 C34725 _1, ATCEA4 C19441 _1	98, 97														(AF120 335) putati ve transp osase [Arabi dopsis thalia na]

143098	ATU005 038	ATL8C2 4698:1 ..2292	gap2	ATCEA4 S1451, ATCEA4 S22358 , ATCEA4 C31884 1, ATCEA4 C9443_1	98, 98, 87, 82	ATL8C2 4698:4 6..150 5	0.91	g40068 29	74	670	5.6e- 73	sapien s] (AC005 970) putati ve protei n kinase [Arabi dopsis thalia na]
143099	ATU005 039	ATL8C5 043:56 3..1	gap2	ATCEA4 S5308	98	ATL8C5 043:49 0..223	0.91	g45875 51	74	128	1.1e- 12	(AC006 577) F15I1. 18 [Arabi dopsis thalia na]
143100	ATU005 040	ATL8C1 3224:1 ..1792	gap2	ATCEA4 C1679_1	98	ATL8C1 3224:1 91..11 47	0.85	g34210 96	74	713	1.0e- 42	(AF043 528) 20S protea some subuni t PAGL [Arabi dopsis thalia na]
143101	ATU005 041	ATL8C2 2017:1 661..4 20	gap2	ATCEA4 S7006	98	ATL8C2 2017:1 514..6 03	0.79	g45875 33	74	196	1.5e- 09	(AC007 060) EST gb AA7 21821 comes from this gene. [Arabi dopsis thalia na]

143102	ATU005 042	ATL8C4 8771:7 46..1	gap2	ATCEA4 C4366_3, ATCEA4 C4366_1, ATCEA4 S26016	98, 89 90, 89	ATL8C4 8771:6 69..20	0.66	g44067 66	74	609	2.4e- 55	(AC006 836) putati ve flavon ol sulfot ransfe rase [Arabi dopsis thalia na]
143103	ATU005 043	ATL8C4 3859:1 ..1935	gap2	ATCEA4 S8909, ATCEA4 C18290 1, ATCEA4 S15962 , ATCEA4 S3492	98, 93, 89, 88	ATL8C4 3859:1 90..18 10	0.64	g37219 26	74	2028		(AB017 480) chloro plast FtSH protea se [Nicot iana tabacu m]
143104	ATU005 044	ATL8C4 45:176 ..3734	gap2	ATCEA4 S29851 , ATCEA4 S29850	98, 97	ATL8C4 45:126 2..361 7	0.51	g38343 04, g45389 17	74, 56	400, 212	1.2e- 29, 0.0002 2	(AC005 679) Contai ns simila rity to [Arabi dopsis thalia na]; (AL049 482) putati ve protei n [Arabi dopsis thalia na]

143105	ATU005 045	ATL8C1 0628:1 970..1 94	gap2	ATCEA4 C27091 1, ATCEA4 C1779 1	98, 86	ATL8C1 0628:1 827..1 94	0.97	g33090 86	73	517	(AF076 253) calcin eurin B-like protei n 3 [Arabi dopsis thalia na]
143106	ATU005 046	ATL8C4 8175:2 91..34 37	gap2	ATCEA4 C15157 1, ATCEA4 S19926 , ATCEA4 C82830 1, ATCEA4 S554	98, 96, 95, 89	ATL8C4 8175:2 97..32 74	0.89	g34508 42	73	1358	(AF080 436) mitoge n activa ted protei n kinase kinase [Oryza sativa]
143107	ATU005 047	ATL8C1 3106:2 142..1	gap2	ATCEA4 S4910	98	ATL8C1 3106:2 026..6 6	0.89	g28282 88	73	1661	(AL021 687) replac ation A protei n-like [Arabi dopsis thalia na]
143108	ATU005 048	ATL8C4 3057:5 43..24 31	gap2	ATCEA4 C6779 1, ATCEA4 C24079 1	98, 92	ATL8C4 3057:6 95..22 26	0.86	g37860 05	73	1312	(AC005 499) putati ve phosph oethan olamin e cytidy lyltra

143109	ATU005 049	ATL8C2 9122:1 072..1	gap2	ATCEA4 C51892 1, ATCEA4 C22398 _1	98, 97	ATL8C2 9122:1 034..8 2	0.84	g40068 48	73	452	1.7e- 52	nsfera se [Arabi dopsis thalia na]
143110	ATU005 050	ATL8C4 2743:1 343..1	gap2	ATCEA4 S6687, ATCEA4 C3524_1	98, 98	ATL8C4 2743:1 319..1 36	0.81	g31579 41	73	397	2.5e- 34	(AJ131 433) seleno cystei ne methyl transf erases [Astra galus bisulc atus]
143111	ATU005 051	ATL8C6 507:20 30..18 9	gap2	ATCEA4 S14816	98	ATL8C6 507:20 30..11 57	0.77	g38785 70	73	677	3.2e- 57	(Z4638 1) simila r to lipoic acid

143113	ATU005 053	ATL8C1 2615:1 ..1395	gap2	ATCEA4 C7389_1, ATCEA4 S34590	98, 94	ATL8C1 2615:9 7..129 7	0.94	g27958 05	72	1179	6.9e- 125	n [Arabi dopsis thalia na]
143114	ATU005 054	ATL8C2 9269:3 375..1 259	gap2	ATCEA4 S29380 , ATCEA4 S33215 , ATCEA4 S26888 , ATCEA4 S28161 , ATCEA4 S32482 , ATCEA4 S34087	98, 95, 94, 90, 90, 89	ATL8C2 9269:3 375..1 631	0.93	g43357 64	72	1032	5.3e- 104	(AC006 284) putati ve WRKY DNA- bindin g protei n [Arabi dopsis thalia na]
143115	ATU005 055	ATL8C7 494:1. ..1129	gap2	ATCEA4 C18158 _1	98	ATL8C7 494:35 4..112 9	0.76	g21314 92, g28276 23	72, 67	250, 181	9.8e- 10, 7.5e- 10	hypoth etical protei n YDR438 w - yeast (Sacch aromyc es cerevi siae)

143116	ATU005056	ATL8C2 9905:3 484..1	gap2	ATCEA4 C78558 1, ATCEA4 C50673 1, ATCEA4 S36139 , ATCEA4 S5402	98, 98, 97, 82	ATL8C2 9905:3 369..1 0	0.75	g44159 12, g33675 68	72, 46	876, 624	5.3e- 67, 1.3e- 60	(AC006 282) putative protease [Arabidopsis thaliana]
143117	ATU005057	ATL8C2 742:68 3..151 3	gap2	ATCEA4 C4460 1	98	ATL8C2 742:68 3..149 8	0.72	g22450 87	72	336	1.3e- 31	(Z9734 3) hypothetical protein [Arabidopsis thaliana]

143118	ATU005 058	ATL8C4 8458:5 59..25 14	gap2	ATCEA4 S17997 , ATCEA4 C8502_1	98, 96	ATL8C4 8458:7 54..24 03	0.69	g41851 39	72	1408	3.8e- 148	thalia na] (AC005 724) putati ve diacyl glycer ol kinase [Arabi dopsis thalia na]
143119	ATU005 059	ATL8C1 0925:7 86..42 56	gap2	ATCEA4 C23312 _1, ATCEA4 C19301 _1, ATCEA4 C95398 _1, ATCEA4 S22055 , ATCEA4 S22053	98, 98, 95, 93, 91	ATL8C1 0925:3 135..4 256, ATL8C1 0925:1 068..2 676	0.58, 0.96	g42042 81	72	320	8.1e- 24	(AC004 146) Hypoth etical protei n [Arabi dopsis thalia na]
143120	ATU005 060	ATL8C1 2284:1 ..1104	gap2	ATCEA4 C24362 _1	98	ATL8C1 2284:1 090..7 4	0.56	g42040 95, g22583 21	72, 40	825, 118	5.4e- 83, 1.4e- 08	(AF030 260) CYP94A 1 [Vicia sativa]; (AF005 475) cytoch rome P450 [Phane rochae te chryso sporiu

143121	ATU005 061	ATL8C2 874:26 90..1	gap2	ATCEA4 S10946	98	ATL8C2 874:26 90..12 1	0.56	g35401 82	72	269	1.9e- 22	m] (AC004 122) Unknown protein [Arabi dopsis thalia na]
143122	ATU005 062	ATL8C3 8404:1 424..1	gap2	ATCEA4 C31101 1, ATCEA4 C31880 2, ATCEA4 C31880 1	98, 95, 95	ATL8C3 8404:1 424..8 61	0.54	g14953 66	72	505	2.4e- 46	(Z6937 0) nitrit e transp orter [Cucum is sativu s]
143123	ATU005 063	ATL8C1 6656:2 213..2 36	gap2	ATCEA4 C11837 4 1, ATCEA4 C67366 1	98, 96	ATL8C1 6656:2 128..4 98	0.51	g25586 60	72	197	6.2e- 21	(AC002 354) No defini tion line found [Arabi dopsis thalia na]
143124	ATU005 064	ATL8C4 3357:8 67..21 13	gap2	ATCEA4 S3531, ATCEA4 C4592 1, ATCEA4 C82061 3	98, 96, 85	ATL8C4 3357:8 67..19 67	0.45	g44907 28	72	303		(AL035 709) putati ve protei n [Arabi dopsis thalia na]
143125	ATU005 065	ATL8C1 2454:1	gap2	ATCEA4 C10986	98			g33866 18	72	377	2.4e- 48	(AC004 665)

143126	ATU005 066	..781	gap2	ATCEA4 S36064 , ATCEA4 C483_1 , ATCEA4 S15306	98, 91, 90				g28268 82	72	190		hypothetical protein [Arabidopsis thaliana]
143127	ATU005 067	ATL8C2 0104:8 37..12 81	gap2	ATCEA4 S7790	98				g45444 64	72	545	4.0e-60	(AJ223634) transcrip- tion factor IIA small subunit [Arabidopsis thaliana]
143128	ATU005 068	ATL8C3 91:128 0..248 7	gap2	ATCEA4 C12108 _1	98				g40084 41	71	334	2.0e-35	(AC006580) puta- tive chlo- roplast nucleo- id DNA bindin- g protei- n [Arabi- dopsis thalia- na]
		ATL8C4 7278:1 953..1	gap2	ATL8C4 7278:1 917..2 06									(AL034488) predic- ted using GeneFi- nder;

143129	ATU005 069	ATL8C6 092:56 1..138 1	gap2	ATCEA4 C23205 _1	98	ATL8C6 092:77 4..130 5	0.96	g48039 60	71	295	1.5e- 33	(AC006 202) putati ve carbon ic anhydr ase	CDNA EST yk433c 6.3 comes from this gene; CDNA EST EMBL:D 72601 comes from this gene; CDNA EST EMBL:D 75524 comes from this gene; CDNA EST EMBL:D yk433c 6.5 comes from this gene [Caeno rhabdi tis elegan s]
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143130	ATU005 070	ATL8C1 4187:1 288..1	gap2	ATCEA4 S16104 , ATCEA4 C70221 _1	98, 82	ATL8C1 4187:1 236..8 8	0.95	g32491 05	71	1256	3.1e- 130	[Arabi dopsis thalia na] (AC003 114) Contai ns simila rity to protei n phosph atase 2C (ABI1) gb X78 886 from A. thalia na. [Arabi dopsis thalia na]
143131	ATU005 071	ATL8C4 5366:1 ..1990	gap2	ATCEA4 C13437 7_1, ATCEA4 C12130 7_1, ATCEA4 C57918 1, ATCEA4 S29530	98, 98, 98, 92	ATL8C4 5366:9 4..197 5	0.91	g42403 05	71	108	2.2e- 07	(AB020 715) KIAA09 08 protei n [Homo sapien s]
143132	ATU005 072	ATL8C3 3614:1 ..3949	gap2	ATCEA4 C23567 1, ATCEA4 C11673 9_1	98, 95	ATL8C3 3614:6 70..35 33	0.82	g13488 9	71	342	1.0e- 27	SIGNAL RECOGN ITION PARTIC LE 68 KD PROTEI

143133	ATU005 073	ATL8C7 785:27 2..198 6	gap2	ATCEA4 C6538_1	98	ATL8C7 785:46 1..193 6	0.66	g45809 53	71	944	4.8e- 84	N (SRP68) [Canis famili aris]
143134	ATU005 074	ATL8C3 8879:1 ..950	gap2	ATCEA4 S6311	98	ATL8C3 8879:1 81..95 0	0.47	g22448 97	71	744	1.1e- 75	(AF117 734) glycer ol kinase -like protei n 2 [Mus muscul us]
143135	ATU005 075	ATL8C1 4005:1 905..1	gap2	ATCEA4 C18562 1, ATCEA4 S20786 , ATCEA4 C4566_1	98, 94, 93			g32128 66	71	284	2.1e- 29	(AC004 005) unknow n protei n [Arabi dopsis thalia na]
143136	ATU005 076	ATL8C1 3269:1 647..1	gap2	ATCEA4 S29709 , ATCEA4 S29708	98, 94	ATL8C1 3269:1 607..7 3	0.99	g38764 68	70	188	5.0e- 17	(Z8107 1) Simila rity to Human Mached O-

143137	ATU005 077	ATL8C1 1424:1 983..1 075	gap2	ATCEA4 C87_1	98	ATL8C1 1424:1 905..1 212	0.97	g72910 2	70	697	1.1e- 61	CHALCO NE-- FLAVON ONE ISOMER ASE [Arabi dopsis thalia na]	Joseph diseas e protei n 1 (SW:P5 4252); cDNA EST EMBL:C 08437 comes from this gene [Caeno rhabdi tis elegan s]
143138	ATU005 078	ATL8C4 6646:1 ..2023	gap2	ATCEA4 C1411_1	98	ATL8C4 6646:4 93..16 81	0.97	g17781 41	70	1071	1.4e- 81	(U6632 1) phosph ate/ph osphoe nolpyr uvate transl ocator precu sor; PPT [Arabi dopsis thalia	

143143	ATU005 083	ATL8C3 1423:1 ..2425	gap2	ATCEA4 C67015 1, ATCEA4 C48992 1_	98, 83	ATL8C3 1423:9 4..237 9	0.57	g38190 99	70	807	2.2e- 82	[Oryza sativa] (AJ009 825) copper amine oxidas e [Cicer arieti num]
143144	ATU005 084	ATL8C1 4551:9 44..15 2	gap2	ATCEA4 S26834 , ATCEA4 C11629 1_1	98, 97	ATL8C1 4551:7 59..15 2	0.49	g31933 18	70	605	2.7e- 47	(AF069 299) No defini tion line found [Arabi dopsis thalia na]
143145	ATU005 085	ATL8C2 10:197 2..1	gap2	ATCEA4 S2040, ATCEA4 C3928_2	98, 83	ATL8C2 10:128 2..38	0.47	g13533 52	70	871	1.3e- 83	(U3197 5) alanin e aminot ransfe rase [Chlam ydomon as reinha rdtill]
143146	ATU005 086	ATL8C3 7893:1 ..1986	gap2	ATCEA4 C24866 2, ATCEA4 C24866 1, ATCEA4 S18192	98, 87 95, 87	ATL8C3 7893:1 68..17 31	0.88	g45444 32	69	760	2.2e- 57	(AC006 955) putati ve mannos e-1- phosph ate guanyl transf

143147	ATU005 087	ATL8C5 406:44 27..1	gap2	ATCEA4 C7378_1, ATCEA4 S4929, ATCEA4 C96372 _1	98, 95, 95, 95	ATL8C5 406:42 81..33	0.70	g34027 13	69	776	5.1e- 55	erase [Arabi dopsis thalia na]
143148	ATU005 088	ATL8C1 9364:1 247..1	gap2	ATCEA4 C812_1 , ATCEA4 S4357	98, 83	ATL8C1 9364:1 210..2 9	0.69	g21467 28, g32942 46	69, 60	1381, 121	9.0e- 134, 5.3e- 07	cyclin cyc1b - Arabid opsis thalia na [Arabi dopsis thalia na]; (AL031 031) putati ve transc riptio nal regula tor [Strep tomyce s coelic olor]
143149	ATU005 089	ATL8C2 0258:4 603..1	gap2	ATCEA4 C10057 _1, ATCEA4 C10057	98, 95, 94, 93, 92,	ATL8C2 0258:4 285..3 4	0.44	g21911 40	69	292	9.6e- 09	(AF007 269) contai ns weak

143150	ATU005 090	ATL8C1 387:30 2..394 5	gap2	3, ATCEA4 S34845 , ATCEA4 S14400 , ATCEA4 C66932 1, ATCEA4 S1914, ATCEA4 S15908	91, 90	ATL8C1 387:20 90..32 4	0.44	g42630 63, g42630 62	69, 63	1561, 446	5.4e- 139, 3.0e- 44	(AC005 142) hypoth etical protein [Arabi dopsis thalia na]; (AC005 142) hypoth etical protein [Arabi dopsis thalia na]
143151	ATU005 091	ATL8C3 6852:9 63..1	gap2	ATCEA4 S14063	98			g45811 52	69	695	1.4e- 61	(AC006 919) hypoth etical protein [Arabi dopsis thalia na]
143152	ATU005	ATL8C1	gap2	ATCEA4	98			g41159	69	506	6.4e-	(AF118

092	3648:5 67..11 03		C37453 _1					35				32	223) contai ns simila rity to Helico bacter pylori peptid e methio nine sulfox ide reduct ase (msrA) (GB:AE 000542) [Arabi dopsis thalia na]
143153	ATU005 093	ATL8C9 09:104 0..473	gap2	ATCEA4 C26232 _1	98			g17698 91	69	211	3.1e- 19	(X9974 7) bZIP transc riptio n factor [Arabi dopsis thalia na]	
143154	ATU005 094	ATL8C3 3818:1 364..1	gap2	ATCEA4 C11805 9_1, ATCEA4 C11236 2_1	98, 95	ATL8C3 3818:1 184..8 2	0.78	g41546 67	68	195		(AE001 454) FRUCTO SE- BISPHO SPHATE ALDOLA SE [Helic	

143155	ATU005 095	ATL8C3 2290:3 094..1	gap2	ATCEA4 S7232, ATCEA4 S325, ATCEA4 S26097 , ATCEA4 S4727	98, 96, 93, 86	ATL8C3 2290:2 794..7 64	0.76	g45804 62	68	1061	9.3e- 106	obacter pylori J99]
143156	ATU005 096	ATL8C4 9063:2 043..1	gap2	ATCEA4 S5183	98	ATL8C4 9063:1 852..9 4	0.76	g45393 51	68	832	3.8e- 74	(AL035 539) putative protein [Arabi dopsis thalia na]
143157	ATU005 097	ATL8C3 5195:2 81..15 75	gap2	ATCEA4 S8062	98	ATL8C3 5195:3 97..15 16	0.71	g27608 32	68	374	1.9e- 22	(AC003 105) similar to barley ids-4 gene produc t [Arabi dopsis thalia na]
143158	ATU005 098	ATL8C1 605:94 9..1	gap2	ATCEA4 C75488 1, ATCEA4 C34841 1	98, 91	ATL8C1 605:94 3..114	0.67	g21328 42	68	306	2.8e- 22	probab le membra ne protei n YOL077 C -

143159	ATU005 099	ATL8C1 1882:1 ..1754	gap2	ATCEA4 C16126 1, ATCEA4 C16126 3	98, 94	ATL8C1 1882:5 0..167 5	0.66	g35229 57	68	2673	1.3e- 258	Yeast (Sacch aromyc es cerevi siae) [Sacch aromyc es cerevi siae] (AC004 411) unknow n protei n [Arabi dopsis thalia na]
143160	ATU005 100	ATL8C3 6559:1 164..1	gap2	ATCEA4 C21891 1, ATCEA4 C28795 1	98, 93	ATL8C3 6559:9 96..21 1	0.63	g24594 32	68	601	1.5e- 60	(AC002 332) CONSTA NS- like protei n [Arabi dopsis thalia na]
143161	ATU005 101	ATL8C1 9314:7 93..15 56	gap2	ATCEA4 C26392 3	98	ATL8C1 9314:9 64..12 98	0.61	g38927 12	68	499	4.4e- 47	(AL033 545) adenin e phosph oribos yltran sferas e (EC 2.4.2. 7)- like protei

143162	ATU005 102	ATL8C3 7707:2 021..1	gap2	ATCEA4 C4068_1	98	ATL8C3 7707:2 021..2 3	0.53	g40068 81	68	611	1.5e- 49	n [Arabi dopsis thalia na] (Z9970 7) putati ve protei n [Arabi dopsis thalia na]
143163	ATU005 103	ATL8C3 7279:1 ..1167	gap2	ATCEA4 S1163	98	ATL8C3 7279:2 60..11 13	0.41	g49491 8	68	33		Lipase (E.C.3 .1.1.3) (Triac ylglyc erol Hydroli ase) Comple xed With N- Hexylp hospho nate Ethyl Ester []
143164	ATU005 104	ATL8C3 4558:1 056..1	gap2	ATCEA4 C26438 1, ATCEA4 C27564 1_	98, 87			g24942 75	68	272	2.4e- 29	ELONGA TION FACTOR P (EF- P) [Synec hococc us PCC794 2]
143165	ATU005	ATL8C2	gap2	ATCEA4	98			g45126	68	763		(AC006

105	7352:1 ..2443		S2881					98				569) hypoth etical protei n [Arabi dopsis thalia na]
143166	ATU005 106	ATL8C3 5172:1 420..1	gap2	ATCEA4 S21339 , ATCEA4 C925_1 , ATCEA4 S10094	98, 97 93, 82	ATL8C3 5172:9 71..10 0	0.95	g10764 02	67	649	1.5e- 62	S-like ribonu clease RNS2 - Arabid opsis thalia na []
143167	ATU005 107	ATL8C4 6268:2 124..1	gap2	ATCEA4 C29882 _1, ATCEA4 C90766 _1	98, 97	ATL8C4 6268:2 114..2 33	0.91	g38508 21	67	1323	1.1e- 125	(Y1835 0) U2 snRNP auxili ary factor , large subuni t [Nicot iana plumba ginifo lia]
143168	ATU005 108	ATL8C5 955:17 72..1	gap2	ATCEA4 C2222_1, ATCEA4 C14168 _2	98, 97	ATL8C5 955:15 84..13 4	0.88	g28282 96	67	1626		(AL021 687) RNase L inhibi tor [Arabi dopsis thalia na]
143169	ATU005 109	ATL8C1 6597:1 ..1750	gap2	ATCEA4 S30947	98, 95	ATL8C1 6597:1 93..13	0.87	g43236 40	67	397	1.4e- 35	(AF102 805) Peter

143170	ATU005 110	ATL8C2 1424:1 ..1485	gap2	ATCEA4 S33289	98, 98	ATL8C2 1424:1 39..10 25	0.82	g41851 31	67	379	3.7e- 40	Pan [Droso phila melano gaster] (AC005 724) putati ve zinc finger protei n [Arabi dopsis thalia na]
143171	ATU005 111	ATL8C2 9128:1 ..843	gap2	ATCEA4 C10486 _2	98	ATL8C2 9128:2 03..84 3	0.81	g48836 11	67	281	2.6e- 13	(AC006 922) putati ve farnes ylated protei n [Arabi dopsis thalia na]
143172	ATU005 112	ATL8C9 892:22 43..1	gap2	ATCEA4 S35120 , ATCEA4 S25631	98, 87	ATL8C9 892:21 67..10 85	0.63	g33193 71, g33193 73	67, 59	1503, 786	1.1e- 157, 3.6e- 72	(AF077 409) Simila r to pectin estera se; T24M8. 6 [Arabi dopsis thalia na]; (AF077 409)

143173	ATU005 113	ATL8C2 3785:3 963..1	gap2	ATCEA4 C6118_1	98	ATL8C2 3785:3 720..9 5	0.61	g45585 55	67	3751	0.0	No defini tion line found [Arabi dopsis thalia na] (AC007 138) hypoth etical protei n [Arabi dopsis thalia na]
143174	ATU005 114	ATL8C3 7054:1 ..1226	gap2	ATCEA4 C136_1	98	ATL8C3 7054:1 083..5 4	0.60	g39142 39	67	1247		PROTEI N PHOSPH ATASE 2C ABI2 (PP2C) [Arabi dopsis thalia na]
143175	ATU005 115	ATL8C3 2049:2 553..1	gap2	ATCEA4 C6826_1	98	ATL8C3 2049:1 803..4 5	0.56	g29207 06	67	713	3.8e- 66	(Y1356 8) beta- xylosi dase [Emeri cella . nidula ns]
143176	ATU005 116	ATL8C3 7952:1 540..1	gap2	ATCEA4 S12847	98	ATL8C3 7952:1 540..1 68	0.56	g30212 73	67	1584	1.0e- 141	(AL022 347) serine /threo nine kinase

143177	ATU005 117	ATL8C4 9029:8 41..1	gap2	ATCEA4 C21599 1, ATCEA4 C24855 1_	98, 90				g26233 11	67	273	5.5e- 31	- like protei n [Arabi dopsis thalia na]
143178	ATU005 118	ATL8C2 3367:2 952..1	gap2	ATCEA4 S1108, ATCEA4 S5052	98, 91				g15076 59, g24628 31	67, 55	63, 107	0.9999 1, 8.8e- 05	(D8324 1) Anther aea pernyi fibroi n [Anthe raea pernyi]; (AF000 657) hypoth etical protei n [Arabi dopsis thalia na]
143179	ATU005 119	ATL8C3 713:1. .1348	gap2	ATCEA4 S29950 , ATCEA4 S30650	98, 97	ATL8C3 713:21 4..110 0	0.94		g13516 76	66	498	1.9e- 27	PROBAB LE PEPTID YL- PROLYL CIS- TRANS

143180	ATU005 120	ATL8C3 2215:8 18..23 00	gap2	ATCEA4 S7704	98	ATL8C3 2215:8 27..22 23	0.93	g40564 37	66	1113	4.8e- 56	ISOMER ASE C21E11 .05C [Schiz osacch aromyc es pombe]
143181	ATU005 121	ATL8C2 2514:2 432..1 383	gap2	ATCEA4 C60010 2, ATCEA4 C60010 _1	98, 88	ATL8C2 2514:2 350..1 766	0.93	g28015 36	66	481	4.1e- 41	(AF039 531) lysoph osphol ipase homolo g [Oryza sativa]
143182	ATU005 122	ATL8C4 1831:3 373..1 631	gap2	ATCEA4 S10552	98	ATL8C4 1831:3 247..1 984	0.90	g45071 41	66	112	8.0e- 09	sortin g nexin 2 [Homo sapien]

143183	ATU005 123	ATL8C2 0612:3 439..8 74	gap2	ATCEA4 C676_1	98	ATL8C2 0612:3 425..1 208	0.90	g45593 39	66	1625	1.8e- 127	s] (AC007 087) putati ve ATP- depend ent RNA helica se [Arabi dopsis thalia na]
143184	ATU005 124	ATL8C2 817:76 ..1310	gap2	ATCEA4 S3204	98	ATL8C2 817:16 9..128 3	0.81	g28945 94	66	85	3.9e- 05	(AL021 889) hypoth etical protei n [Arabi dopsis thalia na]
143185	ATU005 125	ATL8C3 7662:1 ..1427	gap2	ATCEA4 C12207 6_1, ATCEA4 C89664 _1	98, 90	ATL8C3 7662:6 1..138 2	0.79	g40564 62	66	1512	4.2e- 168	(AC005 990) Strong simila rity to gb Y09 876 aldehy de dehydr ogenas e (NAD+) from Nicoti ana tabacu m and a

143186	ATU005 126	ATL8C1 9028:7 83..32 22	gap2	ATCEA4 S27358	98	ATL8C1 9028:7 83..31 29	0.74	g29243 35	66	537	6.7e- 59	member of the aldehy de dehydr ogenas e family PF1001 71. ESTs gb F15 117, gb R83 958 and gb 586 262 come from this gene. [Arabi dopsis thalia na]
143187	ATU005 127	ATL8C1 0378:1 734..1	gap2	ATCEA4 C14464 _1	98	ATL8C1 0378:1 589..7 1	0.73	g30436 94	66	332		(Y1641 4) Export in (tRN A) [Homo sapien s]
143188	ATU005 128	ATL8C3 5066:9	gap2	ATCEA4 S7949,	98, 97	ATL8C3 5066:8	0.66	g43097 36	66	853	6.3e- 84	(AB011 157) K1AA05 85 protei n [Homo sapien s] (AC006 439)

143189	ATU005 129	36..1	gap2	ATCEA4 C60730 _1	98, 92	18..10 0	0.64	g42042 93, g47419 27	66, 66	1470, 1203	7.1e- 116, 2.4e- 102	hypothetical protein [Arabidopsis thaliana] (AC003027) lcl pr t_seq No definition line found [Arabidopsis thaliana]; (AF130252) calcium dependent protein kinase CP4 [Arabidopsis thaliana]
143190	ATU005 130	ATL8C5 658:1. ..2367	gap2	ATCEA4 S10309 , ATCEA4 C35074 _1, ATCEA4 S8766	98, 85 97, 85	ATL8C5 658:73 9..217 1	0.62	g37382 98	66	171		(AC005309) unknown protein [Arabidopsis thaliana]

143191	ATU005 131	ATL8C2 9726:1 862..3 505	gap2	ATCEA4 S5219, ATCEA4 S6075, ATCEA4 S7135	98, 95 96, 95				g29110 73	66	239	8.6e- 20	(AL021 960) putati ve protei n [Arabi dopsis thalia na]
143192	ATU005 132	ATL8C4 8401:2 430..1 554	gap2	ATCEA4 C25730 _1	98				g15523 79	66	893	3.0e- 91	(Y0815 5) pectin methyl estera se [Silen e latifo lia ssp. alba]
143193	ATU005 133	ATL8S1 7354:3 96..1	gap2	ATCEA4 C37649 _1	98				g31504 07	66	415	6.2e- 35	(AC004 165) hypoth etical protei n [Arabi dopsis thalia na]
143194	ATU005 134	ATL8C1 9239:1 ..1525	gap2	ATCEA4 C6943 _1, ATCEA4 S6285	98, 95				g49271 90	66	1176	4.8e- 114	(AF133 659) ATP- bindin g casset te 7 iron transp orter [Homo sapien s]

143195	ATU005 135	ATL8C1 017:1. .1529	gap2	ATCEA4 C29436 1, ATCEA4 C34765 1_	98, 94	ATL8C1 017:16 7..104 5	0.98	g37765 63	65	936	3.0e- 107	(AC005 388) Strong simila rity to gb L04 680 5- epi- aristo lochen e syntha se from Nicoti ana tabacu m and delta cadine ne syntas e gb U88 318 from Gossy pium hirsut um. [Arabi dopsis thalia na]
143196	ATU005 136	ATL8C3 2014:4 11..26 23	gap2	ATCEA4 C1983 1	98	ATL8C3 2014:4 11..25 54	0.92	g12451 82	65	1181	4.5e- 121	(U4939 8) sterol delta- 7 reduct ase [Arabi dopsis thalia

143197	ATU005 137	ATL8C7 698:1. .1334	gap2	ATCEA4 C96318 _1	98	ATL8C7 698:63 ..1154	0.92	g43357 14	65	1519	4.2e- 216	na] (AC006 248) putati ve glucos yltran sferas e [Arabi dopsis thalia na]
143198	ATU005 138	ATL8C3 9344:4 71..19 65	gap2	ATCEA4 S26375 , ATCEA4 S10843 , ATCEA4 C31663 _1, ATCEA4 C79655 _1, ATCEA4 S10844 , ATCEA4 S14508	98, 94, 93, 89, 87, 82	ATL8C3 9344:4 74..15 23	0.91	g22528 63	65	501	1.6e- 46	(AF013 294) simila r to nucleo lin protei n [Arabi dopsis thalia na]
143199	ATU005 139	ATL8C1 4316:3 7..288 6	gap2	ATCEA4 S33303 , ATCEA4 C84220 _1	98, 93	ATL8C1 4316:3 7..232 8	0.87	g24080 68	65	388	7.5e- 29	(Z9916 5) hypoth etical protei n [Schiz osacch aromyc es pombe]
143200	ATU005 140	ATL8C4 8812:1 ..1010	gap2	ATCEA4 C60739 _1	98	ATL8C4 8812:1 01..97 2	0.84	g30687 14	65	161	2.6e- 11	(AF049 236) unknow n

143201	ATU005 141	ATL8C1 0547:3 61..18 09	gap2	ATCEA4 C8123_1, ATCEA4 C8123_2	98, 90	ATL8C1 0547:3 61..17 91	0.74	g36881 70	65	152	[Arabi dopsis thalia na]
143202	ATU005 142	ATL8C4 0173:2 93..65 6	gap2	ATCEA4 C19610 _1	98	ATL8C4 0173:2 97..65 6	0.70	g17033 94	65	335	ADP- RIBOSY LATION FACTOR -LIKE PROTEI N 5 [Rattu s norveg icus]
143203	ATU005 143	ATL8C4 90:44. .1329	gap2	ATCEA4 S35358 , ATCEA4 C61224 _1, ATCEA4 S34014	98, 92, 92, 92	ATL8C4 90:200 ..980	0.70	g48352 34	65	496	[AL049 862) putati ve cold acclim ation protei n [Arabi dopsis thalia na]
143204	ATU005 144	ATL8C4 2091:1 913..1	gap2	ATCEA4 S3505	98	ATL8C4 2091:1 802..6 0	0.69	g22752 01	65	1042	(AC002 337) unknow n protei n [Arabi

143205	ATU005. 145	ATL8C4 1902:1 ..1656	gap2	ATCEA4 C11803 _1, ATCEA4 C76039 _1	98, 98	ATL8C4 1902:1 18..14 39	0.68	g48270 60	65	624	9.7e- 76	dopsis thalia nal
143206	ATU005 146	ATL8C1 2358:1 ..701	gap2	ATCEA4 C78752 _1	98	ATL8C1 2358:1 52..28 6	0.50	g30634 68	65	306	6.2e- 27	(AC003 981) F22013 .30 [Arabi dopsis thalia nal]
143207	ATU005 147	ATL8C2 1931:1 113..4 62	gap2	ATCEA4 C86849 _1, ATCEA4 S19169	98, 84	ATL8C2 1931:8 18..67 7	0.96	g46626 33	64	65	0.97	(AC007 267) hypoth etical protei n [Arabi dopsis thalia nal]
143208	ATU005 148	ATL8C4 4083:5 295..1	gap2	ATCEA4 S5545, ATCEA4 S31639	98, 88	ATL8C4 4083:4 850..2 6	0.93	g11002 53	64	6509	0.0	(D3463 0) acetyl -CoA carbox ylase [Arabi dopsis thalia nal]
143209	ATU005 149	ATL8C1 1803:1 440..1	gap2	ATCEA4 S13494 _1	98, 83	ATL8C1 1803:1 331..1	0.92	g35488 02	64	855	4.8e- 94	(AC005 313) axi 1-

		46		ATCEA4 S12697		46						like protei n [Arabi dopsis thalia na]
143210	ATU005 150	ATL8C2 1625:1 087..2 323	gap2	ATCEA4 C43725 _1	98	ATL8C2 1625:1 104..2 241	0.91	g22135 92	64	773	1.0e- 81	(AC000 348) T7N9.1 2 [Arabi dopsis thalia na]
143211	ATU005 151	ATL8C4 4117:1 ..3535	gap2	ATCEA4 C2132_1	98	ATL8C4 4117:5 9..348 6	0.91	g23160 16	64	4377	0.0	(U9265 0), MRP- like ABC transp orter [Arabi dopsis thalia na]
143212	ATU005 152	ATL8S2 7934:5 70..1	gap2	ATCEA4 C6824_1	98	ATL8S2 7934:4 58..55	0.89	g35229 39	64	409	8.5e- 19	(AC004 411) putati ve squam osa- promot er bindin g protei n [Arabi dopsis thalia na]
143213	ATU005 153	ATL8C1 02:167 0..1	gap2	ATCEA4 S10962	98, 89	ATL8C1 02:130 1..57	0.82	g45726 71	64	1560	2.4e- 126	(AC006 954) putati

143214	ATU005 154	ATL8C1 5133:1 ..1635	gap2	ATCEA4 S630	98, 98 92, 84	ATL8C1 5133:3 3..150 2	0.81	g45390 05	64	374	2.3e- 25	ve cyclic nucleo tide regula ted ion channe l [Arabi dopsis thalia na]
143215	ATU005 155	ATL8C4 3525:2 561..1	gap2	ATCEA4 C10289 2..1, ATCEA4 S11864	98, 98	ATL8C4 3525:2 475..7 7	0.68	g22929 07	64	1975		(Y1009 9) P- glycop rotein homolo gue [Horde um vulgar e]
143216	ATU005 156	ATL8C4 1621:1 ..857	gap2	ATCEA4 C289_1	98	ATL8C4 1621:1 16..58 1	0.67	g73068 8	64	499	1.3e- 32	MITOCH ONDRIA L 40S RIBOSO MAL PROTEI N S19 PRECUR SOR [Arabi dopsis

143217	ATU005 157	ATL8C1 0738:1 ..1370	gap2	ATCEA4 S36255 , ATCEA4 S10433	98, 86	ATL8C1 0738:6 2..137 0	0.62	g42104 51	64	2003	2.6e- 164	thalia nal (AB016 472) ARR2 protei n [Arabi dopsis thalia nal]
143218	ATU005 158	ATL8C3 2682:1 712..1 50	gap2	ATCEA4 C98203 1, ATCEA4 C24219 _1	98, 95	ATL8C3 2682:1 587..4 01	0.61	g48369 48	64	591	2.7e- 65	(AC006 085) Simila r to human CGI-33 protei n [Arabi dopsis thalia nal]
143219	ATU005 159	ATL8C8 511:15 36..1	gap2	ATCEA4 C24421 1, ATCEA4 S16581 , ATCEA4 S4629	98, 86 95, 86	ATL8C8 511:13 85..14 9	0.51	g18711 92	64	1206	9.6e- 130	(U9043 9) Cys3Hi s zinc finger protei n isolog [Arabi dopsis thalia nal]
143220	ATU005 160	ATL8C4 2134:1 ..1222	gap2	ATCEA4 C17656 _1	98			g42401 69, g44328 60	64, 47	156, 103	3.1e- 12, 5.1e- 07	(AB020 647) KIAA08 40 protei n [Homo sapien sl]; (AC006

143221	ATU005 161	ATL8C1 3843:1 846..8 67	gap2	ATCEA4 S27137 , ATCEA4 S31963	98, 87						64	220	4.2e- 21	(AC005 679) F9K20. 25 [Arabi dopsis thalia na]	300) putati ve glucos e- induce d repres sor protei n [Arabi dopsis thalia na]
143222	ATU005 162	ATL8C1 8059:1 114..9 9	gap2	ATCEA4 C95336 1, ATCEA4 S21982	98, 85						64	1222	1.6e- 120	(AB016 819) UDP- glucos e glucos yltran sferas e [Arabi dopsis thalia na]	(AB016 819) UDP- glucos e glucos yltran sferas e [Arabi dopsis thalia na]
143223	ATU005 163	ATL8C1 4049:3 076..1	gap2	ATCEA4 C70140 1, ATCEA4 S5009, ATCEA4 C11425 5 1, ATCEA4	98, 98, 90, 86	ATL8C1 4049:1 354..2 1	0.98	g37902 52	63	91	0.20	(AL031 966) putati ve Zn- protea se [Schiz osacch aromyc	(AL031 966) putati ve Zn- protea se [Schiz osacch aromyc		

143224	ATU005 164	ATL8C7 250:1. .1454	gap2	C45961 1 ATCEA4 C21064 _1	98	ATL8C7 250:57 9..135 2	0.96	g32491 10	63	1157	1.8e- 82	es pombel (AC003 114) T12M4. 6 [Arabi dopsis thalia na]
143225	ATU005 165	ATL8C3 3254:7 44..1	gap2	ATCEA4 C15205 _1	98	ATL8C3 3254:6 92..14 1	0.93	g45443 69	63	467	2.2e- 48	(AC006 920) hypoth etical protei n [Arabi dopsis thalia na]
143226	ATU005 166	ATL8C2 4531:1 ..718	gap2	ATCEA4 C4087 _1	98	ATL8C2 4531:1 0..499	0.92	g34618 33	63	705	1.7e- 67	(AC004 138) putati ve expans in [Arabi dopsis thalia na]
143227	ATU005 167	ATL8C4 7715:2 233..1	gap2	ATCEA4 S350	98	ATL8C4 7715:2 024..3 46	0.89	g30045 52	63	1461	1.3e- 116	(AC003 673) unknow n protei n [Arabi dopsis thalia na]
143228	ATU005 168	ATL8C1 9261:8 95..1	gap2	ATCEA4 C12001 2_1	98	ATL8C1 9261:8 95..26 9	0.87	g22449 39	63	250	8.6e- 14	(Z9733 9) hypoth etical

143229	ATU005 169	ATL8C2 1575:1 156..1	gap2	ATCEA4 S18295 , ATCEA4 C74377 _1	98, 97	ATL8C2 1575:8 92..7	0.85	g10017 94	63	232	1.1e- 12	proteins [Arabidopsis thaliana]
143230	ATU005 170	ATL8C2 2144:1 181..1 869	gap2	ATCEA4 S5616	98	ATL8C2 2144:1 237..1 814	0.79	g45673 11	63	426	3.3e- 43	(AC005 956) putative protein kinase [Arabidopsis thaliana]
143231	ATU005 171	ATL8C4 8133:1 ..918	gap2	ATCEA4 S11658 , ATCEA4 C13982 6.1, ATCEA4 S11659	98, 94, 83	ATL8C4 8133:7 7..870	0.74	g35823 41	63	963	4.5e- 100	(AC005 496) putative flavonol 3- o- glucosyltran- sferase [Arabidopsis thaliana]
143232	ATU005 172	ATL8C1 9505:1 ..2397	gap2	ATCEA4 S2919	98	ATL8C1 9505:4 50..20	0.71	g22449 04	63	2001	5.9e- 165	(Z9733 9) similar

143233	ATU005 173	ATL8C2 3913:1 957..9 3	gap2	ATCEA4 S10667	98	ATL8C2 3913:1 113..9 7	0.55	g37471 07	63	50	0.0001 9	r to hypoth etical protei n C02F5. 7 - Caenor ha [Arabi dopsis thalia na]
143234	ATU005 174	ATL8C1 8383:1 ..2694	gap2	ATCEA4 C16943 1, ATCEA4 S34737	98, 90	ATL8C1 8383:3 ..2240	0.53	g45393 07, g38612 17	63, 57	303, 296	2.3e- 22, 2.1e- 15	(AF095 741) unknow n [Rattu s norveg icus] (AL049 480) putati ve acidic riboso mal protei n [Arabi dopsis thalia na]; (AJ235 272) UBIQUI NONE/M ENAUUI NONE BIOSYN THESIS METHLY TRANSF ERASE

143235	ATU005 175	ATL8C2 8708:1 ..593	gap2	ATCEA4 C17520 1, ATCEA4 C17520 2, ATCEA4 S34662 , ATCEA4 S25938	98, 96, 91, 89	ATL8C2 8708:8 9..425	0.43	g23885 78	63	555	5.7e- 54	UBIE (ubiE) [Ricke ttsia prowaz ekii] (AC000 098) Simila r to Mycoba cteri m RlpF (gb Z8 4395). ESTs gb T75 785,gb R3058 0,gb T 04698 come from this gene. [Arabi dopsis thalia na]
143236	ATU005 176	ATL8C2 6241:3 50..11 91	gap2	ATCEA4 C5173 1	98			g47551 89	63	1094	6.3e- 76	(AC007 018) putati ve cytoch rome P450 [Arabi dopsis thalia na]
143237	ATU005 177	ATL8C4 6998:2 303..7 11	gap2	ATCEA4 S30245 , ATCEA4 C21486	98, 85			g39414 24	63	231	6.4e- 21	(AF062 866) putati ve transc

143238	ATU005 178	ATL8C2 8210:6 63..11 8	gap2	ATCEA4 S22879	98						g19463 72	63	231	1.7e- 24	(U9321 5) yeast hypoth etical protei n YDB1_S CHPO_ isolog [Arabi dopsis thalia na]
143239	ATU005 179	ATL8C4 7081:2 645..1 525	gap2	ATCEA4 C89318 _1	98						g41159 36	63	165	4.6e- 10	(AF118 223) No defini tion line found [Arabi dopsis thalia na]
143240	ATU005 180	ATL8C4 7312:1 899..1	gap2	ATCEA4 S36304	98		ATL8C4 7312:1 899..5 0		0.93		g15652 23	62	1304	6.9e- 131	(Y0830 1) MCM2- relate d protei n [Arabi dopsis thalia na]
143241	ATU005 181	ATL8C3 9279:2	gap2	ATCEA4 S31628	98, 94, 85		ATL8C3 9279:2		0.92		g38325 28	62	366	1.6e- 33	(AF100 167)

143242	ATU005 182	ATL8C1 8646:3 09..18 02	gap2	ATCEA4 S2078, ATCEA4 S8009	98, 85	ATL8C1 8646:4 10..17 33	0.86	g33353 47	62	227	1.5e- 32	unknown [Glycine max]
				ATCEA4 C1071_2, ATCEA4 S9718		807..1 660						(AC004 512) Contai ns simila rity to ARI, RING finger protei n gb X98 309 from Drosop hila melano gaster . ESTs gb T44 383, gb W43 120, gb N65 868, gb H36 013, gb AA0 42241, gb T76 869 and gb AA0 42359 come from this

143243	ATU005 183	ATL8C4 6511:7 20..1	gap2	ATCEA4 C725_1	98	ATL8C4 6511:4 90..9	0.74	g32420 71	62	737	1.6e- 51	gene. [Arabi dopsis thalia na] (AJ007 289) myb- like protei n [Arabi dopsis thalia na]
143244	ATU005 184	ATL8C2 7782:1 ..967	gap2	ATCEA4 C5518_1	98	ATL8C2 7782:1 08..83 5	0.50	g45195 39	62	840		(AB016 256) NAD- depend ent sorbit ol dehydr ogenas e [Malus domest ica]
143245	ATU005 185	ATL8C1 0957:1 ..3604	gap2	ATCEA4 C90487 1, ATCEA4 C7012_1, ATCEA4 C21237 1, ATCEA4 S35140 , ATCEA4 C11041 8_1, ATCEA4 S25800	98, 93, 93, 93, 90, 85, 82	ATL8C1 0957:1 95..27 59	0.90	g31766 90	61	3076	1.6e- 305	(AC003 671) Simila r to ubiqui tin ligase gblD63 905 from S. cerevi siae. EST gblR65 295 comes

143246	ATU005 186	ATL8C5 0115:4 948..1	gap2	ATCEA4 S5810	98	ATL8C5 0115:4 893..6 1	0.88	944671 26	61	4449	0.0	(AL035 538) guanin e nucle otide- exchan ge protei n-like [Arabi dopsis thalia na]
143247	ATU005 187	ATL8C1 4100:1 ..2297	gap2	ATCEA4 C13745 51, ATCEA4 S26539	98, 92	ATL8C1 4100:4 7..112 9	0.72	942621 54	61	511	1.3e- 41	(AC005 275) putati ve ,protei n phosph atase regula tory subuni t [Arabi dopsis thalia na]
143248	ATU005 188	ATL8C4 8149:1 ..1227	gap2	ATCEA4 C35454 _1	98	ATL8C4 8149:2 58..12 27	0.96	934209 82	60	369	1.8e- 24	(Z9762 8) Simila rity to Brugia peptid ylprol

143249	ATU005 189	ATL8C2 386:43 9..715	gap2	ATCEA4 C13055 3_1	98	ATL8C2 386:48 3..659	0.93	g31525 85	60	171	2.8e- 12	(AC002 986) Contai ns simila rity to auxin- induce d protei n TM018A 10.6 from A. thalia na BAC gb AF0 13294. [Arabi dopsis thalia na]
143250	ATU005 190	ATL8C4 2719:1 204..2 76	gap2	ATCEA4 S29732	98	ATL8C4 2719:1 100..2 82	0.90	g54219 0	60	212	5.8e- 27	hypoth etical protei n 1087 - maize [Zea mays]
143251	ATU005 191	ATL8C2 6718:3 379..1	gap2	ATCEA4 S12996	98, 96, 82	ATL8C2 6718:3 250..1	0.85	g22451 07	60	554	5.3e- 48	(Z9734 3) thioes

	195	318:1. .440		C1849_1		318:10 1..280	70				06	906) J8 [Arabi dopsis thalia na]
143256	ATU005 196	ATL8C3 4914:1 619..1	gap2	ATCEA4 C120_1 , ATCEA4 S31723 , ATCEA4 S30933	98, 97, 87	ATL8C3 4914:1 619..9 0	g30246 66	59	816	9.3e- 78		STRICT OSIDIN E SYNTHA SE 1/2 PRECUR SOR [Arabi dopsis thalia. na]
143257	ATU005 197	ATL8C4 1660:5 66..15 22	gap2	ATCEA4 C6959_1	98	ATL8C4 1660:6 25..14 89	g46783 52	59	955	1.8e- 99		(AL049 659) putati ve protei n [Arabi dopsis thalia na]
143258	ATU005 198	ATL8C9 326:1. .774	gap2	ATCEA4 C54559 1, ATCEA4 S31736 , ATCEA4 S33755 , ATCEA4 C88797 1	98, 93, 92, 82	ATL8C9 326:81 ..708	g44690 20	59	583	3.3e- 47		(AL035 602) putati ve protei n (fragm ent) [Arabi dopsis thalia na]
143259	ATU005 199	ATL8C3 7779:1 908..1 7	gap2	ATCEA4 C25378 1, ATCEA4 C15907 1,	98, 95, 88	ATL8C3 7779:1 908..1 166	g40334 19	59	281	2.4e- 17		INORGA NIC PYROPH OSPHAT ASE (PYROP

					ATCEA4 C4155_1											HOSP H TE PHOSPH O- HYDROL ASE) (PPASE) [Droso phila melano gaster]
143260	ATU005 200	ATL8C3 5415:1 ..1263	gap2	ATCEA4 S2384, ATCEA4 C7685_1	98, 93	ATL8C3 5415:8 6..126 3	0.79	g13993 80	59	701	4.3e- 63	(U4368 3) S- adenos yl-L- methio nine:d elta24 - sterol -C- methyl transf erase [Glyci ne max]				
143261	ATU005 201	ATL8C3 3306:7 51..1	gap2	ATCEA4 C61855 1, ATCEA4 S13620	98, 87	ATL8C3 3306:5 51..14 3	0.78	g42204 81	59	340	1.4e- 20	(AC006 069) unknow n protei n [Arabi dopsis thalia na]				
143262	ATU005 202	ATL8C3 1616:1 ..4611	gap2	ATCEA4 C25910 1, ATCEA4 S14609	98, 96 97, 96	ATL8C3 1616:3 6..402 2	0.78	g31525 87	59	2635	1.4e- 248	(AC002 986) Simila r to CREB- bindin				

143263	ATU005 203	ATL8C1 4221:1 285..2 02	gap2	ATCEA4 S7935, ATCEA4 S4981	98, 91	ATL8C1 4221:1 272..2 02	0.74	g17854 86	59	757	5.1e- 80	g protei n homolo g gb U88 570 from D. melano gaster and contai ns simila rity to callus - associ ated protei n gb U01 961 from Nicoti ana tabacu m. EST gb W43 427 comes from this gene. [Arabi dopsis thalia na]
												(D1458 9) flavon oid

143264	ATU005 204	ATL8C4 0700:1 ..1610	gap2	ATCEA4 S26762 , ATCEA4 S2567	98, 86	ATL8C4 0700:3 07..14 10	0.68	g24941 25	59	1059	5.3e- 91	(AC002 376) Strong simila rity to Cucumi s acetyl -CoA acyltr ansfer ase (gb D7 0895). [Arabi dopsis thalia na]
143265	ATU005 205	ATL8C2 1263:1 316..3 349	gap2	ATCEA4 C6093 1	98	ATL8C2 1263:1 452..3 129	0.54	g33554 80	59	454	5.3e- 22	(AC004 218) Medica go noduli n N21- like protei n [Arabi dopsis thalia na]
143266	ATU005 206	ATL8C8 185:13 52..22 45	gap2	ATCEA4 C18878 _1	98	ATL8C8 185:15 63..19 96	0.46	g28298 71	59	869	1.6e- 69	(AC002 396) Hypoth etical protei

143267	ATU005 207	ATL8C4 780:14 31...62 4	gap2	ATCEA4 C5225_1, ATCEA4 S31771	98, 92					g32560 35	59	483	3.7e- 37	(Y1427 4) putative serine /threonine protein kinase [Sorghum bicolor]
143268	ATU005 208	ATL8C1 0831:1 ...293	gap2	ATCEA4 S32603, ATCEA4 C18817 1, ATCEA4 S13104	98, 92 96,					g45586 63	59	219	1.1e- 10	(AC007 063) unknown protein [Arabidopsis thaliana]
143269	ATU005 209	ATL8C2 2634:2 600...2 94	gap2	ATCEA4 C50643 1, ATCEA4 C74765 _1	98, 95	ATL8C2 2634:2 395...4 71				g34510 74	58	747	5.6e- 77	(AL031 326) putative protein [Arabidopsis thaliana]
143270	ATU005 210	ATL8C3 5359:2 218...1	gap2	ATCEA4 S3642, ATCEA4 S1333	98, 89	ATL8C3 5359:2 173...4 08				g31352 70	58	1243	5.4e- 122	(AC003 058) putative protein

143271	ATU005 211	ATL8C4 8127:1 527..1	gap2	ATCEA4 S4158, ATCEA4 C562_1	98, 96	ATL8C4 8127:1 032..9 6	0.70	g27813 61	58	987	5.7e- 82	kinase [Arabi dopsis thalia na]
143272	ATU005 212	ATL8C2 99:1.. 2170	gap2	ATCEA4 S5425	98	ATL8C2 99:138 ..621, ATL8C2 99:107 0..205 1	0.69, 0.96	g29824 64	58	980	8.3e- 103	(AL022 223) putati ve protei n [Arabi dopsis thalia na]
143273	ATU005 213	ATL8C1 0842:5 55..45 43	gap2	ATCEA4 S32, ATCEA4 S727	98, 89	ATL8C1 0842:5 55..45 33	0.69	g45103 96	58	344	5.1e- 35	(AC006 587) hypoth etical protei n [Arabi dopsis thalia na]
143274	ATU005 214	ATL8C2 5121:1 56..99 8	gap2	ATCEA4 C186_2 , ATCEA4 C1987_ 1	98, 84	ATL8C2 5121:3 58..94 3	0.54	g30367 99	58	429	6.6e- 31	(AL022 373) ras- relate d small GTP- bindin g protei n [Arabi

143275	ATU005 215	ATL8C2 3497:1 215..1	gap2	ATCEA4 C11883 1, ATCEA4 S1178, ATCEA4 C24565 1_	98, 83 94, 83	ATL8C2 3497:9 29..11 77	0.53	g26186 84	58	870	1.5e- 44	dopsis thalia na] (AC002 510) putati ve UDP-N- acetyl glucos amine- - dolich yl- phosph ate N- acetyl glucos aminep hospho transf erase [Arabi dopsis thalia na]
143276	ATU005 216	ATL8C1 319:28 0..514 8	gap2	ATCEA4 C7212_ 1, ATCEA4 C80618 1, ATCEA4 C52809 1, ATCEA4 C3087_ 1	98, 96, 95, 93	ATL8C1 319:28 9..514 8	0.41	g22449 10	58	260	1.3e- 20	(Z9733 9) unname d protei n produc t [Arabi dopsis thalia na]
143277	ATU005 217	ATL8C3 1942:1 191..1 48	gap2	ATCEA4 C49564 1, ATCEA4 C2628_ 1	98, 95			g16850 05	58	367	1.6e- 45	(U3264 4) immedi ate- early salicy late-

143278	ATU005 218	ATL8C2 4078:5 57..14 0	gap2	ATCEA4 C83973 _1	98					g29613 83	58	290	5.8e- 28	(Al022 141) putati ve protei n [Arabi dopsis thalia na]	induce d glucos yltran sferas e [Nicot iana tabacu m]
143279	ATU005 219	ATL8S3 906:8. .510	gap2	ATCEA4 C23280 _1, ATCEA4 S32270	98, 91					g45876 09	58	205	5.4e- 09	(AC006 951) unknow n protei n [Arabi dopsis thalia na]	
143280	ATU005 220	ATL8C2 5453:1 156..7 24	gap2	ATCEA4 S3395	98				ATL8C2 5453:1 095..7 24	g31932 89	57	220	2.4e- 24	(AF069 298) simila r to severa l small protei ns (~100 aa) that are induce d by	

143281	ATU005 221	ATL8C4 0053:1 ..895	gap2	ATCEA4 C5542_1	98	ATL8C4 0053:7 99..62 0	0.92	g42205 27	57	538	3.9e- 46	(AL035 356) putative protein [Arabi dopsis thaliana]
143282	ATU005 222	ATL8C1 0324:1 ..1066	gap2	ATCEA4 C11723 _1	98	ATL8C1 0324:1 05..83 9	0.89	g30061 42	57	374	(AL022 299) hypothetical protein [Schiz osaccharomycetes]	

143285	ATU005 225	ATL8C7 19:1.. 1541	gap2	ATCEA4 S28927 , ATCEA4 S32581	98, 85	ATL8C7 19:243 ..1253	0.77	g36876 52	57	457	2.7e- 45	tis elegan s]
143286	ATU005 226	ATL8C1 6400:4 64..39 75	gap2	ATCEA4 S2565, ATCEA4 S16782 , ATCEA4 S16783	98, 94, 93	ATL8C1 6400:5 61..39 75	0.75	g45393 83	57	373	2.3e- 34	(AF047 352) rubisc o activa se precur sor [Datis ca glomer ata]
143287	ATU005 227	ATL8C2 4322:7 25..43 77	gap2	ATCEA4 C17635 1, ATCEA4 C70242 1, ATCEA4 C19614 1, ATCEA4 S34395	98, 97, 95, 94	ATL8C2 4322:8 00..42 37	0.73	g38735 50	57	46	0.97	(AL033 534) serine -rich protei n [Schiz osacch aromyc es pombe]
143288	ATU005 228	ATL8C1 5176:1 019..1 440	gap2	ATCEA4 S30053	98	ATL8C1 5176:1 207..1 072	0.67	g42637 08	57	707	1.6e- 44	(AC006 223) hypoth etical protei n [Arabi

143289	ATU005 229	ATL8S2 6068:1 ..606	gap2	ATCEA4 C3198_1	98	ATL8S2 6068:1 9..565	0.61	g485510	57	187	5.6e-10	dopsis thaliana
143290	ATU005 230	ATL8C1 0809:1 125..7 369	gap2	ATCEA4 S941, ATCEA4 S10846 , ATCEA4 C64428 _1	98, 98, 89	ATL8C1 0809:1 203..5 621, ATL8C1 0809:5 749..6 846	0.47, 0.81	g3600044	57	1438	3.1e-152	(AF080119) contains similarity to proteases [Arabis dopsis thaliana]
143291	ATU005 231	ATL8C1 4787:1 284..1	gap2	ATCEA4 C3167_1, ATCEA4 S26889 , ATCEA4 C22267 _1	98, 89, 86	ATL8C1 4787:8 19..23 5	0.46	g3201633	57	1781	3.9e-155	(AC004669) putative cell division protein [Arabis dopsis thaliana]
143292	ATU005	ATL8C4	gap2	ATCEA4	98	ATL8C4	0.92	g16526	56	355	1.1e-	(D9090)

232	9193:1 41..10 21		C61229 _1		9193:4 13..98 1		49				29	7) hypoth etical protei n [Synec hocyst is sp.]
143293	ATU005 233	ATL8C3 4946:8 89..13 95	gap2	ATCEA4 C26002 _1	98	ATL8C3 4946:9 76..12 26	0.91	g29110 66	56	233	2.7e- 15	(AL021 960) adreno dixin- like protei n [Arabi dopsis thalia na]
143294	ATU005 234	ATL8C3 2522:3 299..1	gap2	ATCEA4 C70556 _1, ATCEA4 C32693 _1	98, 95	ATL8C3 2522:3 102..2 6	0.85	g33556 26	56	616	6.7e- 46	(Y0920 4) histid inol- phosph ate aminot ransfe rase [Nicot iana tabacu m]
143295	ATU005 235	ATL8C1 7262:1 376..1	gap2	ATCEA4 S105, ATCEA4 C5417 _1	98, 83	ATL8C1 7262:7 88..11 6	0.84	g45104 01	56	465	6.9e- 48	(AC006 587) putati ve genera l negati ve regula tor of transc riptio

143296	ATU005 236	ATL8C6 496:74 0..516 9	gap2	ATCEA4 C35120 1, ATCEA4 C44015 1_	98, 93	ATL8C6 496:81 1..516 3	0.76	g96145 0	56	340	4.6e- 30	n [Arabi dopsis thalia na]
143297	ATU005 237	ATL8C3 8654:5 63..17 06	gap2	ATCEA4 C21840 1, ATCEA4 C36461 1_	98, 94	ATL8C3 8654:5 84..16 29	0.64	g28943 78	56	611	5.0e- 56	(Y1457 3) putati ve riboph orin I homolo gue [Horde um vulgar e]
143298	ATU005 238	ATL8S2 7043:5 77..1	gap2	ATCEA4 C1274_	98	ATL8S2 7043:4 93..16 8	0.59	g46227 3	56	454	4.0e- 33	IMIDAZ OLEGLY CEROL- PHOSPH ATE DEHYDR ATASE (IGPD) [Arabi dopsis thalia na]

143306	ATU005 246	ATL8C3 5302:3 213..1	gap2	ATCEA4 S2632, ATCEA4 C8964_1	98, 93	ATL8C3 5302:3 207..4 4	0.89	g49271 90	55	743	3.7e- 39	n [Arabi dopsis thalia na]
143307	ATU005 247	ATL8C4 7693:2 253..1 86	gap2	ATCEA4 S6992, ATCEA4 S36099 , ATCEA4 S32638	98, 94, 90	ATL8C4 7693:2 228..8 84	0.86	g48369 01	55	276	6.3e- 27	(AC007 369) Unknown protein [Arabi dopsis thalia na]
143308	ATU005 248	ATL8C2 8664:1 ..1544	gap2	ATCEA4 C2746_1	98	ATL8C2 8664:1 03..12 36	0.84	g17081 52	55	315	8.3e- 31	PROBAB LE ATP- DEPEND ENT RNA HELICA SE DBP5 (HELIC ASE CA5/6) [Sacch aromyc es cerevi siae]

143309	ATU005 249	ATL8C4 6303:1 944..1 066	gap2	ATCEA4 C26068 _1	98		ATL8C4 6303:1 887..1 297	0.84		g37383 29	55	241	1.2e- 16	(AC005 170) unknown protein [Arabi dopsis thalia na]
143310	ATU005 250	ATL8C2 8050:7 60..1	gap2	ATCEA4 C838_1 , ATCEA4 S33526 , ATCEA4 C838_3 , ATCEA4 S33997	98, 97, 87, 84		ATL8C2 8050:7 10..26 3	0.84		g44552 53	55	478	4.2e- 42	(AL035 523) superoxide dismutase (EC 1.15.1 .1) (Fe) (f ragmen t) [Arabi dopsis thalia na]
143311	ATU005 251	ATL8C2 5307:3 801..2 686	gap2	ATCEA4 C25974 _1	98		ATL8C2 5307:3 657..3 505	0.83		g37023 33	55	133	5.2e- 13	(AC005 397) hypothetical protein [Arabi dopsis thalia na]
143312	ATU005 252	ATL8C1 8017:3 395..6 568	gap2	ATCEA4 S13703 , ATCEA4 S2180, ATCEA4 C24396 _1, ATCEA4	98, 96, 96, 94, 84		ATL8C1 8017:3 465..6 470	0.80		g29147 00	55	2246	1.7e- 167	(AC003 974) tRNA- processing protein [Arabi dopsis thalia na]

143313	ATU005 253	ATL8C3 1638:1 280..1	gap2	S883, ATCEA4 S8414	98, 96, 88, 84, 82, 82	ATL8C3 1638:1 143..3 01	0.80	g40986 47	55	1124	2.8e- 123	[Arabi dopsis thalia na] (U8066 8) homoge nizatio n 1,2- dioxyg enase [Arabi dopsis thalia na]
143314	ATU005 254	ATL8C8 652:41 30..1	gap2	ATCEA4 C348_1 , ATCEA4 S32066	98, 94	ATL8C8 652:34 51..83	0.78	g23424 27, g39281 02	55, 48	1302, 194	1.2e- 127, 0.0002 3	(AB000 799) NPK1- relate d protei n kinase 3 [Arabi dopsis thalia na]; (AC005 770) putati ve protei n kinase [Arabi dopsis thalia na]

[illegible]

143319	ATU005 259	ATL8C1 0999:3 062..6 3	gap2	ATCEA4 S33712 , ATCEA4 S3445, ATCEA4 C11645 2, ATCEA4 S31428 , ATCEA4 S34455 , ATCEA4 S2833, ATCEA4 S11463	98, 98, 95, 94, 93, 91, 82	ATL8C1 0999:6 3..292 2	0.64	g32567 46	55	100	0.0013	thalia nal (AF000 002) 109aa long hypoth etical protei n [Pyroc occus horiko shii]
143320	ATU005 260	ATL8C4 226:1. .1615	gap2	ATCEA4 C41245 _1	98	ATL8C4 226:76 ..682	0.51	g20886 58	55	1219	1.1e- 33	(AF002 109) unknow n protei n [Arabi dopsis thalia nal]
143321	ATU005 261	ATL8C3 8530:8 56..1	gap2	ATCEA4 C45784 _1	98			g45803 94	55	648	1.2e- 62	(AC007 171) putati ve fatty acid elonga se [Arabi dopsis thalia nal]
143322	ATU005 262	ATL8C4 9320:1 ..720	gap2	ATCEA4 C56752 _1,	98, 95			g33416 85	55	89	0.0020	(AC003 672) unknow

143323	ATU005 263	ATL8C4 1958:1 665..2 83	gap2	ATCEA4 S33760	98					g42635 22	55	1038	2.7e- 104	n protei n [Arabi dopsis thalia na]
143324	ATU005 264	ATL8C5 0162:1 ..2937	gap2	ATCEA4 C89081 _1	98					g17861 38	55	293	4.1e- 23	(AC004 044) hypoth etical protei n [Arabi dopsis thalia na]
143325	ATU005 265	ATL8C1 5359:7 88..1	gap2	ATCEA4 S1407	98					g38505 69	55	421	3.1e- 37	(AC005 278) ESTs gb T21 276, gb T45 403, and gb AA5 86113. come from this gene. [Arabi dopsis thalia na]
143326	ATU005 266	ATL8C4 9451:7	gap2	ATCEA4 S13049	98					g20621 60	54	399	2.1e- 37	(AC001 645) hypoth etical protei n [Arabi dopsis thalia na]

143327	ATU005 267	56..17 9	gap2	ATCEA4 C367_2 , ATCEA4 S36246	98, 96	40..29 2	0.94	g22805 28	54	348	8.4e- 38	jasmonate inducible protein isolog [Arabi dopsis thalia na] (AB005 888) ATMYB3 [Arabi dopsis thalia na] (AC006 234)
143328	ATU005 268	ATL8C1 9355:1 .894	gap2	ATCEA4 S6654	98	ATL8C9 731:14 5..845	0.94	g44544 80	54	846	7.7e- 88	putative (1-4)-beta-mannan endohydrolase [Arabi dopsis thalia na] (AC006 234)
143329	ATU005 269	ATL8C3 0453:8 31..1	gap2	ATCEA4 S11784	98	ATL8C3 0453:5 54..24 9	0.89	g34027 18	54	625	1.5e- 64	hypothetical protein [Arabi dopsis thalia na] (AC004 261)
143330	ATU005 270	ATL8C2 3977:8 05..1	gap2	ATCEA4 C1794_1,	98, 89	ATL8C2 3977:6 37..44	0.86	g37905 87	54	820	1.1e- 58	hypothetical protein [Arabi dopsis thalia na] (AF079 182) RING-

143331	ATU005 271	ATL8C1 0556:1 478..1	gap2	ATCEA4 S3525	98, 93	ATL8C1 0556:1 254..6 7	0.79	g41153 87	54	1107		H2 finger protein RHF2a [Arabi dopsis thalia na]
143332	ATU005 272	ATL8C4 771:18 16..29 44	gap2	ATCEA4 S6097	98	ATL8C4 771:18 16..28 74	0.66	g44553 53	54	822	9.1e- 86	(AL035 524) putati ve protei n [Arabi dopsis thalia na]
143333	ATU005 273	ATL8C3 8354:1 ..646	gap2	ATCEA4 S13850	98	ATL8C3 8354:2 39..62 6	0.61	g45593 84	54	478	2.4e- 53	(AC006 526) unknow n protei n [Arabi

143334	ATU005 274	ATL8C7 6:1..2 197	gap2	ATCEA4 C11936 1, ATCEA4 S29993 , ATCEA4 S3956, ATCEA4 S36202	98, 98, 96, 83	ATL8C7 6:108. .2197	0.59	g40068 48	54	449	3.1e- 45	dopsis thalia na]
143335	ATU005 275	ATL8S5 046:1. .739	gap2	ATCEA4 C5140_ 1, ATCEA4 C93068 _1	98, 95	ATL8S5 046:56 ..545	0.41	g29807 95	54	502	1.4e- 52	(AL022 197) putati ve protei n [Arabi dopsis thalia na]
143336	ATU005 276	ATL8C9 85:144 ..1324	gap2	ATCEA4 C41014 1, ATCEA4 S284	98, 87			g43771 80	54	338	3.1e- 33	(AE001 667) Phosph oglyce rate Mutase [Chlam ydia pneumo niae]
143337	ATU005 277	ATL8C1 4927:1 ..919	gap2	ATCEA4 S4603	98			g31933 09	54	86	1.2e- 05	(AF069 300) No defini tion line found [Arabi dopsis thalia

143345	284	6521:2 527..1		C71136 1, ATCEA4 S19682		6521:2 527..6 9	61				16	063) Rab escort protei n homolo g [Droso phila melano gaster]
	ATU005 285	ATL8C2 6570:1 000..1	gap2	ATCEA4 C11000 _3	98	ATL8C2 6570:9 37..23 9	0.80	g10865 86	53	84	0.0002 9	(U4100 7) simila r to G beta repeat s (PROSI TE:PSO 0670) [Caeno rhabdi tis elegan s]
143346	ATU005 286	ATL8C4 4543:4 09..27 87	gap2	ATCEA4 C20618 _1	98	ATL8C4 4543:4 09..25 27	0.79	g22448 65	53	1305	4.1e- 90	(Z9733 7) hypoth etical protei n [Arabi dopsis thalia na]
143347	ATU005 287	ATL8C3 899:25 64..13 8	gap2	ATCEA4 C75948 1, ATCEA4 C11066 _1	98, 97	ATL8C3 899:15 92..19 0	0.76	g38787 37	53	182	7.0e- 13	(Z7342 8) predic ted using Genefi nder; cDNA

143348	ATU005 288	ATL8C2 2541:2 863..1	gap2	ATCEA4 C64961 2, ATCEA4 C14954 1, ATCEA4 C64961 1,	98, 98, 92, 89	ATL8C2 2541:2 763..3 00	0.74	g45054 99	53	630	1.4e- 45	O- GlcNAc transf erase (uridi ne diphos pho-N- acetyl
												EST EMBL:T 01774 comes from this gene; CDNA EST Yk470a 9.3 comes from this gene; CDNA EST Yk470a 9.5 comes from this gene; CDNA EST Yk476b 6.5 comes from this gene [Caeno rhabdi tis elegan s]

143349	ATU005 289	ATL8C8 533:1. .618	gap2	ATCEA4 C27462 _1	98	ATL8C8 533:57 6..160	0.73	g42043 08	53	926	1.1e- 46	(AC003 027) lcl pr t_seq No defini tion line found [Arabi dopsis thalia na]
143350	ATU005 290	ATL8C4 4407:1 ..1074	gap2	ATCEA4 S32191 , ATCEA4 S27468 , ATCEA4 C9729 2, ATCEA4 C9729 _1	98, 97, 96, 91	ATL8C4 4407:1 94..90 1	0.72	g48368 97	53	487	2.1e- 38	(AC007 369) Hypoth etical protei n [Arabi dopsis thalia na]
143351	ATU005 291	ATL8C3 0658:9 71..1	gap2	ATCEA4 S10507	98	ATL8C3 0658:9 71..61 0	0.67	g48368 81	53	739	4.8e- 56	(AC007 260) lcl pr t_seq No defini

143355	ATU005 295	ATL8S1 3011:1 ..588	gap2	ATCEA4 C7556_1	98	ATL8S1 3011:1 13..51 7	0.49	g29824 56	53	144	3.7e- 13	na] (AL022 223) putati ve protei n [Arabi dopsis thalia na]
143356	ATU005 296	ATL8C1 95:271 1..19	gap2	ATCEA4 S29523 , ATCEA4 C2813_1	98, 98	ATL8C1 95:271 1..246	0.46	g17311 46	53	263		HYPOTH ETICAL 42.1 KD PROTEI N ZK1307 .9 IN CHROMO SOME III [Caeno rhabdi tis elegan s]
143357	ATU005 297	ATL8C6 036:1. .645	gap2	ATCEA4 S28934 , ATCEA4 S34018	98, 97			g23426 86	53	669	1.1e- 67	(AC000 106) Simila r to Saccha romyce s hypoth etical protei n YDR051 C (gb Z4 9209) . ESTs gb T44 436, gb

143358	ATU005 298	ATL8C4 0097:1 ..1000	gap2	ATCEA4 S36375	98					g86264 2	53	356	2.1e- 30	(U2018 3) MADS- box protei n AGL13 [Arabi dopsis thalia na]	142252 come from this gene. [Arabi dopsis thalia na]
143359	ATU005 299	ATL8C2 3739:1 671..2 538	gap2	ATCEA4 C8093_ 1, ATCEA4 C434_1 , ATCEA4 C6412_ 1, ATCEA4 S819	98, 91, 88, 86					g45586 63	53	281	1.4e- 18	(AC007 063) unknow n protei n [Arabi dopsis thalia na]	
143360	ATU005 300	ATL8C2 6488:2 43..82 3	gap2	ATCEA4 C52728 _1	98					g27499 43	53	484	1.0e- 47	(U7124 4) pathog enesis - relate d group 5 protei n [Brass ica rapa]	

143361	ATU005 301	ATL8C1 8429:3 98..1	gap2	ATCEA4 C1299- 1, ATCEA4 S24598 , ATCEA4 S31422 , ATCEA4 S19895	98, 98, 97, 83				921467 33	53	171	0.26	GAST1 protei n homolo g (clone GAS1) - Arabid opsis thalia na []
143362	ATU005 302	ATL8C2 1958:3 23..72 8	gap2	ATCEA4 C20781 1, ATCEA4 C22639 1, ATCEA4 S21554	98, 83, 82				941394 93	53	140	5.8e- 12	Rub1 []
143363	ATU005 303	ATL8C4 0078:1 ..364	gap2	ATCEA4 C14592 3_1	98				930969 29	53	200	1.1e- 09	(AL023 094) putati ve protei n [Arabi dopsis thalia na]
143364	ATU005 304	ATL8C2 4349:1 ..2047	gap2	ATCEA4 S7672	98				928274 3	53	422	3.8e- 50	gene cob intron 3 protei n - liverw ort (March antia polymo rpha) mitoch ondrio n

143365	ATU005 305	ATL8C3 3588:1 ..2134	gap2	ATCEA4 C10454 1, ATCEA4 C10454 2	98, 94	ATL8C3 3588:1 259..1 957	0.98	945875 25	52	293	2.6e- 35	[March antia polymo rpha] (AC007 060) Contai ns the PF1006 50 CRAL/T RIO phosph atidyl - inosit ol- transf er protei n domain ESTs gb T76 582, gb N06 574 and gb Z25 700 come from this gene. [Arabi dopsis thalia na]
143366	ATU005 306	ATL8C1 6849:2 37..68 3	gap2	ATCEA4 C53301 1	98	ATL8C1 6849:2 65..49 1	0.97	942622 41	52	300	4.4e- 30	(AC006 200) unknow n protei n

143367	ATU005 307	ATL8C4 574:1. .999	gap2	ATCEA4 S33415	98	ATL8C4 574:74 ..884	0.92	g42494 10	52	1021	7.5e- 101	[Arabi dopsis thalia na] (AC006 072) unknow n protei n [Arabi dopsis thalia na]
143368	ATU005 308	ATL8C4 0054:1 171..1	gap2	ATCEA4 S278, ATCEA4 S6934	98, 95	ATL8C4 0054:1 127..3 80	0.90	g62971 4	52	837	5.5e- 88	1- aminoc yclopr opane- 1- carbox ylate syntha se (EC 4.4.1. 14) - potato [Solan um tubero sum]
143369	ATU005 309	ATL8C4 6950:1 ..1288	gap2	ATCEA4 C364_2 , ATCEA4 S11893 , ATCEA4 S30710 , ATCEA4 S3061, ATCEA4 C364_1 , ATCEA4	98, 94, 94, 88, 84 86, 84	ATL8C4 6950:1 48..12 11	0.90	g24469 81	52	920	1.9e- 91	(AB005 560) AtGDI2 [Arabi dopsis thalia na]

143370	ATU005 310	ATL8C3 3241:9 10..1	gap2	S33781 ATCEA4 C20920 1, ATCEA4 C20920 2	98, 93	ATL8C3 3241:5 38..12 6	0.84	g22450 61	52	370	1.4e- 40	(Z9734 2) Clp protei nase homolo g [Arabi dopsis thalia na]
143371	ATU005 311	ATL8C2 13:1.. 1807	gap2	ATCEA4 S31369 , ATCEA4 S31562	98, 95	ATL8C2 13:455 ..1686	0.84	g47034 0	52	234	2.4e- 14	(U0004 3) simila r to beta- mannos yltran sferase [Caeno rhabdi tis elegan s]
143372	ATU005 312	ATL8C2 4669:2 013..5 8	gap2	ATCEA4 S3877, ATCEA4 S6322	98, 98	ATL8C2 4669:1 918..8 22	0.84	g22535 82	52	212	2.9e- 15	(U7872 1) Serine protei nase (stubb le) isolog [Arabi dopsis thalia na]
143373	ATU005 313	ATL8C3 2595:1 739..7 0	gap2	ATCEA4 C66895 1, ATCEA4 C66256 1, ATCEA4 S12079	98, 95 98,	ATL8C3 2595:1 678..2 63	0.82	g18144 24	52	859	2.4e- 83	(U8525 4) homeod omain protei n AHDP [Arabi dopsis

143374	ATU005 314	ATL8C2 7504:1 .818	gap2	ATCEA4 S12192 , ATCEA4 S7759, ATCEA4 S29774	98, 85 96, 85	ATL8C2 7504:2 0..774	0.81	g11748 62	52	136	thalia nal
143375	ATU005 315	ATL8C9 584:1. .2143	gap2	ATCEA4 S5121	98	ATL8C9 584:10 79..20 36	0.77	g40380 30	52	576	PUTATI VE UBIQUI TIN CARBOX YL- TERMIN AL HYDROL ASE C13A11 .04C (UBIQU ITIN THIOLE STERAS E) (UBIQU ITIN- SPECIF IC PROCES SING PROTEA SE) (DEUBI QUITIN ATING ENZYME) [Schiz osacch aromyc es pombel] (AC005 936) putati ve protei n kinase , 5,

143376	ATU005 316	ATL8C3 2813:1 948..8 73	gap2	ATCEA4 C34261 3, ATCEA4 C77417 1, ATCEA4 C34261 1, ATCEA4 S17846	98, 98, 95, 84	ATL8C3 2813:1 948..1 139	0.75	g22450 66	52	573	2.2e- 57	partia 1 [Arabi dopsis thalia na] (Z9734 2) Beta- Amylas e [Arabi dopsis thalia na]
143377	ATU005 317	ATL8C4 3619:1 182..1	gap2	ATCEA4 C1010_ 1, ATCEA4 C121_1 , ATCEA4 S31059	98, 96, 94	ATL8C4 3619:1 080..2 3	0.68	g11693 40	52	298		DEHYDR IN XERO 1 [Arabi dopsis thalia na]
143378	ATU005 318	ATL8C4 4770:2 477..1	gap2	ATCEA4 S1689, ATCEA4 S1464	98, 93	ATL8C4 4770:2 378..3 8	0.67	g49144 52	52	2119	5.6e- 123	(AL050 398) putati ve protei n [Arabi dopsis thalia na]
143379	ATU005 319	ATL8C4 497:1. .3328	gap2	ATCEA4 S14836 , ATCEA4 S11452 , ATCEA4 C26714 _1	98, 97, 84	ATL8C4 497:64 ..678, ATL8C4 497:13 43..33 28	0.66, 0.57	g44690 09	52	317	1.1e- 21	(AL035 602) putati ve protei n [Arabi dopsis thalia na]

143380	ATU005 320	ATL8C3 3540:1 332..1	gap2	ATCEA4 S6989, ATCEA4 C51298 _1	98, 94	ATL8C3 3540:1 032..1 09	0.57	g22890 03	52	190	2.4e- 11	(AC002 335) membra ne transp orter D1 isolog [Arabi dopsis thalia na]
143381	ATU005 321	ATL8S2 7965:1 ..539	gap2	ATCEA4 S16249	98	ATL8S2 7965:5 7..538	0.55	g36081 28	52	253	9.2e- 28	(AC005 314) hypoth etical protei n [Arabi dopsis thalia na]
143382	ATU005 322	ATL8C2 6952:1 185..2 383	gap2	ATCEA4 C4395_ 1	98	ATL8C2 6952:1 410..2 240	0.40	g40068 29	52	580	2.4e- 55	(AC005 970) putati ve protei n kinase [Arabi dopsis thalia na]
143383	ATU005 323	ATL8C3 1614:6 80..1	gap2	ATCEA4 C13036 _1	98			g33866 07	52	704	1.3e- 54	(AC004 665) hypoth etical protei n [Arabi dopsis thalia na]
143384	ATU005 324	ATL8C2 575:63	gap2	ATCEA4 C15878	98			g24353 95	52	903	6.0e- 84	(U6355 0)

143385	ATU005 325	1..1	gap2	ATCEA4 S26939 , ATCEA4 C4220_1, ATCEA4 S31949	98, 94 93, 90					g36680 83	52	184	0.59	(AC004 667) hypoth etical protei n [Arabi dopsis thalia na]	pectat e lyase [Fraga ria x ananas sa]
143386	ATU005 326	ATL8C1 4238:1 238..1	gap2	ATCEA4 C2355_1, ATCEA4 S2315	98, 94	ATL8C1 4238:3 58..76	0.98			g40068 87	51	759	1.3e- 76	(Z9970 8) putati ve protei n [Arabi dopsis thalia na]	(Z9970 8) putati ve protei n [Arabi dopsis thalia na]
143387	ATU005 327	ATL8C4 8178:1 01..14 66	gap2	ATCEA4 C12882 _1	98	ATL8C4 8178:2 63..14 56	0.94			g27085 32	51	455	9.3e- 35	(AF029 351) putati ve RNA bindin g protei n [Nicot iana tabacu m]	(AF029 351) putati ve RNA bindin g protei n [Nicot iana tabacu m]
143388	ATU005 328	ATL8C4 985:1. .612	gap2	ATCEA4 S36360	98	ATL8C4 985:62 ..601	0.91			g37029 66	51	407	1.4e- 23	(AF079 486) rac GTP bindin g	(AF079 486) rac GTP bindin g

143389	ATU005 329	ATL8C4 3778:1 ..2665	gap2	ATCEA4 S7621, ATCEA4 S33811 , ATCEA4 S35025 , ATCEA4 S1048, ATCEA4 S35363	98, 93, 92, 85, 83	ATL8C4 3778:1 68..20 82	0.89	g28424 89	51	1881		protein Arac8 [Arabi dopsis thalia na]
143390	ATU005 330	ATL8C3 7430:2 210..5 61	gap2	ATCEA4 C67563 1, ATCEA4 C67563 2	98, 97	ATL8C3 7430:1 859..9 86	0.83	g46803 81	51	205		(AF139 131) beclin 1 [Homo sapien s]
143391	ATU005 331	ATL8C1 3979:6 39..1	gap2	ATCEA4 C19667 1	98	ATL8C1 3979:6 39..30 4	0.81	g38941 58	51	722	1.3e- 64	(AC005 312) simila r to phloem - specif ic lectin [Arabi dopsis thalia na]
143392	ATU005 332	ATL8C4 5379:1 344..1	gap2	ATCEA4 C8722 1	98	ATL8C4 5379:1 344..1 41	0.78	g28646 14	51	910	1.4e- 68	(AL021 811) putati ve protein

143393	ATU005 333	ATL8C1 8345:1 184..1	gap2	ATCEA4 S26095 , ATCEA4 S671	98, 98	ATL8C1 8345:1 008..3 32	0.77	g42205 14	51	531	5.2e- 62	[Arabi dopsis thalia na] (AL035 356) putati ve protei n [Arabi dopsis thalia na]
143394	ATU005 334	ATL8C3 810:56 9..1	gap2	ATCEA4 C120_2 , ATCEA4 C13486 4_1, ATCEA4 S16133	98, 93, 84	ATL8C3 810:56 9..92	0.72	g30246 66	51	638	2.3e- 64	STRICT OSIDIN E SYNTHA SE 1/2 PRECUR SOR [Arabi dopsis thalia na]
143395	ATU005 335	ATL8C4 7873:1 466..5 37	gap2	ATCEA4 S7441	98	ATL8C4 7873:1 320..5 37	0.52	g37859 79	51	221	1.9e- 16	(AC005 560) putati ve serine protea se [Arabi dopsis thalia na]
143396	ATU005 336	ATL8C3 4301:1 255..7 87	gap2	ATCEA4 C608_1	98	ATL8C3 4301:1 185..9 61	0.50	g18715 77	51	266	5.4e- 24	(Y1155 3) putati ve 21kD protei n precu sor

143397	ATU005 337	ATL8C3 3650:1 ..543	gap2	ATCEA4 C4195_1	98						g13071 8	51	226	1.0e- 15	ACID PHOSPH ATASE PRECUR SOR 1 [Lycop ersico n escule ntum]	[Medic ago sativa]
143398	ATU005 338	ATL8C6 848:18 00..1	gap2	ATCEA4 C8201_1, ATCEA4 C32719 1, ATCEA4 S13800	98, 85 96, 85		ATL8C6 848:16 48..28 5	0.97			g23426 90	50	838	5.4e- 63	(AC000 106) Simila r to Homo copine I (gb U8 3246). [Arabi dopsis thalia na]	
143399	ATU005 339	ATL8C2 2547:2 64..12 19	gap2	ATCEA4 S2684, ATCEA4 S1243, ATCEA4 S5630	98, 82 97, 82		ATL8C2 2547:4 87..11 49	0.94			g13522 43	50	1211	2.7e- 107	LIGHT- MEDIAT ED DEVELO PMENT PROTEI N DET1 [Arabi dopsis thalia na]	
143400	ATU005 340	ATL8C3 2259:1 ..780	gap2	ATCEA4 C10471 9_1	98		ATL8C3 2259:8 ..777	0.89			g36183 20	50	376	6.2e- 25	(AB001 888) zinc finger protei n [Oryza	

143401	ATU005 341	ATL8C3 9764:6 94..1	gap2	ATCEA4 C5710_1, ATCEA4 C12316 5_1, ATCEA4 S22905	98, 90, 85	ATL8C3 9764:4 92..15 1	0.89	g16286 22	50	498	8.0e- 50	sativa J (U7263 1) flavon ol syntha se [Arabi dopsis thalia na]
143402	ATU005 342	ATL8C3 0029:1 ..527	gap2	ATCEA4 C602_1	98	ATL8C3 0029:3 5..65	0.86	g19466 90	50	278	2.1e- 24	(U9449 5) glutat hione peroxi dase [Arabi dopsis thalia na]
143403	ATU005 343	ATL8C6 95:138 1..675	gap2	ATCEA4 C11723 2_1	98	ATL8C6 95:128 0..675	0.84	g48862 82	50	152	7.5e- 08	(AL050 300) putati ve protei n [Arabi dopsis thalia na]
143404	ATU005 344	ATL8C3 2345:1 275..1	gap2	ATCEA4 C11276 _1	98	ATL8C3 2345:1 275..1 09	0.83	g45593 53	50	1034	1.7e- 86	(AC006 585) putati ve extrag enic suppre ssor protei n [Arabi dopsis thalia na]

143405	ATU005 345	ATL8C1 7297:5 046..4 53	gap2	ATCEA4 S3424, ATCEA4 S11501 , ATCEA4 S11578	98, 85 89, 85	ATL8C1 7297:5 046..4 53	0.80	g40068 68	50	215	6.2e- 12	na] (Z9970 7) putati ve protei n [Arabi dopsis thalia na]
143406	ATU005 346	ATL8C9 060:1. .1522	gap2	ATCEA4 C74672 _1	98	ATL8C9 060:21 0..129 3	0.72	g22447 80	50	852		(Z9733 5) hypoth etical protei n [Arabi dopsis thalia na]
143407	ATU005 347	ATL8C1 1915:7 29..17 56	gap2	ATCEA4 S7858, ATCEA4 S263	98, 89	ATL8C1 1915:7 29..12 21	0.72	g41651 83	50	131	0.0056	(AJ132 349) SAP1 protei n [Antir rhinum majus]
143408	ATU005 348	ATL8C3 4531:3 52..23 68	gap2	ATCEA4 C16581 _1, ATCEA4 S5900	98, 95	ATL8C3 4531:3 52..23 50	0.71	g45811 09	50	1215	1.4e- 118	(AC005 825) unknow n protei n [Arabi dopsis thalia na]
143409	ATU005 349	ATL8C1 3017:2 397..1	gap2	ATCEA4 S19885 , ATCEA4 C1706	98, 97	ATL8C1 3017:2 388..4 48	0.67	g33355 16	50	2002	1.2e- 200	(AF053 941) nonpho totrop ic

143410	ATU005 350	ATL8C3 9822:1 639..1	gap2	ATCEA4 C20243 _1	98	ATL8C3 9822:1 581..2 0	0.67	g25009 59	50	919	3.4e- 89	hypoco tyl 2 [Arabi dopsis thalia na]
143411	ATU005 351	ATL8C1 8705:1 108..3 56	gap2	ATCEA4 S29510	98	ATL8C1 8705:1 108..3 56	0.61	g42630 46	50	168	1.2e- 16	(AC005 142) hypoth etical protei n [Arabi dopsis thalia na]
143412	ATU005 352	ATL8C1 0448:4 647..1	gap2	ATCEA4 S5197, ATCEA4 C21564 _1, ATCEA4 C31758 _1	98, 96, 85	ATL8C1 0448:4 647..2 9	0.60	g33353 41	50	142		(AC004 512) T8F5.1 0 [Arabi dopsis thalia na]
143413	ATU005 353	ATL8C3 7529:9 00..27 16	gap2	ATCEA4 C49560 _2, ATCEA4 S27735	98, 87	ATL8C3 7529:9 18..22 86	0.49	g29807 88	50	254		(AL022 197) putati ve protei n

143414	ATU005 354	ATL8C3 8876:7 19..14 24	gap2	ATCEA4 C13974 1, ATCEA4 S33905	98, 96					g48875 43	50	556	4.6e- 59	[Arabi dopsis thalia na]
143415	ATU005 355	ATL8C8 077:64 0..1	gap2	ATCEA4 S30218 , ATCEA4 C1232_ 4, ATCEA4 C1232_ 2, ATCEA4 S7832, ATCEA4 S27470	98, 96, 95, 93, 86					g42638 18	50	171	2.0e- 08	(AC006 067) unknow n protei n [Arabi dopsis thalia na]
143416	ATU005 356	ATL8C9 387:77 6..1	gap2	ATCEA4 C192_2 , ATCEA4 C192_1 , ATCEA4 S35105 , ATCEA4 S28255 , ATCEA4 S7172	98, 98, 95, 86, 82	ATL8C9 387:43 9..320	1.00			g26876 86	49	168	1.9e- 15	(AJ000 110) cystat in [Arabi dopsis thalia na]

143417	ATU005 357	ATL8C1 0667:2 114..2 96	gap2	ATCEA4 S12686	98	ATL8C1 0667:1 960..2 96	1.00	g29824 52	49	975		(AL022 223) recept or protei n kinase -like protei n [Arabi dopsis thalia na]
143418	ATU005 358	ATL8C2 2358:1 ..2409	gap2	ATCEA4 S1798, ATCEA4 C24565 _1	98, 92	ATL8C2 2358:1 60..32 3, ATL8C2 2358:1 530..1 017	0.93, 0.56	g26186 84, g45593 82	49, 40	426, 79	9.7e- 21, 4.9e- 07	(AC002 510) putati ve UDP-N- acetyl glucos amine- dolich yl- phosph ate N- acetyl glucos aminep hospho transf erase [Arabi dopsis thalia na]; (AC006 526) putati ve DNA bindin g protei n

143419	ATU005 359	ATL8C4 8445:9 04..1	gap2	ATCEA4 C2111_1	98	ATL8C4 8445:8 18..36 3	0.92	g18421 11	49	330	2.4e- 33	[Arabi dopsis thalia na]
143420	ATU005 360	ATL8C2 6187:1 880..2 470	gap2	ATCEA4 C6414_1, ATCEA4 S10540	98, 93	ATL8C2 6187:1 982..2 406	0.88	g14189 90	49	482	3.3e- 48	(Z7552 4) unknow n [Lycop ersico n escule ntum]
143421	ATU005 361	ATL8C3 6103:1 ..4018	gap2	ATCEA4 C811_1 , ATCEA4 S140, ATCEA4 S19925	98, 98, 95	ATL8C3 6103:2 84..40 18	0.88	g10763 30	49	398	1.6e- 37	heat shock transc riptio n factor HSF1 - Arabid opsis thalia na []
143422	ATU005 362	ATL8C6 465:24 60..1	gap2	ATCEA4 C76752 _1	98	ATL8C6 465:21 92..11 0	0.88	g22449 65	49	1426	1.4e- 119	(Z9734 0) unname d protei n produc t [Arabi dopsis thalia na]
143423	ATU005	ATL8C3	gap2	ATCEA4	98	ATL8C3	0.82	g27022	49	1318	6.8e-	(AC003

143426	ATU005 366	ATL8C2 410:18 64..10	gap2	ATCEA4 S13063 , ATCEA4 C52592 _1	98, 97	ATL8C2 410:18 18..51	0.72	g49143 87	49	1040	1.6e- 83	(AC007 167) putati ve heat- shock protei n [Arabi dopsis thalia na]	/three nine kinase NPK15 gblD31 737 from Nicoti ana tabacu m. [Arabi dopsis thalia na]
143427	ATU005 367	ATL8C4 8987:1 ..1650	gap2	ATCEA4 C9271_1	98	ATL8C4 8987:1 52..15 24	0.65	g28277 00	49	667	8.2e- 51	(AL021 684) DEAD box ATP depend ent helica se protei n [Arabi dopsis thalia na]	
143428	ATU005 368	ATL8C6 543:10 55..1	gap2	ATCEA4 C70162 _1	98	ATL8C6 543:77 0..470	0.61	g22450 05	49	784	7.0e- 77	(Z9734 1) hypoth	

143429	ATU005 369	ATL8C4 6807:2 537..4 7	gap2	ATCEA4 C24245 _1	98	ATL8C4 6807:2 401..4 7	0.58	g34026 72	49	1552	9.6e- 146	etical protei n [Arabi dopsis thalia na]
143430	ATU005 370	ATL8C2 6560:1 21..10 36	gap2	ATCEA4 C1453 _1, ATCEA4 C20265 _1, ATCEA4 S25769	98, 96, 93	ATL8C2 6560:1 39..10 26	0.56	g37194 55	49	456	2.7e- 41	(AF094 831) iron supero xide dismut ase [Zante deschi a aethio pica]
143431	ATU005 371	ATL8C1 115:10 82..1	gap2	ATCEA4 S30362	98	ATL8C1 115:10 82..38 4	0.53	g13526 79	49	268	1.4e- 12	PROTEI N PHOSPH ATASE 2C ABI1 (PP2C) [Arabi dopsis thalia na]
143432	ATU005 372	ATL8C3 3275:1 683..1	gap2	ATCEA4 S13724 , ATCEA4	98, 94, 94, 85	ATL8C3 3275:1 603..1 63	0.49	g48952 21	49	601	4.3e- 38	(AC007 660) unknow n

143437	ATU005 377	ATL8S1 4565:5 69..1	gap2	ATCEA4 S1795, ATCEA4 C16694 1, ATCEA4 S31216	98, 94, 93					49	629	2.5e- 49	E. coli YecD hypoth etical 21.8 KD protei n in asps 5'regi on and to isocho rismat ase [Bacil lus subtil is]
143438	ATU005 378	ATL8C2 4109:1 264..1	gap2	ATCEA4 C364_1 , ATCEA4 S17992 , ATCEA4 C364_2 , ATCEA4 S32657	98, 90, 87, 85	ATL8C2 4109:1 069..5 8	0.97	g16554 24	48	858	3.7e- 93	(D8353 1) GDP dissoc iation inhibi tor [Arabi dopsis thalia na]	
143439	ATU005 379	ATL8C1 5823:1 02..26 05	gap2	ATCEA4 C95864 1, ATCEA4	98, 95, 92	ATL8C1 5823:8 25..23 34	0.95	g22451 07	48	483	6.9e- 45	(29734 3) thioes terase	

143440	ATU005 380	ATL8C4 4367:1 895..5 892	gap2	ATCEA4 C32816 _1	98	ATL8C4 4367:2 225..5 595	0.92	g46789 43	48	2931	9.6e- 225	homolog [Arabi dopsis thalia na]
143441	ATU005 381	ATL8C2 1529:1 120..8 5	gap2	ATCEA4 C13437 _1	98	ATL8C2 1529:7 28..85	0.91	g21296 23	48	83	1.9e- 12	immuno philin FKBP15 -2 - Arabid opsis thalia na [Arabi dopsis thalia na]
143442	ATU005 382	ATL8C1 6422:3 005..2 92	gap2	ATCEA4 C28942 _1	98	ATL8C1 6422:2 955..4 86	0.87	g38853 34	48	1259	3.5e- 96	(AC005 623) putati ve argona ute protei n [Arabi dopsis thalia na]
143443	ATU005 383	ATL8C4 05:107 6..377	gap2	ATCEA4 C18125 _1	98	ATL8C4 05:100 6..381	0.86	g43357 37	48	242	4.0e- 13	(AC006 248) putati ve serine

143444	ATU005 384	ATL8C9 838:18 44..1	gap2	ATCEA4 S5058	98	ATL8C9 838:16 30..31 5	0.79	g41851 41	48	498	3.4e- 44	/threo nine kinase [Arabi dopsis thalia na]
143445	ATU005 385	ATL8C2 8935:1 ..454	gap2	ATCEA4 C632_1 , ATCEA4 S30846 , ATCEA4 S10901 , ATCEA4 S8216	98, 94, 92, 88	ATL8C2 8935:8 5..282	0.76	g21295 83	48	546	1.1e- 42	ferrit in - Arabid opsis thalia na [Arabi dopsis thalia na]
143446	ATU005 386	ATL8C1 1580:9 32..23 87	gap2	ATCEA4 C19042 _1, ATCEA4 C32532 _1	98, 85	ATL8C1 1580:9 32..23 71	0.67	g24627 53	48	782	1.7e- 51	(AC002 292) putati ve polyga lactur onase [Arabi dopsis thalia na]
143447	ATU005 387	ATL8C4 8549:1	gap2	ATCEA4 S1701,	98, 95	ATL8C4 8549:1	0.66	g48352 35	48	741	5.0e- 75	(AL049 862)

143448	ATU005 388	306..1	ATCEA4 S1156	98	ATL8C1 3673:8 38..41 9	0.55	g46512 04	48	280	7.3e- 24	putative protein [Arabidopsis thaliana]
143449	ATU005 389	ATL8C2 3131:6 09..15 85	ATCEA4 S31079 , ATCEA4 C21567 _1	98, 85			g34829 75	48	396	2.0e- 44	(AL031 369) putative protein [Arabidopsis thaliana]
143450	ATU005 390	ATL8C2 7128:5 85..1	ATCEA4 C54244 _1, ATCEA4 S14744	98, 82			g33675 21	48	685	2.8e- 68	(AC004 392) Simila r to gb U08 285 membrane- associated salt-inducible protein from Nicotiana tabacu

143451	ATU005 391	ATL8C5 47:269 ..1369	gap2	ATCEA4 C13265 _1	98							48	1348	3.2e- 95	m. ESTs gb T44 131 and gb T04 378 come from this gene. [Arabi dopsis thalia na]
143452	ATU005 392	ATL8C3 6179:7 62..1	gap2	ATCEA4 C7059 _1	98							47	111	0.0088	(AC002 534) putati ve histon e deacet ylase [Arabi dopsis thalia na]
143453	ATU005 393	ATL8C6 338:46 9..1	gap2	ATCEA4 S1830, ATCEA4 S2402	98, 91							47	225	7.5e- 15	(AC006 439) hypoth etical protei

143454	ATU005 394	ATL8C3 643:89 6..1	gap2	ATCEA4 C60245 _1	98	ATL8C3 643:41 7..48	0.89	g36081 40	47	367	3.8e- 36	n [Arabi dopsis thalia na]
143455	ATU005 395	ATL8C3 4384:1 168..1 7	gap2	ATCEA4 S15315 , ATCEA4 C6318 _3, ATCEA4 S33154	98, 92 96,	ATL8C3 4384:1 054..9 4	0.88	g26224 28	47	65	4.0e- 06	(AE000 896) conser ved protei n [Metha nobact erium thermo autotr ophicu m]
143456	ATU005 396	ATL8C4 3788:1 833..1	gap2	ATCEA4 C2091 _1, ATCEA4 C31758 _1	98, 88	ATL8C4 3788:1 833..4	0.83	g40986 47	47	1002	(U8066 8) homoge ntisat e 1,2- dioxyg enase [Arabi dopsis thalia na]	
143457	ATU005 397	ATL8C2 6500:1 950..9 21	gap2	ATCEA4 C18292 _1, ATCEA4 C73124 _1	98, 97	ATL8C2 6500:1 950..1 155	0.82	g48061 8	47	333	8.9e- 35	ATAF1 protei n - Arabid opsis thalia

143461	ATU005 401	ATL8C2 6147:8 20..1	gap2	ATCEA4 C8400_2, ATCEA4 S19352	98, 86	ATL8C2 6147:5 61..39	0.80	g29795 59	47	252	9.9e- 27	thalia na] (AC003 680) putati ve DNA bindin g protei n [Arabi dopsis thalia na]
143462	ATU005 402	ATL8S4 917:1. .515	gap2	ATCEA4 C738_1 , ATCEA4 S3456, ATCEA4 S2844, ATCEA4 S2612, ATCEA4 S2892	98, 96, 95, 94, 82	ATL8S4 917:17 0..354	0.76	g36463 34	47	271	2.0e- 26	(AJ001 681) MdMADS 8 [Malus domest ica]
143463	ATU005 403	ATL8C3 1538:2 532..1 415	gap2	ATCEA4 S9924, ATCEA4 S10439 , ATCEA4 S13124	98, 91, 88	ATL8C3 1538:2 371..1 579	0.68	g24995 35	47	1147	1.6e- 88	2- OXOGLU TARATE /MALAT E TRANSL OCATOR PRECUR SOR [Spina cia olerac ea]
143464	ATU005 404	ATL8C1 0298:1 473..9 8	gap2	ATCEA4 C29739 1, ATCEA4 S18960 , ATCEA4	98, 86, 82	ATL8C1 0298:8 57..56 5	0.66	g28646 16	47	144		(AL021 811) hypothe tical protei n [Arabi

143465	ATU005 405	ATL8C2 3630:5 81..1	gap2	S27045	98	ATL8C2 3630:4 81..27 5	0.57	g11408 6	47	348	6.0e- 27	RAS- RELATE D PROTEI N ARA- 2 [Arabi dopsis thalia na]
143466	ATU005 406	ATL8C2 1854:1 ..2138	gap2	ATCEA4 S9938, ATCEA4 S3669, ATCEA4 C36982 1, ATCEA4 S9939	98, 90, 90, 83	ATL8C2 1854:8 ..1615	0.57	g29824 64	47	261	5.0e- 27	(AL022 223) putati ve protei n [Arabi dopsis thalia na]
143467	ATU005 407	ATL8C2 779:12 2..298 1	gap2	ATCEA4 C98200 1, ATCEA4 S36280	98, 94	ATL8C2 779:12 2..204 1	0.52	g11704 10	47	1317	9.1e- 121	HOMEOB OX PROTEI N HAT3.1 [Arabi dopsis thalia na]
143468	ATU005 408	ATL8C4 8186:1 02..85 6	gap2	ATCEA4 C7157_1	98	ATL8C4 8186:1 43..64 9	0.48	g11684 70	47	827	8.8e- 81	PROTEI N KINASE APK1A [Arabi dopsis thalia na]
143469	ATU005 409	ATL8C5 808:87 9..362	gap2	ATCEA4 S7648, ATCEA4 C8493	98, 96			g29824 66	47	476		(AL022 223) putati ve

143470	ATU005 410	ATL8C2 3657:1 ..1415	gap2	ATCEA4 C22851 1, ATCEA4 S35525	98, 91	ATL8C2 3657:1 86..14 15	0.94	g22621 05	46	992	4.3e- 99	protein [Arabi dopsis thalia na]
143471	ATU005 411	ATL8C4 3231:3 626..1	gap2	ATCEA4 S10434	98	ATL8C4 3231:3 290..2 9	0.90	g22448 81, g22448 80	46, 37	2183, 402	2.9e- 195, 1.2e- 35	(Z9733 8) PDR5- like ABC transp orter [Arabi dopsis thalia na]; (Z9733 8) ABC transp orter homolo g [Arabi dopsis thalia na]
143472	ATU005 412	ATL8C1 292:19 09..1	gap2	ATCEA4 C12540 _1	98	ATL8C1 292:19 09..62 2	0.90	g42204 62	46	1560	2.4e- 151	(AC006 216) Strong simila rity to gb Z50 851

143473	ATU005 413	ATL8C2 4743:1 ..1170	gap2	ATCEA4 S4408	98	ATL8C2 4743:7 1..116 4	0.85	g39280 78	46	1125	3.3e- 123	HD-zip (athb- 8) gene from Arabid opsis thalia na contai ning Homeob ox PF1000 46 and bZIP PF1001 70 domain s. [Arabi dopsis thalia na]
143474	ATU005 414	ATL8C4 7201:1 ..1607	gap2	ATCEA4 C50487 1, ATCEA4 S2643	98, 98	ATL8C4 7201:2 53..14 21	0.84	g45859 66	46	885	8.6e- 61	(AC005 770) putati ve protei n kinase , calciu m depend ent [Arabi dopsis thalia na]
												(AC005 287) Putati ve dihydr

143475	ATU005 415	ATL8S3 843:1. .743	gap2	ATCEA4 C32043 _1	98	ATL8S3 843:47 0..695	0.83	g46802 12	46	103	2.9e- 07	olipoa mide acetyl transf erases [Arabi dopsis thalia na]
143476	ATU005 416	ATL8C4 7188:6 38..17 49	gap2	ATCEA4 C1445_ 1, ATCEA4 S17803 , ATCEA4 S24093	98, 95, 90	ATL8C4 7188:6 60..13 57	0.81	g24400 33	46	1007	1.2e- 95	(X9854 3) endo- 1,4- beta- glucan ase [Arabi dopsis thalia na]
143477	ATU005 417	ATL8C2 5825:1 ..1407	gap2	ATCEA4 S1989	98	ATL8C2 5825:1 34..13 42	0.81	g32709	46	491	7.5e- 39	(X6257 0) IFP53 [Homo sapien s]
143478	ATU005 418	ATL8C3 7201:3 344..1	gap2	ATCEA4 S2491, ATCEA4 C12873 2_1	98, 92	ATL8C3 7201:3 244..1 81	0.67	g28269 00	46	1547		(AB004 461) DNA polyme rase alpha cataly tic, subuni

143479	ATU005 419	ATL8C1 1837:5 64..11 85	gap2	ATCEA4 C19570 _1	98	ATL8C1 1837:5 93..81 5	0.45	g37383 33	46	262	1.1e- 17	t [Oryza sativa] (AC005 170) unknown n protei n [Arabi dopsis thalia na]
143480	ATU005 420	ATL8C1 3908:3 378..1	gap2	ATCEA4 S253	98	ATL8C1 3908:1 376..3 36	0.43	g33778 16	46	1573	2.0e- 133	(AF076 275) contai ns simila rity to Arabid opsis thalia na retrot ranspo son Athila (GB:X8 1801) [Arabi dopsis thalia na]
143481	ATU005 421	ATL8C2 9732:4 1..627	gap2	ATCEA4 C12583 _1, ATCEA4 S9677, ATCEA4 C12583 _3	98, 93, 85			g13370 9	46	106	9.3e- 08	CYANEL LE 30S RIBOSO MAL PROTEI N S10 [Cyano phora parado xa]

143482	ATU005 422	ATL8C4 8594:1 137..1	gap2	ATCEA4 S413	98				g46806 59	46	339	1.1e- 36	(AF132 944) CGI-10 protei n [Homo sapien s]
143483	ATU005 423	ATL8C4 1224:1 ..2222	gap2	ATCEA4 S986, ATCEA4 C5631_1	98, 98	ATL8C4 1224:8 72..20 49	0.95	g45301 26	45	472	3.7e- 42	(AF078 082) recept or- like protei n kinase homolo g RK20-1 [Phase olus vulgar is]	
143484	ATU005 424	ATL8C4 9403:1 990..1	gap2	ATCEA4 S1740	98	ATL8C4 9403:1 854..1 75	0.91	g21082 52	45	1135	1.0e- 105	(Y1022 8) P- glycop rotein -2 [Arabi dopsis thalia na]	
143485	ATU005 425	ATL8C1 9803:2 095..1	gap2	ATCEA4 S34243	98	ATL8C1 9803:1 827..1 6	0.90	g35229 43	45	2534	6.3e- 244	(AC004 411) putati ve p- glycop rotein [Arabi dopsis thalia na]	
143486	ATU005 426	ATL8C1 0514:6 90..25	gap2	ATCEA4 S4372, ATCEA4	98, 93	ATL8C1 0514:1 384..2	0.90	g45672 50	45	112		(AC007 070) hypoth	

143487	ATU005 427	72	C19108 _1		351	0.89	g29824 64	45	1241	1.0e- 130	(AL022 223) putative protein [Arabi dopsis thalia na]
143488	ATU005 428	ATL8C2 8946:1 281..1	gap2	ATCEA4 C44801 _1	98	ATL8C2 8946:1 206..6 2	0.88	g38222 23	45	590	(AF077 955) branch ed- chain alpha keto- acid dehydr ogenas e El alpha subuni t [Arabi dopsis thalia na]
143489	ATU005 429	ATL8C3 61:404 8..98	gap2	ATCEA4 S4849, ATCEA4 S30962 , ATCEA4 C29072 _1, ATCEA4 C11121	98, 97, 93, 90, 88	ATL8C3 61:404 8..656	0.88	g39476 90	45	736	(AJ131 245) Sec24B protein [Homo sapien s]

143490	ATU005 430	ATL8C4 1282:1 749..1	gap2	ATCEA4 C66808 1	98, 98	ATL8C4 1282:1 332..3 36	0.87	g37860 14	45	442	2.8e- 32	(AC005 499) hypoth etical protei n [Arabi dopsis thalia na]
143491	ATU005 431	ATL8C3 6253:1 ..886	gap2	ATCEA4 C31717 1	98	ATL8C3 6253:1 31..86 0	0.87	g49024 76	45	652	7.9e- 68	(AJ238 802) MAP kinase [Arabi dopsis thalia na]
143492	ATU005 432	ATL8C3 8051:1 778..1	gap2	ATCEA4 C30460 1, ATCEA4 S12488	98, 96	ATL8C3 8051:1 012..1 34	0.84	g37639 16	45	236	1.0e- 16	(AC004 450) unknow n protei n [Arabi dopsis thalia na]
143493	ATU005 433	ATL8C2 509:19 53..1	gap2	ATCEA4 C18479 1, ATCEA4 S23558	98, 86	ATL8C2 509:17 32..10 8	0.78	g28298 81	45	563	1.0e- 35	(AC002 396) Hypoth etical protei n [Arabi dopsis thalia na]
143494	ATU005 434	ATL8C2 0210:7	gap2	ATCEA4 C7791	98, 97, 90	ATL8C2 0210:6	0.77	g10719 13	45	646	1.8e- 55	cystei ne

143495	ATU005 435	53..1	gap2	2, ATCEA4 S11745 , ATCEA4 C7791_1	98, 95, 94, 88, 88	ATL8C4 113:20 12..1	60..16 0	0.75	g44553 23	45	1701	3.0e- 168	syntha se (EC 4.2.99 .8) C precu sor, mitoch ondria l - spinac h [Spina cia olerac ea]
143496	ATU005 436	ATL8C4 9424:3 38..61 4	gap2	ATCEA4 S12196 , ATCEA4 S19085 , ATCEA4 C5867_1, ATCEA4 C16185 _1, ATCEA4 S13399	98	ATL8C4 9424:3 38..53 8	ATL8C4 113:20 00..43	0.65	g29976 86	45	104	0.14	(AF053 303) putati ve transc riptio nal co- activa tor [Arabi dopsis thalia na]
143497	ATU005 437	ATL8C1 9243:1	gap2	ATCEA4 C17966	98, 93	ATL8C1 9243:1	ATL8C1 9243:1	0.62	g43097 31	45	139	9.1e- 10	(AC006 439)

143498	ATU005 438	914..1	gap2	ATCEA4 S11772	98, 98	ATL8C3 9194:1 45..25 0	0.59	g41509 63	45	223	6.1e- 20	(Y1862 0) DsPTP1 protein [Arabi dopsis thalia na]
143499	ATU005 439	ATL8C4 340:1. .3954	gap2	ATCEA4 C494_1	98	ATL8C4 340:27 9..382 1	0.57	g31933 09	45	402	1.7e- 32	(AF069 300) No defini tion line found [Arabi dopsis thalia na]
143500	ATU005 440	ATL8C2 5096:1 ..853	gap2	ATCEA4 C32663 _1	98	ATL8C2 5096:7 3..692	0.55	g48951 91	45	211	1.5e- 19	(AC007 661) hypoth etical protein [Arabi dopsis thalia na]
143501	ATU005 441	ATL8C7 014:19 78..1	gap2	ATCEA4 C12475 _1	98			g27233 93	45	113	2.8e- 12	(AB009 284) EXTR2 [Homo sapien s]

143502	ATU005 442	ATL8C1 4003:2 321..4 932	gap2	ATCEA4 C47349 _1	98				g16535 13	45	289	9.9e- 20	(D9091 4) hypoth etical protei n [Synec hocyst is sp.]
143503	ATU005 443	ATL8C1 2502:1 ..762	gap2	ATCEA4 S33321	98				g34134 24	45	239	6.6e- 22	(AJ006 309) hypoth etical protei n [Arabi dopsis thalia na]
143504	ATU005 444	ATL8C1 7222:1 767..3 539	gap2	ATCEA4 S12715	98				g35505 19	45	597	2.3e- 54	(AJ007 630) oxygen ase [Nicot iana tabacu m]
143505	ATU005 445	ATL8C4 8266:9 79..1	gap2	ATCEA4 S36326 , ATCEA4 C1409_ 1	98, 97	ATL8C4 8266:9 13..11 4			g29118 76	44	58	0.0021	(AF047 662) contai ns strong simila rity to RNA recogn ition motifs (RNP) (PS:PS 00030) [Caeno rhabdi tis

143506	ATU005 446	ATL8C1 0748:1 212..1	gap2	ATCEA4 S12409	98	ATL8C1 0748:1 146..1 2	0.98	g26548 70	44	600	1.4e- 59	(AF015 302) RbohAO sp [Oryza sativa]
143507	ATU005 447	ATL8C1 291:36 82..1	gap2	ATCEA4 C5611- 1, ATCEA4 S3139	98, 95	ATL8C1 291:34 80..99 6	0.96	g42181 22, g33554 73	44, 33	205, 181	7.7e- 22, 2.5e- 10	(AL035 353) putati ve protei n [Arabi dopsis thalia na]; (AC004 218) hypoth etical protei n [Arabi dopsis thalia na]
143508	ATU005 448	ATL8C8 405:11 29..24 7	gap2	ATCEA4 C11990 3_1	98	ATL8C8 405:10 62..24 7	0.90	g38860 24	44	370	5.5e- 28	(AF106 576) contai ns simila rity to WD domain s [Caeno rhabdi tis elegan s]
143509	ATU005 449	ATL8C3 2051:1	gap2	ATCEA4 C18323	98, 94 96, 94	ATL8C3 2051:1	0.85	g47586 68	44	583	5.2e- 50	serine palmit

143510	ATU005 450	454..1	gap2	ATL8C4 7271:1 4..604	1, ATCEA4 S31288 , ATCEA4 S1843	98, 91	ATL8C4 7271:6 2..463	0.85	g13896 99	44	479	2.0e- 49	(U3884 5) nitri ase 1 [Arabi dopsis thalia na]
143511	ATU005 451	ATL8C3 7921:1 264..1	gap2	ATL8C3 7921:1 057..4 75	ATCEA4 C13434 7 1, ATCEA4 C21148 1, ATCEA4 S18505	98, 90 98, 90	ATL8C3 7921:1 057..4 75	0.85	g45803 97	44	830	3.1e- 84	(AC007 171) putati ve RNA helica se [Arabi dopsis thalia na]
143512	ATU005 452	ATL8C4 5096:6 151..3 18	gap2	ATL8C4 5096:1 931..3 23	ATCEA4 S442, ATCEA4 C50_1	98, 98	ATL8C4 5096:1 931..3 23	0.82	g11765 85, g33193 72	44, 43	188, 904	1.8e- 06, 8.1e- 98	HYPOTH ETICAL 53.1 KD TRP- ASP REPEAT S CONTAI NING PROTEI N IN HXT14- PHA2 INTERG ENIC REGION [Sacch aromyc

143513	ATU005 453	ATL8C3 1130:2 03..13 95	gap2	ATCEA4 S331	98	ATL8C3 1130:2 03..73 1	0.79	g35488 05	44	390	2.4e- 33	es cerevi siae]; (AF077 409) simila r to revers e transc riptas es (PFam: rvt.hm m, score: 60.13) [Arabi dopsis thalia na]
143514	ATU005 454	ATL8S6 586:37 0..1	gap2	ATCEA4 S10828	98	ATL8S6 586:36 7..16	0.76	g21296 34	44	267		lectin -like protei n - Arabid opsis thalia na [Arabi dopsis thalia na]
143515	ATU005 455	ATL8C1 1012:1	gap2	ATCEA4 C98384	98, 82	ATL8C1 1012:8	0.75	g48357 56	44	604	3.8e- 52	(AC007 202)

143516	ATU005 456	ATL8C3 7077:2 105..1	gap2	ATCEA4 C7722_1	98	ATL8C3 7077:2 059..8 6	0.67	g30045 65	44	1381			Is a member of the PF100044 glycer aldehyde 3-phosphate dehydrogenase family . ESTs gb T43985, gb N38667, gb N65037, gb AA713069 and gb AI099548 come from this gene. [Arabis dopsis thaliana]
..1211				1, ATCEA4 C4940_1									
						4..373							

143517	ATU005 457	ATL8C3 3878:1 ..2385	gap2	ATCEA4 S16213	98	ATL8C3 3878:1 48..19 83	0.64	g26529 38	44	611		na] (Z4755 4) orf [Zea mays]
143518	ATU005 458	ATL8C1 2365:8 48..1	gap2	ATCEA4 S19901 , ATCEA4 C75807 _1	98, 97	ATL8C1 2365:8 20..21 8	0.63	g12084 96	44	269	5.6e- 32	(D3812 4) EREBP- 3 [Nicot iana tabacu m]
143519	ATU005 459	ATL8C4 7703:6 20..20 16	gap2	ATCEA4 C4229 _1	98	ATL8C4 7703:1 041..1 902	0.62	g39351 87	44	531	1.1e- 57	(AC004 557) F17L21 .30 [Arabi dopsis thalia na]
143520	ATU005 460	ATL8C2 119:1. .1197	gap2	ATCEA4 S6642, ATCEA4 C13315 2_1	98, 98	ATL8C2 119:53 0..112 6	0.58	g45672 79	44	1126	2.2e- 109	(AC006 841) putati ve serine /threo nine protei n kinase [Arabi dopsis thalia na]
143521	ATU005 461	ATL8C3 6487:2 52..17 15	gap2	ATCEA4 S1966	98	ATL8C3 6487:8 62..16 75	0.48	g34260 36	44	693	1.7e- 70	(AC005 168) unknow n protei n [Arabi dopsis thalia

143522	ATU005 462	ATL8C1 288:35 30..15 51	gap2	ATCEA4 C3933 1	98	ATL8C1 288:33 99..15 60	0.45	g39351 49	44	1484	1.3e- 143	na] (AC005 106) T25N20 .13 [Arabi dopsis thalia na]
143523	ATU005 463	ATL8C1 7534:1 ..965	gap2	ATCEA4 S35194 , ATCEA4 S26109 , ATCEA4 S30790	98, 86 95, 86			g29795 66	44	285	1.2e- 22	(AC003 680) MADS box protei n AGL20 [Arabi dopsis thalia na]
143524	ATU005 464	ATL8C3 9950:1 431..3 63	gap2	ATCEA4 S3245, ATCEA4 S16119	98, 89			g38343 30	44	195	7.3e- 15	(AC005 679) F9K20. 17 [Arabi dopsis thalia na]
143525	ATU005 465	ATL8C3 27:1.. 1077	gap2	ATCEA4 C25002 _1	98			g25831 13	44	359	1.7e- 31	(AC002 387) hypoth etical protei n [Arabi dopsis thalia na]
143526	ATU005 466	ATL8C1 9020:7 22..1	gap2	ATCEA4 S3574	98			g42180 00, g24649 01	44, 42	220, 394	8.6e- 16, 1.1e- 34	(AC006 135) putati ve membra ne

143527	ATU005 467	ATL8S8 063:29 2..744	gap2	ATCEA4 C95785 _1	98	ATL8S8 063:32 5..633	0.96	g33353 72	43	301	2.6e- 33	(AC003 028) putati ve SRG1 protei n [Arabi dopsis thalia na]
143528	ATU005 468	ATL8C3 1445:1 ..2210	gap2	ATCEA4 C9386 _1	98	ATL8C3 1445:5 4..204 3	0.83	g17503 76	43	1873	9.8e- 172	(U8080 8) ubiqui tin activa ting enzyme [Arabi dopsis thalia na]
143529	ATU005 469	ATL8C1 2255:6 8..905	gap2	ATCEA4 S3813	98	ATL8C1 2255:8 26..38 9	0.75	g32928 16	43	680	5.4e- 52	(AI031 018) putati ve fizzy- relate d

													protein [Arabidopsis thaliana]
143530	ATU005 470	ATL8C1 0349:1 ..3338	gap2	ATCEA4 C26148 _1	98	ATL8C1 0349:7 83..23 93	0.75	g41603 02	43	97			(AJ011 894) cyclin D3.2 protein [Nicotiana tabacum]
143531	ATU005 471	ATL8C5 380:1. ..1347	gap2	ATCEA4 C2022 _1	98	ATL8C5 380:78 ..1347	0.75	g44551 93	43	1121	2.1e- 122		(AL035 440) fimbri n-like protein [ATFIM1] [Arabidopsis thaliana]
143532	ATU005 472	ATL8C1 6963:5 322..1	gap2	ATCEA4 C30781 _1, ATCEA4 S18032	98, 84	ATL8C1 6963:5 303..1 419	0.68	g24627 45	43	506	1.5e- 48		(AC002 292) Hypothetical protein [Arabidopsis thaliana]
143533	ATU005 473	ATL8C3 0281:1 ..1349	gap2	ATCEA4 C34229 _2	98	ATL8C3 0281:2 22..10 85	0.63	g31228 61	43	60	0.0006 0		D-3- PHOSPHOGLYCE RATE DEHYDR OGENASE

143534	ATU005 474	ATL8C3 3149:7 30..1	gap2	ATCEA4 C29479 _1	98	ATL8C3 3149:7 30..48 5	0.58	g44328 39	43	596	5.1e- 60	(PGDH) [Archa eoglob us fulgid us]
143535	ATU005 475	ATL8C1 7114:1 512..1	gap2	ATCEA4 S29959	98	ATL8C1 7114:1 486..2 52	0.56	g36680 96	43	492	2.3e- 30	(AC004 667) hypo thetical protein [Arabi dopsis thalia na]
143536	ATU005 476	ATL8C1 1664:1 04..11 26	gap2	ATCEA4 S11994 , ATCEA4 S8092	98, 94	ATL8C1 1664:3 19..76 5	0.50	g31525 60	43	506	1.3e- 49	(AC002 986) Strong simila rity to ser/th r protei n kinase s, especi ally gbIX97 980 from solanu m

143537	ATU005 477	ATL8C3 584:96 0..83	gap2	ATCEA4 C25929 1, ATCEA4 S29648	98, 97						43	367	1.6e- 33	(Y1427 4) putati ve serine /threo nine protei n kinase [Sorgh um bicolo r]	bertha ultii, gb X90 990 from solanu m tubero sum and gb D10 909 from A. thalia na. [Arabi dopsis thalia na]
143538	ATU005 478	ATL8C1 6650:1 ..543	gap2	ATCEA4 C7399 2, ATCEA4 S13530 , ATCEA4 S31672 , ATCEA4 S33662	98, 95, 90, 83						43	208	3.9e- 20	(AC004 218) putati ve riboso mal protei n I35 [Arabi dopsis thalia	

143539	ATU005 479	ATL8C4 0830:1 ..613	gap2	ATCEA4 C19052 1, ATCEA4 S23394 , ATCEA4 S26132	98, 88 97, 88				g11346 5	43	258	5.9e- 13	na] ADP,AT P CARRIE R PROTEI N (ADP/A TP TRANSL OCASE) (ADENI NE NUCLEO TIDE TRANSL OCATOR) (ANT) [Chlam ydomon as reinha rdtiil]
143540	ATU005 480	ATL8C9 529:12 61..1	gap2	ATCEA4 C1516 1, ATCEA4 S14105	98, 97				g33341 23	43	502	1.4e- 14	ATP SYNTHA SE GAMMA CHAIN, MITOCH ONDRIA L PRECUR SOR [Arabi dopsis thalia na]
143541	ATU005 481	ATL8C2 8838:1 ..594	gap2	ATCEA4 C6972 2, ATCEA4 C6972 1	98, 90				g21601 82	43	129	2.0e- 06	(AC000 132) ESTs gb ATT S1236, gb T43 334, gb

143542	ATU005 482	ATL8C1 2765:1 ..1324	gap2	ATCEA4 C10075 22, ATCEA4 S24502	98, 90						g31282 32	43	420	1.6e- 35	[N9701 9,gb A A39520 3 come from this gene. [Arabi dopsis thalia na]
143543	ATU005 483	ATL8C2 2229:4 030..4 419	gap2	ATCEA4 S34051	98	ATL8C2 2229:4 058..4 355	0.98				g29824 63	42	413	9.3e- 40	[AL022 223) putati ve protei n [Arabi dopsis thalia na]
143544	ATU005 484	ATL8S6 037:66 3..1	gap2	ATCEA4 C229_1 , ATCEA4 S18744	98, 94	ATL8S6 037:46 1..354	0.98				g22857 92	42	209	7.9e- 22	[AB004 568) cyanas e [Arabi dopsis thalia na]
143545	ATU005 485	ATL8C3 5546:1 ..567	gap2	ATCEA4 C12075 7_1	98	ATL8C3 5546:4 8..410	0.96				g48743 05	42	594	3.7e- 07	[AC006 053) unknow n protei

143546	ATU005 486	ATL8C4 0116:8 69..1	gap2	ATCEA4 S2125	98	ATL8C4 0116:6 89..10 5	0.93	g23179 01	42	349	5.1e- 34	n [Arabi dopsis thalia na]
143547	ATU005 487	ATL8C2 9130:1 044..1	gap2	ATCEA4 C26964 _1	98	ATL8C2 9130:1 044..1 20	0.83	g11763 25	42	533	3.6e- 51	GTP- BINDIN G PROTEI N TYPA/B IPA HOMOLO G [Haemo philus influe nzae Rd]
143548	ATU005 488	ATL8C9 688:1. .1716	gap2	ATCEA4 S26071 , ATCEA4 C12005 4_1, ATCEA4 S33387	98, 88 96, 88	ATL8C9 688:42 ..1319	0.80	g36953 88	42	406	2.0e- 35	(AF096 371) No defini tion line found [Arabi

143549	ATU005 489	ATL8C1 9189:1 537..1	gap2	ATCEA4 C30447 _1.	98	ATL8C1 9189:6 42..56	0.69	g47319 12	42	235	3.1e- 23	dopsis thalia na] (AF111 941) develo pment protei n DG1148 [Dicty osteli um discoi deum]
143550	ATU005 490	ATL8C2 4739:1 730..1	gap2	ATCEA4 C82686 _1, ATCEA4 S15391 , ATCEA4 S636	98, 97, 97	ATL8C2 4739:1 528..1 6	0.66	g30436 56	42	657	3.5e- 60	(AB011 138) KIAA05 66 protei n [Homo sapien s]
143551	ATU005 491	ATL8C3 903:1. .2898	gap2	ATCEA4 S32352	98	ATL8C3 903:11 18..28 98	0.48	g45393 59	42	59	0.053	(AL049 525) putati ve protei n [Arabi dopsis thalia na]
143552	ATU005 492	ATL8C3 8414:1 ..605	gap2	ATCEA4 S5, ATCEA4 S5973	98, 82	ATL8C3 8414:4 6..548	0.44	g26233 06	42	555	5.0e- 57	(AC002 409) unknow n protei n [Arabi dopsis thalia na]

143553	ATU005 493	ATL8C3 7948:1 ..727	gap2	ATCEA4 S6301	98				g44540 51	42	493	7.9e- 46	(AL035 394) putati ve polyga lactur onase [Arabi dopsis thalia na]
143554	ATU005 494	ATL8C1 2781:7 45..1	gap2	ATCEA4 C3514_ 1	98				g30333 77	42	488	2.2e- 39	(AC004 238) putati ve berber ine bridge enzyme [Arabi dopsis thalia na]
143555	ATU005 495	ATL8C2 1823:1 ..1129	gap2	ATCEA4 S13637	98				g24438 84	42	1281	2.4e- 133	(AC002 294) Simila r to RPS-2 diseas e resist ance protei n [Arabi dopsis thalia na]
143556	ATU005 496	ATL8C3 4586:1 122..1	gap2	ATCEA4 S29902	98				g45393 94	42	422	1.7e- 41	(AL035 526) putati ve protei n [Arabi

143557	ATU005 497	ATL8C3 4573:8 31..17 5	gap2	ATCEA4 C7807_2	98							g33193 41	42	366	2.8e- 23	dopsis thalia nal (AF077 407) simila r to Medica go sativa nuclei c acid bindin g protei n Alfin- 1 (GB:I0 7291) [Arabi dopsis thalia nal]
143558	ATU005 498	ATL8C4 4707:2 319..3 181	gap2	ATCEA4 S7816	98							g28326 06	42	401	2.0e- 19	(AL021 635) predic ted protei n [Arabi dopsis thalia nal]
143559	ATU005 499	ATL8S1 6361:1 ..543	gap2	ATCEA4 C60710 1, ATCEA4 S29072	98, 83							g25058 79	42	107	3.8e- 07	(Y1277 6) hypoth etical protei n [Arabi dopsis thalia nal]
143560	ATU005	ATL8C4	gap2	ATCEA4	98							g32362	42	413	6.5e-	(AC004

143561	500	7446:1 073..1	gap2	ATCEA4 C5368_1, ATCEA4 S1401	98, 94					37		42	809	1.0e- 79	684) putati ve riboto l dehydr ogenas e [Arabi dopsis thalia na]
143562	ATU005 502	ATL8S7 653:1. .608	gap2	ATCEA4 S29626 , ATCEA4 C61032 _1, ATCEA4 S1770	98, 84, 83					g24649 13		42	727	3.0e- 64	(Z9970 8) sugar transp orter like protei n [Arabi dopsis thalia na]
143563	ATU005 503	ATL8C2 6140:1 ..1158	gap2	ATCEA4 C55747 _1	98	ATL8C4 4941:8 59..41 6	0.96			g37460 59		41	270	2.1e- 26	(AC005 311) putati ve cystei nyl- tRNA synthe tase [Arabi dopsis thalia na]
										g29110 68		41			(Al021 960) G10- like protei n [Arabi dopsis

143564	ATU005 504	ATL8C1 3953:5 46..1	gap2	ATCEA4 C4042_1	98	ATL8C1 3953:5 33..13 3	0.93	g54363 2	41	409	2.7e- 44	thalia nal aldehy de reduct ase (EC 1.1.1.1. 21), NADPH- depend ent - bromeg rass [Bromu s inermi s]
143565	ATU005 505	ATL8S8 926:1. .580	gap2	ATCEA4 C135_1 , ATCEA4 S15272	98, 86	ATL8S8 926:10 ..172	0.91	g19441 32	41	703	1.1e- 74	(AB002 560) CUC2 [Arabi dopsis thalia nal]
143566	ATU005 506	ATL8C4 5341:1 755..1	gap2	ATCEA4 S3026	98	ATL8C4 5341:1 737..6 43	0.88	g27393 66	41	181	0.58	(AC002 505) SF16 like protei n [Arabi dopsis thalia nal]
143567	ATU005 507	ATL8C1 9386:4 717..1	gap2	ATCEA4 C14983 1, ATCEA4 S6717, ATCEA4 S27072	98, 96, 87	ATL8C1 9386:4 717..1 84	0.80	g25010 67	41	590	3.0e- 44	VALYL- TRNA SYNTH E-- E-- TRNA LIGASE) (VALRS

143568	ATU005 508	ATL8C4 5284:2 52..10 85	gap2	ATCEA4 C22482 1, ATCEA4 S7109	98, 96	ATL8C4 5284:2 52..10 06	0.78	g38853 28	41	354	1.6e- 24	(AC005 623) putati ve serine /threo nine protei n kinase [Arabi dopsis thalia na]
143569	ATU005 509	ATL8C4 7590:1 073..1	gap2	ATCEA4 C27976 _1	98	ATL8C4 7590:9 54..10 4	0.73	g44328 44	41	609	1.7e- 59	(AC006 283) unknow n protei n [Arabi dopsis thalia na]
143570	ATU005 510	ATL8C4 3675:6 53..1	gap2	ATCEA4 S1376	98	ATL8C4 3675:6 53..84	0.72	g26560 04	41	94		(Z9898 0) hypoth etical protei n [Schiz osacch aromyc es pombe]
143571	ATU005 511	ATL8C3 8074:6 092..1 968	gap2	ATCEA4 C13040 1, ATCEA4 S10306	98, 95	ATL8C3 8074:6 092..2 854	0.70	g16537 87	41	134	1.8e- 06	(D9091 6) hypoth etical protei

143572	ATU005 512	ATL8C4 575:76 9..1	gap2	ATCEA4 C115_1 , ATCEA4 C115_3 , ATCEA4 C115_6 , ATCEA4 S13614 , ATCEA4 C115_5 , ATCEA4 S29113	98, 95, 95, 95, 86, 86	ATL8C4 575:37 0..201	0.69	g45103 59	41	109	2.5e- 11	n [Synec hocyst is sp.] (AC006 921) putati ve ubiqui tin- riboso mal extens ion protei n CEP52, 5, partia l [Arabi dopsis thalia na]
143573	ATU005 513	ATL8C1 0257:5 96..16 73	gap2	ATCEA4 S14869 , ATCEA4 S804, ATCEA4 S761	98, 96, 93	ATL8C1 0257:1 188..6 37	0.69	g44159 08	41	159		(AC006 282) unknow n protei n [Arabi dopsis thalia na]
143574	ATU005 514	ATL8C4 9127:9 93..16 29	gap2	ATCEA4 S10991 , ATCEA4 S5024	98, 98	ATL8C4 9127:1 010..1 488	0.67	g17699 68	41	259	2.2e- 22	(Y1015 6) myrosi nase- associ ated protei n [Brass ica

143575	ATU005 515	ATL8C2 3577:7 5..149 5	gap2	ATCEA4 S11282 , ATCEA4 C84080 2, ATCEA4 C84080 1	98, 93 94, 93	ATL8C2 3577:5 59..13 05	0.56	g28326 23	41	290	8.0e- 20	napus] (AL021 711) protei n kinase - like protei n [Arabi dopsis thalia na]
143576	ATU005 516	ATL8C2 6507:9 38..1	gap2	ATCEA4 S29759 , ATCEA4 C13198 0 1, ATCEA4 S33931 , ATCEA4 S35641	98, 93, 93, 86			g24628 22	41	984	7.8e- 96	(AF000 657) hypoth etical protei n [Arabi dopsis thalia na]
143577	ATU005 517	ATL8C4 6668:1 ..707	gap2	ATCEA4 C6646 1, ATCEA4 C57020 1	98, 88	ATL8C4 6668:2 1..654	1.00	g38941 78	40	339	2.9e- 31	(AC005 312) putati ve nucle ic acid bindin g protei n [Arabi dopsis thalia na]
143578	ATU005 518	ATL8C4 5276:1 ..735	gap2	ATCEA4 S36344	98			g35825 20	41	472	2.0e- 27	(AF016 265) FUSCA3 [Arabi dopsis thalia na]

143579	ATU005 519	ATL8C1 2717:3 610..2 176	gap2	ATCEA4 C70910 _1	98	ATL8C1 2717:3 538..2 182	0.95	g37023 31	40	743	1.9e- 58	(AC005 397) hypoth etical protei n [Arabi dopsis thalia na]
143580	ATU005 520	ATL8C4 0721:2 38..86 3	gap2	ATCEA4 C17470 _1, ATCEA4 S35946	98, 94	ATL8C4 0721:3 20..76 4	0.94	g41933 20	40	641	2.7e- 66	(AF045 473) histon e deacet ylase [Zea mays]
143581	ATU005 521	ATL8C3 7401:5 89..15 81	gap2	ATCEA4 C13411 _1	98	ATL8C3 7401:6 32..14 78	0.94	g29470 62	40	375		(AC002 521) unknow n protei n [Arabi dopsis thalia na]
143582	ATU005 522	ATL8C2 2397:2 580..1	gap2	ATCEA4 C8164 _1, ATCEA4 S27313 , ATCEA4 S32653	98, 97, 87	ATL8C2 2397:2 497..1 14	0.93	g22136 20	40	749	6.6e- 77	(AC000 103) F21J9. 13 [Arabi dopsis thalia na]
143583	ATU005 523	ATL8C1 4228:2 25..41 91	gap2	ATCEA4 C11310 _1	98	ATL8C1 4228:2 49..41 91	0.93	g22816 97	40	118	3.0e- 17	(AF010 138) transc riptio n factor [Mus muscul us]

143584	ATU005 524	ATL8C3 2863:1 ..586	gap2	ATCEA4 S2385	98	ATL8C3 2863:4 0..522	0.93	g48352 45	40	390	1.9e- 36	(AL049 862) putati ve mitoch ondria l protei n [Arabi dopsis thalia na]
143585	ATU005 525	ATL8C2 0232:1 ..1383	gap2	ATCEA4 C61449 1, ATCEA4 S10684 , ATCEA4 C6650 1	98, 91, 85	ATL8C2 0232:5 4..112 6	0.89	g44552 10	40	629	2.1e- 43	(AL035 440) putati ve aspart ate- trNA ligase [Arabi dopsis thalia na]
143586	ATU005 526	ATL8C1 7708:2 112..1	gap2	ATCEA4 S7571, ATCEA4 S14444 , ATCEA4 S33746	98, 82, 82	ATL8C1 7708:2 112..5 1	0.86	g42622 39	40	415	9.1e- 38	(AC006 200) putati ve membra ne transp orter [Arabi dopsis thalia na]
143587	ATU005 527	ATL8C3 3771:3 081..1	gap2	ATCEA4 C7364 1, ATCEA4 S13824	98, 96	ATL8C3 3771:3 081..1 61	0.85	g39129 17	40	471	1.5e- 38	(AF001 308) putati ve NAK- like ser/th r

143588	ATU005 528	ATL8C2 3755:1 824..1 036	gap2	ATCEA4 S1030, ATCEA4 S7227	98, 89	ATL8C2 3755:1 761..1 036	0.84	g45860 49	40	624	1.4e- 45	prote n kinase [Arabi dopsis thalia na]
143589	ATU005 529	ATL8C2 988:54 3..136 4	gap2	ATCEA4 C31147 1, ATCEA4 S14495	98, 86	ATL8C2 988:56 1..132 6	0.82	g44689 84	40	651	1.9e- 68	(AL035 605) putati ve protei n [Arabi dopsis thalia na]
143590	ATU005 530	ATL8C1 2742:8 69..1	gap2	ATCEA4 C24780 _1	98	ATL8C1 2742:5 66..23 0	0.77	g28327 08	40	642	4.1e- 66	(AL021 713) beta- 1, 3- glucan ase- like protei n [Arabi dopsis thalia na]
143591	ATU005 531	ATL8C2 1359:2 148..6 76	gap2	ATCEA4 S14745 , ATCEA4 S5346	98, 98	ATL8C2 1359:2 148..1 083	0.65	g37859 77	40	976	1.5e- 70	(AC005 560) putati ve growth

143592	ATU005 532	ATL8C4 7812:9 95..1	gap2	ATCEA4 C8965_1, ATCEA4 C8761_1	98, 94	ATL8C4 7812:4 37..16 8	0.62	g45444 57	40	264	3.2e- 21	regula tor protei n [Arabi dopsis thalia na]
143593	ATU005 533	ATL8C4 8397:1 014..1 630	gap2	ATCEA4 C78898 1, ATCEA4 S14309	98, 96	ATL8C4 8397:1 014..1 565	0.61	g45443 99	40	988	1.2e- 99	(AC007 047) putati ve beta- ketoac yl-CoA syntha se [Arabi dopsis thalia na]
143594	ATU005 534	ATL8C4 2469:1 ..1169	gap2	ATCEA4 C89110 2, ATCEA4 S18386	98, 92	ATL8C4 2469:1 04..60 6	0.52	g44159 47	40	906	2.0e- 60	(AC006 418) putati ve laccas e [Arabi dopsis thalia na]
143595	ATU005 535	ATL8C2 7757:9	gap2	ATCEA4 S1987,	98, 88	ATL8C2 7757:8	0.43	g22136 29	40	450		(AC000 103)

143596	ATU005 536	ATL8S3 0949:1 ..625	gap2	ATCEA4 S32631	98	85..25 1	g31933 09	40	369	3.5e- 38	F21J9. 21 [Arabi dopsis thalia na]
143597	ATU005 537	ATL8C2 6256:1 ..515	gap2	ATCEA4 S27230	98		g41917 91	40	585	2.6e- 51	(AF069 300) No defini tion line found [Arabi dopsis thalia na]
143598	ATU005 538	ATL8S1 3588:1 ..572	gap2	ATCEA4 S5078, ATCEA4 C23611 _1	98, 93		g45389 59	40	139	1.1e- 09	(AC005 917) putati ve sf21 {Helia nthus annuus } protei n [Arabi dopsis thalia na]
143599	ATU005 539	ATL8C3 2631:1 ..517	gap2	ATCEA4 C5363_2	98		g45804 61	40	288	3.4e- 27	(AI049 488) putati ve protei n [Arabi dopsis thalia na]
											(AC006 081) unknow

143600	ATU005 540	ATL8C4 9326:1 143..1	gap2	ATCEA4 S34851 , ATCEA4 C15068 _2	98, 98					g48743 02	40	494	4.5e- 30	(AC006 053) putati ve beta- glucos idase [Arabi dopsis thalia na]	n protei n [Arabi dopsis thalia na]
143601	ATU005 541	ATL8C4 5054:1 508..1	gap2	ATCEA4 C11875 9_1	98	ATL8C4 5054:1 508..2 76	0.97			g40637 43	39	118	6.4e- 10	(AC005 851) hypoth etical protei n [Arabi dopsis thalia na]	n protei n [Arabi dopsis thalia na]
143602	ATU005 542	ATL8C4 9302:1 ..1585	gap2	ATCEA4 S6236	98	ATL8C4 9302:2 90..15 69	0.95			g32016 11	39	180	1.3e- 08	(AC004 669) unknow n protei n [Arabi dopsis thalia na]	n protei n [Arabi dopsis thalia na]
143603	ATU005 543	ATL8C9 686:98 6..1	gap2	ATCEA4 C42280 _1	98	ATL8C9 686:96 4..362	0.94			g25831 13	39	263	5.3e- 28	(AC002 387) hypoth etical protei n [Arabi dopsis thalia na]	n protei n [Arabi dopsis thalia na]

143604	ATU005 544	ATL8C2 3795:4 404..1	gap2	ATCEA4 C34609 _1	98	ATL8C2 3795:4 224..6 5	0.91	g44159 26	39	1643	1.0e- 131	dopsis thalia na]
143605	ATU005 545	ATL8C3 4844:1 ..1195	gap2	ATCEA4 S12481 , ATCEA4 C17609 _1	98, 96	ATL8C3 4844:8 73..11 89	0.88	g44553 54	39	69	0.079	(AL035 524) putati ve protei n [Arabi dopsis thalia na]
143606	ATU005 546	ATL8C2 7366:1 ..1891	gap2	ATCEA4 C23202 _1, ATCEA4 C81973 _1	98, 96	ATL8C2 7366:2 19..16 29	0.80	g44544 77	39	105		(AC006 234) hypoth etical protei n [Arabi dopsis thalia na]
143607	ATU005 547	ATL8C2 3901:9 39..1	gap2	ATCEA4 S2379	98	ATL8C2 3901:6 93..17 9	0.76	g24437 51	39	459	8.4e- 40	(AF020 303) fumara se [Arabi dopsis thalia na]
143608	ATU005 548	ATL8C3 041:35 4..1	gap2	ATCEA4 S13987	98	ATL8C3 041:35 1..65	0.67	g45859 77	39	290	1.3e- 31	(AC005 287) Unknown

143609	ATU005 549	ATL8C3 4405:1 ..623	gap2	ATCEA4 C1919_1	98	ATL8C3 4405:3 6..416	0.67	g86265 0	39	294	3.9e- 12	n protei n [Arabi dopsis thalia nal]
143610	ATU005 550	ATL8C2 6926:2 253..1 431	gap2	ATCEA4 C48853 _1	98	ATL8C2 6926:2 173..1 431	0.65	g49143 74	39	445	1.5e- 32	(AC007 584) putati ve protei n kinase [Arabi dopsis thalia nal]
143611	ATU005 551	ATL8C2 1101:1 ..594	gap2	ATCEA4 C8563_1	98	ATL8C2 1101:3 4..436	0.64	g14028 88	39	552	1.2e- 43	(X9813 0) unknow n [Arabi dopsis thalia nal]
143612	ATU005 552	ATL8C4 5503:1 042..1	gap2	ATCEA4 C11243 2, ATCEA4 C21361 _1	98, 97	ATL8C4 5503:1 041..2 1	0.59	g37859 77	39	285	4.3e- 14	(AC005 560) putati ve growth regula tor protei

143613	ATU005 553	ATL8C3 609:62 3..1	gap2	ATCEA4 C76554 _1	98	ATL8C3 609:53 6..330	0.55	g32362 55	39	456	6.6e- 46	(AC004 684) hypoth etical protei n [Arabi dopsis thalia na]
143614	ATU005 554	ATL8C1 7465:2 31..12 82	gap2	ATCEA4 S13843 , ATCEA4 S35793	98, 97	ATL8C1 7465:8 92..10 84	0.52	g31528 80	39	449	2.0e- 44	(AF063 246) cell wall invert ase; beta- fructo furano sidase [Pisum sativu m]
143615	ATU005 555	ATL8C1 6660:2 307..3 242	gap2	ATCEA4 S32504	98			g45860 56	39	1224	6.4e- 92	(AC007 020) unknow n protei n [Arabi dopsis thalia na]
143616	ATU005 556	ATL8C1 7944:1 181..1	gap2	ATCEA4 C25339 _1	98			g45444 40	39	1290		(AC006 592) unknow n protei n [Arabi dopsis thalia na]

143617	ATU005 557	ATL8S1 3357:1 81..51 0	gap2	ATCEA4 C8970_1, ATCEA4 C8970_2	98, 88					g45305 85	39	98	8.5e- 07	dopsis thalia na] (AF130 978) B12D protei n [Ipomo ea batata s]
143618	ATU005 558	ATL8C1 4809:1 362..7 75	gap2	ATCEA4 S12670 , ATCEA4 S4421	98, 95					g12053 9	39	142	2.5e- 06	NADH- PLASTO QUINON E OXIDOR EDUCTA SE SUBUNI T I (FRXB PROTEI N) [Nicot iana tabacu m]
143619	ATU005 559	ATL8C3 5506:8 19..1	gap2	ATCEA4 C35680 _1	98					g45390 08	39	312	3.3e- 19	(AL049 481) lipase -like protei n [Arabi dopsis thalia na]
143620	ATU005 560	ATL8C9 317:13 65..49 4	gap2	ATCEA4 C64233 _1, ATCEA4 S34283	98, 88	ATL8C9 317:11 52..56 9	0.97			g32582 82	38	102	3.6e- 06	(AP000 007) 381aa long hypoth etical protei

143621	ATU005 561	ATL8C1 9293:1 799..1	gap2	ATCEA4 C23128 _1	98	ATL8C1 9293:1 711..1 63	0.92	g48503 99	38	1106	3.4e- 63	(AC007 357) F3F19. 18 [Arabi dopsis thalia na]
143622	ATU005 562	ATL8S2 179:1. .592	gap2	ATCEA4 S11513 , ATCEA4 C942_1	98, 98	ATL8S2 179:83 ..369	0.92	g11685 29	38	468	1.9e- 32	SERINE /THREO NINE- PROTEI N KINASE ASK1 [Arabi dopsis thalia na]
143623	ATU005 563	ATL8C6 917:1. .1726	gap2	ATCEA4 C33488 _1	98	ATL8C6 917:16 6..171 6	0.88	g24433 29	38	999	5.6e- 100	(D8612 2) Mei2- like protei n [Arabi dopsis thalia na]
143624	ATU005 564	ATL8C1 7305:1 525..6 86	gap2	ATCEA4 C1343 _2, ATCEA4 C1271_1	98, 91	ATL8C1 7305:1 308..8 74	0.88	g13512 21	38	485	7.6e- 29	TRANSC RIPTIO N INITIA TION FACTOR IIB (TFIIB) [Arabi dopsis

143625	ATU005 565	ATL8C1 197:71 4..1	gap2	ATCEA4 C8539_1	98	ATL8C1 197:62 1..68	0.86	g32818 48	38	247	1.6e- 24	thalia na] (AL031 004) putati ve protei n [Arabi dopsis thalia na]
143626	ATU005 566	ATL8C1 8952:8 90..1	gap2	ATCEA4 S7046, ATCEA4 C15623 1, ATCEA4 S21393	98, 96, 82	ATL8C1 8952:4 87..30 7	0.74	g44540 32	38	165	9.5e- 15	(AL035 394) putati ve protei n [Arabi dopsis thalia na]
143627	ATU005 567	ATL8C2 2093:1 ..1475	gap2	ATCEA4 C6806_1, ATCEA4 S19235 , ATCEA4 S31385 , ATCEA4 S19431 , ATCEA4 C6806_6, ATCEA4 C6806_2	98, 97, 93, 92, 91, 85	ATL8C2 2093:4 65..12 93	0.72	g62960 2	38	1174	4.1e- 111	probab le imbibi tion protei n - wild cabbag e [Brass ica olerac ea]
143628	ATU005 568	ATL8C4 7305:1 688..1	gap2	ATCEA4 S6939	98	ATL8C4 7305:1 634..2 2	0.68	g29824 52	38	663	3.8e- 75	(AL022 223) recept or protei

143629	ATU005 569	ATL8C2 9060:3 38..78 7	gap2	ATCEA4 C10816 1_1	98	ATL8C2 9060:3 38..68 0	0.41	g34618 18	38	124	9.4e- 10	n kinase -like protei n [Arabi dopsis thalia na]
143630	ATU005 570	ATL8C4 2621:2 663..4 524	gap2	ATCEA4 S2497	98	ATL8C4 2621:2 663..3 699	0.40	g38853 40	38	1226	8.6e- 32	(AC005 623) unknow n protei n [Arabi dopsis thalia na]
143631	ATU005 571	ATL8C2 68:455 ..1580	gap2	ATCEA4 S351	98			g38314 44	38	951	2.4e- 69	(AC005 819) putati ve protei n kinase [Arabi dopsis thalia na]
143632	ATU005 572	ATL8C4 9688:5	gap2	ATCEA4 C51413	98			g40918 06	38	494	2.6e- 49	(AF052 585)

143633	ATU005 573	52..97 0	gap2	ATCEA4 S32463 , ATCEA4 C12310 9_1	98, 96					g48952 30	38	448	2.6e- 42	(AC007 660) unknown protein [Arabi dopsis thalia na]	CONSTA NS- like protein 2 [Malus domest ica]
143634	ATU005 574	ATL8C4 305:1. .1772	gap2	ATCEA4 S7737, ATCEA4 S434	98, 85	ATL8C8 305:12 1..177 2				g34149 30	37	103	0.0020	(AF076 599) FutA [Dicty osteli um discoi deum]	
143635	ATU005 575	ATL8C2 2232:6 2..125 5	gap2	ATCEA4 C5005_ 1	98	ATL8C2 2232:6 2..121 0				g22448 93	37	594	4.7e- 50	(Z9733 8) simila rity to cytoch rome P450 [Arabi dopsis thalia na]	
143636	ATU005 576	ATL8C4 7860:3 94..10 63	gap2	ATCEA4 C384_1	98	ATL8C4 7860:3 94..97 3				g41764 20	37	724	6.3e- 78	(AB008 097) cytoch rome P450 [Arabi dopsis]	

143637	ATU005 577	ATL8C4 8340:1 ..2393	gap2	ATCEA4 S5304	98	ATL8C4 8340:3 3..234 6	0.84	g45593 29	37	269	1.4e- 22	thalia na] (AC007 087) putati ve protei n kinase MAP3K [Arabi dopsis thalia na]
143638	ATU005 578	ATL8C2 5186:1 ..1458	gap2	ATCEA4 C1571_1	98	ATL8C2 5186:6 34..12 05	0.77	g41025 98	37	1291	1.2e- 99	(AF013 466) auxin respon se factor 4 [Arabi dopsis thalia na]
143639	ATU005 579	ATL8C5 552:1. .567	gap2	ATCEA4 C467_1 , ATCEA4 S20756	98, 90	ATL8C5 552:15 4..267	0.73	g25982 27	37	407	3.6e- 22	(AJ222 585) AT- hook protei n 1 [Arabi dopsis thalia na]
143640	ATU005 580	ATL8C7 800:1. .859	gap2	ATCEA4 C11505 2, ATCEA4 S8378	98, 84	ATL8C7 800:68 ..822	0.72	g44551 80	37	640	4.8e- 44	(AL035 521) putati ve protei n [Arabi dopsis thalia na]

143645	ATU005 585	ATL8C2 6889:2 471..7 13	gap2	ATCEA4 S15633 , ATCEA4 S763, ATCEA4 S26012	98, 96, 94	ATL8C2 6889:2 207..7 13	0.43	g41851 39	37	679	2.2e- 62	(AC005 724) putati ve diacyl glycer ol kinase [Arabi dopsis thalia na]	DNAJ heatsh ock protei n gb U32 803 from Haemop hilus influe nzae. [Arabi dopsis thalia na]
143646	ATU005 586	ATL8S3 10:368 ..1	gap2	ATCEA4 S14944 , ATCEA4 C5703_1	98, 98			g45586 78	37	271	9.5e- 16	(AC006 586) unknow n protei n [Arabi dopsis thalia na]	(AC006 586) unknow n protei n [Arabi dopsis thalia na]
143647	ATU005 587	ATL8C3 3512:4 23..15 85	gap2	ATCEA4 S619, ATCEA4 S2479, ATCEA4 C1165_6	98, 97, 94			g28297 92	37	327	3.5e- 36	SOLUBL E GLYCOG EN (STARC H) SYNTHA	SOLUBL E GLYCOG EN (STARC H) SYNTHA

143652	ATU005 592	ATL8C3 6399:1 733..1	gap2	ATCEA4 C2516_1	98	ATL8C3 6399:1 506..5 0	0.89	g28326 25	36	356	7.9e- 34	RNA- bindin g protei n [Schiz osacch aromyc es pombel] (AL021 711) putati ve protei n [Arabi dopsis thalia na]
143653	ATU005 593	ATL8C2 5209:1 791..3 21	gap2	ATCEA4 S2759, ATCEA4 C2020_1	98, 97	ATL8C2 5209:1 586..7 41	0.87	g20523 83	36	474	5.3e- 18	(U6634 5) calret iculin [Arabi dopsis thalia na]
143654	ATU005 594	ATL8S2 5316:5 59..1	gap2	ATCEA4 S12165	98	ATL8S2 5316:4 37..53	0.83	g22448 35	36	509	3.2e- 50	(Z9733 7) protei n kinase homolo g [Arabi dopsis thalia na]
143655	ATU005 595	ATL8S2 7033:5 66..1	gap2	ATCEA4 C40471 _1	98	ATL8S2 7033:4 27..12 4	0.83	g42205 23	36	647	6.9e- 67	(AL035 356) putati ve alliin lyase

143656	ATU005 596	ATL8C5 629:51 9..135 3	gap2	ATCEA4 C1826_1, ATCEA4 C32473 ATCEA4 S27298	98, 89 97, 89	ATL8C5 629:59 3..101 8	0.79	g38224 03	36	766	[Arabi dopsis thalia na] (AF087 932) hydrop eroxid e lyase [Arabi dopsis thalia na]
143657	ATU005 597	ATL8C5 259:29 3..511 4	gap2	ATCEA4 S2122, ATCEA4 S5551	98, 85	ATL8C5 259:36 7..501 6	0.73	g31525 87	36	1493	(AC002 986) Simila r to CREB- bindin g protei n homolo g gb U88 570 from D. melano gaster and contai ns simila rity to callus - associ ated protei n gb U01 961

143658	ATU005 598	ATL8C3 5448:6 82...1	gap2	ATCEA4 S33899 , ATCEA4 C11544 4_1	98, 98	ATL8C3 5448:6 69...73	0.73	g38745 63	36	192	2.1e- 15	(Z8104 2) simila r to Yeast hypothe tical protei n YFY6 like; cDNA EST yk206h 5.3 comes from this gene; cDNA EST yk206h 5.5 comes from this gene; cDNA EST yk303h
												from Nicoti ana tabacu m. EST gb W43 427 comes from this gene. [Arabi dopsis thalia nal

143659	ATU005 599	ATL8C2 2719:2 97..88 9	gap2	ATCEA4 C24810 _1	98	ATL8C2 2719:2 97..52 2	0.72	g39280 85	36	262	9.0e- 17	(AC005 770) unknown protein [Arabi dopsis thalia na]	1.3 comes from this gene; cDNA EST yk303h 1.5 comes from this gene; cDNA ...
143660	ATU005 600	ATL8C2 9321:1 ..4076	gap2	ATCEA4 S23846 , ATCEA4 S851	98, 87	ATL8C2 9321:9 4..407 6	0.65	g29807 90	36	569	1.6e- 54	(AL022 197) hypoth etical protein [Arabi dopsis thalia na]	comes from this gene; cDNA EST yk303h 1.5 comes from this gene; cDNA ...
143661	ATU005 601	ATL8C4 9836:1 ..815	gap2	ATCEA4 S27406	98	ATL8C4 9836:5 6..786	0.59	g45393 83	36	374	3.4e- 22	(AL035 526) putati ve protein (fragm ent). [Arabi	comes from this gene; cDNA EST yk303h 1.5 comes from this gene; cDNA ...

143662	ATU005 602	ATL8C1 0023:1 286..1	gap2	ATCEA4 C46464 1, ATCEA4 S32220	98, 96	ATL8C1 0023:8 24..12 3	0.51	g39253 63	36	613	(AF067 961) homeod omain protei n [Malus domest ical]
143663	ATU005 603	ATL8C1 1744:1 ..1261	gap2	ATCEA4 C5009 1	98	ATL8C1 1744:2 79..11 64	0.50	g48369 17	36	482	(AC007 153) 80099 [Arabi dopsis thalia na]
143664	ATU005 604	ATL8C3 2607:1 114..1	gap2	ATCEA4 C11798 4_1	98	ATL8C3 2607:9 53..49	0.45	g21321 89	36	59	hypoth etical protei n YPL107 w - yeast (Sacch aromyc es cerevi siae) [Sacch aromyc es cerevi siae]
143665	ATU005 605	ATL8C5 134:11 40..1	gap2	ATCEA4 C65366 _1	98	ATL8C5 134:59 8..98	0.40	g28326 57	36	171	(AL021 710) putati ve protei n [Arabi dopsis thalia

143666	ATU005 606	AT18C4 9436:1 ..552	gap2	ATCEA4 C3357_2, ATCEA4 S14723, ATCEA4 C3357_4	98, 97, 95					36	939278 38	551	0.020	(AC005 727) unknown protein [Arabidopsis thaliana]
143667	ATU005 607	AT18C4 0487:1 116..1 597	gap2	ATCEA4 C78019 3, ATCEA4 C78019 1, ATCEA4 S28957	98, 94, 90					36	943371 75	153	3.0e- 15	(AC006 416) ESTs gb T20 589, gb T04 648, gb AA5 97906, gb T04 111, gb R84 180, gb R65 428, gb T44 439, gb T76 570, gb R90 004, gb T45 020, gb T42 457, gb T20 921, gb AA0 42762 and gb AA7 20210 come from

143668	ATU005 608	ATL8C2 1173:2 984..2 103	gap2	ATCEA4 S24943	98					g43371 96	36	863	1.3e- 90	(AC006 403) putati ve serine /threo nine recept or kinase [Arabi dopsis thalia na]	this gene. [Arabi dopsis thalia na]
143669	ATU005 609	ATL8S1 88:1.. 438	gap2	ATCEA4 C10320 _1	98					g28574 1	36	256	1.3e- 23	(D1455 0) EDGP precur sor [Daucu s carota]	
143670	ATU005 610	ATL8C1 2055:1 ..771	gap2	ATCEA4 C11916 2_1	98					g22450 14	36	597	2.4e- 58	(Z9734 1) glucos yltran sferas e homolo g [Arabi dopsis thalia na]	
143671	ATU005 611	ATL8C1 4165:1 045..1	gap2	ATCEA4 C30174 _1	98					g45062 15	35	343	3.8e- 28	protea some (proso me,	

143672	ATU005 612	ATL8C4 8555:2 357..1	gap2	ATCEA4 S34049 , ATCEA4 C10880 _2	98, 90	ATL8C4 8555:2 306..1 887	0.96	g28276 46	35	285	5.0e- 27	macrop ain) 26S subuni t, ATPase , 6 [Homo sapien s]
143673	ATU005 613	ATL8C3 6661:1 34..10 62	gap2	ATCEA4 S2590	98	ATL8C3 6661:4 10..10 54	0.95	g73193 5	35	107	0.0001 3	HYPOTH ETICAL 66.4 KD PROTEI N IN SMC3- MRPL8 INTERG ENIC REGION [Sacch. aromyc es cerevi siae]
143674	ATU005 614	ATL8C3 7377:1 ..1309	gap2	ATCEA4 C12715 0_1, ATCEA4 S35135	98, 93	ATL8C3 7377:8 1..120 5	0.94	g31232 86	35	373		LEUCYL -TRNA SYNTHE TASE (LEUCI NE--

143679	ATU005 619	ATL8C2 1290:4 71..11 67	gap2	ATCEA4 C12539 1, ATCEA4 S8115	98, 96	ATL8C2 1290:4 71..95 1	0.88	g42185 35	35	325	1.6e- 30	proteins [Arabidopsis thaliana] (AJ010829) GRAB1 protein [Triticum sp.]
143680	ATU005 620	ATL8C2 1821:8 03..1	gap2	ATCEA4 C72892 1, ATCEA4 S26011	98, 97	ATL8C2 1821:7 59..22 9	0.86	g39831 03	35	310	7.4e- 35	(AF097441) phenylalanine e-tRNA synthetase [Homo sapiens]
143681	ATU005 621	ATL8C1 4655:1 053..1	gap2	ATCEA4 C11547 31, ATCEA4 S29023 , ATCEA4 S29039 , ATCEA4 S29048	98, 97, 85, 85	ATL8C1 4655:1 017..2 06	0.86	g58474 1	35	219	3.1e- 13	ANKYRI N REPEAT PROTEIN (AKRP) [Arabidopsis thaliana]
143682	ATU005 622	ATL8C3 0635:1 146..1	gap2	ATCEA4 S7179	98	ATL8C3 0635:8 94..26 5	0.86	g36872 30	35	697	5.9e- 60	(AC005169) hypothetical protein [Arabidopsis thaliana]

143683	ATU005 623	ATL8C2 6605:3 518..1 349	gap2	ATCEA4 C704_1	98	ATL8C2 6605:3 280..1 576	0.85	g44328 27	35	1434	3.0e- 100	(AC006 593) putati ve ADP- ribose polyme rase [Arabi dopsis thalia na]
143684	ATU005 624	ATL8C3 7320:1 614..1	gap2	ATCEA4 S7794	98	ATL8C3 7320:1 561..1 08	0.85	g18414 68	35	411		(Y1099 0) Tyrosy l-tRNA synthe tase [Nicot iana tabacu m]
143685	ATU005 625	ATL8C2 5830:1 ..698	gap2	ATCEA4 S30500 , ATCEA4 S1943	98, 86	ATL8C2 5830:1 43..49 5	0.82	g22450 83	35	459	2.3e- 22	(Z9734 3) hypoth etical protei n [Arabi dopsis thalia na]
143686	ATU005 626	ATL8C3 0550:1 ..3220	gap2	ATCEA4 C18924 _1	98	ATL8C3 0550:1 093..2 817	0.79	g30236 51	35	200	0.0001 1	D- LACTAT E DEHYDR OGENAS E [Kluyv eromyc es lactis]
143687	ATU005 627	ATL8C4 3872:3	gap2	ATCEA4 C4417	98, 82	ATL8C4 3872:3	0.74	g39278 25	35	492	1.3e- 45	(AC005 727)

143688	ATU005 628	ATL8C4 0041:1 ..598	gap2	ATCEA4 C29396 _1	98	ATL8C4 0041:1 57..51 8	0.74	g29825 83	35	374	6.8e- 32	(AJ003 135) polyga lactur onase [Arabi dopsis thalia na]
143689	ATU005 629	ATL8C2 6046:8 78..1	gap2	ATCEA4 C46708 _1	98	ATL8C2 6046:7 94..78	0.73	g16528 92	35	332	8.5e- 34	(D9090 9) ABC transp orter [Synec' hocyst is sp.]
143690	ATU005 630	ATL8C4 104:1. .779	gap2	ATCEA4 C15797 _2	98	ATL8C4 104:18 ..647	0.73	g22448 06	35	454	1.3e- 48	(Z9733 6) hypoth etical protei n [Arabi dopsis thalia na]
143691	ATU005 631	ATL8S9 23:685 ..93	gap2	ATCEA4 S6789	98	ATL8S9 23:578 ..93	0.71	g42205 27	35	289	3.0e- 29	(AL035 356) putati ve protei n [Arabi

143692	ATU005 632	ATL8C4 7172:1 ..1681	gap2	ATCEA4 S27087 , ATCEA4 S34503	98, 84	ATL8C4 7172:1 54..16 81	0.68	g24648 65	35	896	4.0e- 92	(Z9970 7) pectin esterase like protein [Arabi dopsis thalia na]
143693	ATU005 633	ATL8C1 0916:4 05..11 83	gap2	ATCEA4 C40545 _2	98	ATL8C1 0916:8 48..11 22	0.44	g34618 45	35	149	8.7e- 14	(AC005 315) hypoth etical protein [Arabi dopsis thalia na]
143694	ATU005 634	ATL8C1 7130:6 99..21 90	gap2	ATCEA4 C6491_1	98			g27393 76	35	841	9.5e- 65	(AC002 505) putative permease [Arabi dopsis thalia na]
143695	ATU005 635	ATL8C9 738:1. .1527	gap2	ATCEA4 C62282 _1	98			g11704 10	35	252	1.6e- 12	HOMEOB OX PROTEIN HAT3.1 [Arabi dopsis thalia na]

143696	ATU005 636	ATL8C2 8598:7 71..1	gap2	ATCEA4 C75319 _2	98	ATL8C2 8598:7 68..98	0.99	g21941 25	34	868	1.0e- 91	(AC002 062) ESTs gb R30 459,gb IN3844 1 come from this gene. [Arabi dopsis thalia na]
143697	ATU005 637	ATL8C4 4443:1 188..1	gap2	ATCEA4 C17162 _1, ATCEA4 S15809 , ATCEA4 S29732	98, 82 90, 82	ATL8C4 4443:8 82..28	0.99	g26739 61	34	143	6.0e- 07	(U7047 7) astroc ytic NOVA- like RNA- bindin g protei n [Homo sapien s]
143698	ATU005 638	ATL8C4 6014:7 45..1	gap2	ATCEA4 S6198	98	ATL8C4 6014:6 99..38	0.98	g39278 36	34	942	3.1e- 89	(AC005 727) unknow n protei n [Arabi dopsis thalia na]
143699	ATU005 639	ATL8C6 703:27 0..99	gap2	ATCEA4 S33775 , ATCEA4 C279_9 , ATCEA4	98, 92, 86	ATL8C6 703:27 0..210	0.98	g11459 1	34	172	4.1e- 13	ATP SYNTHA SE EPSILO N CHAIN [Arabi

143700	ATU005 640	ATL8C9 64:133 6..115	gap2	ATCEA4 C585_1	98	ATL8C9 64:126 0..377	0.93	g21547 15	34	856	2.5e- 70	dopsis thalia na] (Y0941 8) CDPK- relate d protei n kinase [Arabi dopsis thalia na]
143701	ATU005 641	ATL8C1 7699:9 58..1	gap2	ATCEA4 S336	98	ATL8C1 7699:8 74..29 8	0.91	g22621 05	34	369	3.2e- 36	(AC002 343) unknow n protei n [Arabi dopsis thalia na]
143702	ATU005 642	ATL8C2 4812:3 209..1	gap2	ATCEA4 C812_1 , ATCEA4 S4357	98, 84	ATL8C2 4812:3 105..1 5	0.89	g47046 62	34	216	1.1e- 16	(AF116 860) uracil phosph oribos yltran sferase 1. [Arabi dopsis thalia na]
143703	ATU005 643	ATL8C4 143:34 10..1	gap2	ATCEA4 S28936 , ATCEA4 C4837_1, ATCEA4 S35618	98, 93 96, 93	ATL8C4 143:31 42..52 5	0.81	g30636 99	34	233	3.4e- 19	(AL022 537) putati ve protei n [Arabi dopsis

143704	ATU005 644	ATL8C4 0251:2 21..95 9	gap2	ATCEA4 C6582_ 1, ATCEA4 S13876 , ATCEA4 S19628	98, 98, 92	ATL8C4 0251:2 99..78 2	0.73	g26233 03	34	817	5.6e- 84	thalia nal (AC002 409) putati ve cytoch rome P450 [Arabi dopsis thalia nal]
143705	ATU005 645	ATL8C8 506:16 38..1	gap2	ATCEA4 C84760 1, ATCEA4 C33574 1, ATCEA4 S30111	98, 97, 94	ATL8C8 506:16 21..97	0.73	g23520 96	34	56	7.9e- 05	(U9702 2) orf; simila r to serine /threo nine protei n phosph atase [Fervi dobact erium island icum]
143706	ATU005 646	ATL8C1 0961:4 050..1	gap2	ATCEA4 S63	98	ATL8C1 0961:4 050..6 0	0.67	g45835 46	34	179	9.7e- 14	(AJ010 819) GrpE protei n [Arabi dopsis thalia nal]
143707	ATU005 647	ATL8C2 5391:1 ..1797	gap2	ATCEA4 C37954 1	98	ATL8C2 5391:5 6..169 1	0.56	g33554 77	34	2220	2.3e- 178	(AC004 218) putati ve P- glycop rotein

143708	ATU005 648	ATL8S1 0401:5 98..1	gap2	ATCEA4 C25336 1, ATCEA4 S35393	98, 97	ATL8S1 0401:5 44..40 9	0.55	g23524 92	34	435	3.4e- 42	(AF005 047) transp ort inhibi tor respon se 1 [Arabi dopsis thalia na]
143709	ATU005 649	ATL8C3 1901:1 ..639	gap2	ATCEA4 S4066	98	ATL8C3 1901:8 3..639	0.54	g10200 96	34	496	1.8e- 50	(D4983 2) stearo yl- acyl carrie r protei n desatu rase [Sesam um indicu m]
143710	ATU005 650	ATL8C1 6364:2 61..15 38	gap2	ATCEA4 S30588	98	ATL8C1 6364:4 37..15 38	0.41	g27603 25	34	369	2.7e- 24	(AC002 130) F1N21. 10 [Arabi dopsis thalia na]
143711	ATU005 651	ATL8C2 0901:1 526..2 049	gap2	ATCEA4 C14066 1, ATCEA4 S17791	98, 95			g22450 05	34	645	3.6e- 54	(Z9734 1) hypoth etical protei

143712	ATU005 652	ATL8C2 4193:5 46..1	gap2	ATCEA4 C1589_2	98					g29245 16	34	521	3.1e- 50	(AL022 023) WD-40 repeat protei n (MSI3) [Arabi dopsis thalia na]
143713	ATU005 653	ATL8C2 401:1. .680	gap2	ATCEA4 C30592 _1	98					g45389 41	34	849	1.4e- 69	(AL049 483) NPR1 like protei n [Arabi dopsis thalia na]
143714	ATU005 654	ATL8C9 709:1. .380	gap2	ATCEA4 C1315_1, ATCEA4 S18080	98, 84					g11729 77	34	253	4.4e- 22	60S RIBOSO MAL PROTEI N L18 [Arabi dopsis thalia na]
143715	ATU005 655	ATL8C3 9285:3 48..1	gap2	ATCEA4 C72195 _1, ATCEA4 S14273	98, 95					g39803 93	34	378	1.7e- 34	(AC004 561) putati ve glutat hione S- transf erase [Arabi na]

143716	ATU005 656	ATL8C2 6404:7 05..1	gap2	ATCEA4 S11990	98						g44328 46	34	188	2.6e- 20	(AC006 283) unknown protein [Arabi dopsis thalia na]
143717	ATU005 657	ATL8C4 7328:1 ..1455	gap2	ATCEA4 C51804 1, ATCEA4 C26087 1	98, 94	ATL8C4 7328:5 1..134 4	0.97	g39132 40	33	918	3.0e- 74				MAGNES IUM- CHELAT ASE SUBUNI T CHLD PRECUR SOR (MG- PROTOP ORPHYR IN IX CHELAT ASE) (MG- CHELAT ASE SUBUNI T D) [Nicot iana tabacu m]
143718	ATU005 658	ATL8C4 7474:1 ..799	gap2	ATCEA4 C1791 1	98	ATL8C4 7474:2 54..73 0	0.97	g38060 98	33	1020	1.6e- 94				(AF079 100) argini ne- tRNA- protei n transf erase

143719	ATU005 659	ATL8C7 595:49 0..1	gap2	ATCEA4 C2586_1	98	ATL8C7 595:15 0..18	0.96	g45390 05	33	189	1.0e- 17	1: Atelp [Arabi dopsis thalia nal] (AL049 481) putati ve oxidor educta se [Arabi dopsis thalia nal]
143720	ATU005 660	ATL8S1 9347:1 ..708	gap2	ATCEA4 C7087_1, ATCEA4 S990	98, 97	ATL8S1 9347:4 29..69 8	0.83	g49143 17	33	278	1.1e- 27	(AC005 489) FL4N23 .3 [Arabi dopsis thalia nal]
143721	ATU005 661	ATL8C3 8977:9 87..1	gap2	ATCEA4 C23737_1	98	ATL8C3 8977:8 08..22	0.81	g35112 23	33	400	7.7e- 32	(AF069 528) plant adhesi on molecu le 1 [Arabi dopsis thalia nal]
143722	ATU005 662	ATL8C3 8408:8 37..57	gap2	ATCEA4 C16792_1	98	ATL8C3 8408:7 29..57	0.73	g45393 35	33	512	1.6e- 51	(AL035 539) putati ve protei n [Arabi dopsis thalia

143723	ATU005 663	ATL8C2 2978:1 086..1 691	gap2	ATCEA4 C4311_2, ATCEA4 C4311_1, ATCEA4 S10348, ATCEA4 C4311_3	98, 97, 87, 87	ATL8C2 2978:1 192..1 687	0.70	g25116 93	33	286	1.7e- 28	na] (Z9995 4) cystei ne protei nase precu sor [Phase olus vulgar is]
143724	ATU005 664	ATL8C1 8644:4 42..27 54	gap2	ATCEA4 C28504 1, ATCEA4 S19118	98, 86	ATL8C1 8644:5 37..27 30	0.68	g22526 32	33	613	1.2e- 45	(U9597 3) Barley Mlo protei n isolog [Arabi dopsis thalia na]
143725	ATU005 665	ATL8C1 8575:1 036..2 820	gap2	ATCEA4 C16523 1, ATCEA4 S32443	98, 92	ATL8C1 8575:1 634..2 449	0.64	g39280 78	33	285	8.8e- 32	(AC005 770) putati ve protei n kinase , calciu m depend ent [Arabi dopsis thalia na]
143726	ATU005 666	ATL8C1 3281:7 70..1	gap2	ATCEA4 C13228 1, ATCEA4 S6206	98, 91	ATL8C1 3281:7 70..13 3	0.57	g30803 71	33	338	2.3e- 34	(AL022 580) putati ve pectin

143727	ATU005 667	ATL8C3 9998:3 22..82 3	gap2	ATCEA4 S30008 , ATCEA4 S6361	98, 93	ATL8C3 9998:3 22..69 8	0.54	g44540 16	33	140	0.0042	(AL035 396) UMP/CM P kinase like protei n [Arabi dopsis thalia na]
143728	ATU005 668	ATL8C4 8520:1 993..1	gap2	ATCEA4 C84570 _1	98	ATL8C4 8520:1 037..1 95	0.53	g22890 11	33	1217	2.3e- 124	(AC002 335) MYB transc riptio n factor isolog [Arabi dopsis thalia na]
143729	ATU005 669	ATL8C2 5099:1 105..1	gap2	ATCEA4 S7809	98	ATL8C2 5099:1 059..2 32	0.53	g36881 78	33	1005	1.4e- 103	(AL031 804) putati ve protei n [Arabi dopsis thalia na]
143730	ATU005 670	ATL8C9 987:1.	gap2	ATCEA4 C76050	98, 97, 94			g42622 33	33	468	1.5e- 46	(AC006 200)

143731	ATU005 671	.1026	gap2	2, ATCEA4 S5845, ATCEA4 S15853	98, 97					g29593 58	33	152	0.050	(X96758) clathrin coat assembly protein API7 [Zea mays]
143732	ATU005 672	ATL8C1 336:53 23..43 20	gap2	ATCEA4 S33395 , ATCEA4 C12062 1_1	98, 88					g22451 17	33	141	4.1e-11	(Z97343) hypothetical protein [Arabi dopsis thaliana]
143733	ATU005 673	ATL8C1 0629:7 56..1	gap2	ATCEA4 C1779_1, ATCEA4 S3123	98, 94					g29824 50	33	360		(AL02223) putative protein [Arabi dopsis thaliana]
143734	ATU005 674	ATL8C3 8015:2 65..17 11	gap2	ATCEA4 C14761 _1	98					g29795 59	33	281	1.4e-26	(AC003680) putative DNA binding

143738	ATU005 678	ATL8C3 764:1. .1719	gap2	ATCEA4 S11806	98	ATL8C3 764:18 1..170 9	0.91	g25823 81	32	1292	2.7e- 132	(AJ002 414) hnRNP- like protein [Arabi dopsis thalia na]
143739	ATU005 679	ATL8C1 5559:1 ..727	gap2	ATCEA4 S3252	98	ATL8C1 5559:3 47..72 7	0.88	g22451 07	32	744	5.3e- 72	(Z9734 3) thioes terase homolo g [Arabi dopsis thalia na]
143740	ATU005 680	ATL8C1 3506:1 092..1 606	gap2	ATCEA4 C44505 _1	98	ATL8C1 3506:1 092..1 602	0.86	g27390 02	32	221	1.6e- 20	(AF022 460) CYP83D lp [Glyci ne max]
143741	ATU005 681	ATL8C4 2274:2 94..22 14	gap2	ATCEA4 S1884	98	ATL8C4 2274:2 94..21 90	0.80	g41043 21	32	224	2.1e- 18	(AF034 582) vesicle associated

143742	ATU005 682	ATL8C2 2390:3 517..7 552	gap2	ATCEA4 C2559_1	98	ATL8C2 2390:3 608..6 584	0.77	g40068 20	32	582	1.3e- 59	protein [Rattus norvegicus] (AC005 970) putative serine carboxy peptidase [Arabi dopsis thaliana]
143743	ATU005 683	ATL8C2 4624:1 ..990	gap2	ATCEA4 S10473	98	ATL8C2 4624:4 43..89 8	0.76	g22448 34	32	946	2.3e- 75	(Z9733 7) hypothetical protein [Arabi dopsis thaliana]
143744	ATU005 684	ATL8C2 8162:1 226..1	gap2	ATCEA4 C5949_1	98	ATL8C2 8162:1 069..3 33	0.75	g39351 50	32	472	5.1e- 43	(AC005 106) T25N20 .14 [Arabi dopsis thaliana]
143745	ATU005 685	ATL8C9 854:10 69..1	gap2	ATCEA4 C11928 4_1, ATCEA4 S27025	98, 91	ATL8C9 854:98 4..1	0.74	g30804 21	32	1244	1.6e- 113	(AL022 604) putative protein [Arabi dopsis thaliana]

143746	ATU005 686	ATL8S2 4752:7 3..594	gap2	ATCEA4 C11681 9_1	98	ATL8S2 4752:7 3..474	0.70	g10013 55	32	67	0.0019	na] (D6400 6) auxin- induce d protei n [Synec hocyst is sp.]
143747	ATU005 687	ATL8C3 3817:1 128..2 12	gap2	ATCEA4 C99059 _1	98	ATL8C3 3817:1 060..3 95	0.69	g34829 18	32	436		(AC003 970) Simila r to ATP- citrat e- lyase [Arabi dopsis thalia na]
143748	ATU005 688	ATL8C2 9222:1 ..679	gap2	ATCEA4 C726_1	98	ATL8C2 9222:3 63..60 9	0.61	g40496 32	32	448	7.1e- 47	(AF039 406) pyruva te dehydr ogenas e kinase [Arabi dopsis thalia na]
143749	ATU005 689	ATL8C4 3571:7 32..1	gap2	ATCEA4 C98737 _1	98	ATL8C4 3571:5 18..25 7	0.58	g37899 17	32	65		(AF084 928) erythr oblast macrop hage protei n EMP [Homo

143750	ATU005 690	ATL8C1 595:84 6..1	gap2	ATCEA4 C5637_1	98	ATL8C1 595:57 6..118	0.53	g46462 03	32	331	1.0e- 29	sapien s] (AC007 230) Belong s to PF 000 26 Eukary otic aspart yl protea se family . [Arabi dopsis thalia na]
143751	ATU005 691	ATL8C4 3223:1 182..1	gap2	ATCEA4 C15007_1	98	ATL8C4 3223:1 179..5 58	0.52	g46789 47	32	413	1.8e- 28	(AL049 711) putati ve protei n [Arabi dopsis thalia na]
143752	ATU005 692	ATL8C7 370:83 6..169 9	gap2	ATCEA4 S10372	98	ATL8C7 370:83 6..148 4	0.49	g46782 33	32	317	6.2e- 32	(AC007 265) unknow n protei n [Arabi dopsis thalia na]
143753	ATU005 693	ATL8C3 0107:8 84..22 41	gap2	ATCEA4 S374	98	ATL8C3 0107:2 002..1 208	0.42	g22449 10	32	444	3.4e- 37	(Z9733 9) unname d protei

143754	ATU005 694	ATL8C4 304:1. .1140	gap2	ATCEA4 C89302 _1	98					g45393 94	32	488	4.5e- 47	(AL035 526) putative protein [Arabi dopsis thalia na]
143755	ATU005 695	ATL8C2 6639:6 00..1	gap2	ATCEA4 C419_1 , ATCEA4 C419_3	98, 86					g32282 19	32	481	5.0e- 49	(AJ006 871) MAP2k beta [Arabi dopsis thalia na]
143756	ATU005 696	ATL8C1 0804:1 350..1	gap2	ATCEA4 C203_1 , ATCEA4 S24582	98, 97					g31228 58	32	852	2.6e- 81	D-3- PHOSPH OGLYCE RATE DEHYDR OGENAS E PRECUR SOR [Arabi dopsis thalia na]
143757	ATU005 697	ATL8C4 4560:1 863..2 296	gap2	ATCEA4 S1511	98					g26421 58	32	451	1.6e- 44	(AC003 000) hypoth etical protein [Arabi

143758	ATU0005 698	ATL8C3 7011:1 486..2 075	gap2	ATCEA4 C29444 _1	98							32	358		dopsis thalia na]
143759	ATU0005 699	ATL8C3 30:905 ..1355	gap2	ATCEA4 S801, ATCEA4 S34245	98, 96							32	81	0.0013	(Z9734 4) hypoth etical protei n [Arabi dopsis thalia na]
143760	ATU0005 700	ATL8C1 7702:8 4..115 1	gap2	ATCEA4 S32132 , ATCEA4 C98725 _1	98, 97	ATL8C1 7702:9 97..62 9	0.96					31	374	3.6e- 31	(AC006 931) hypoth etical protei n [Arabi dopsis thalia na]

143761	ATU005 701	ATL8C2 8028:1 ..548	gap2	ATCEA4 C18466 _1	98	ATL8C2 8028:1 21..37 1	0.93	g36680 69	31	272	2.3e- 27	(U2800 7) Pto kinase intera ctor 1 [Lycop ersico n escule ntum]
143762	ATU005 702	ATL8C1 1032:1 ..1422	gap2	ATCEA4 C34355 _1, ATCEA4 S34909	98, 92	ATL8C1 1032:4 18..14 22	0.91	g23410 42	31	680	1.7e- 45	(AC000 104) F19P19 .26 [Arabi dopsis thalia na]
143763	ATU005 703	ATL8C4 7045:3 057..2 154	gap2	ATCEA4 C27770 _1, ATCEA4 S30200	98, 97	ATL8C4 7045:2 961..2 281	0.87	g17056 78	31	886	1.3e- 67	CELL DIVISI ON CYCLE PROTEI N 48 HOMOLO G (VALOS IN CONTAI NING PROTEI N HOMOLO G) (VCP) [Glyci ne max]
143764	ATU005 704	ATL8C1 1431:3 31..96 0	gap2	ATCEA4 C4832 _1	98			g17084 20	31	262	2.4e- 26	ISOFLA VONE REDUCT ASE HOMOLO G P3 [Arabi

143765	ATU005 705	ATL8S8 544:48 1..1	gap2	ATCEA4 S440	98					934618 21	31	345	5.1e- 30	dopsis thalia na] (AC004 138) putati ve nucleo side triphos phata se [Arabi dopsis thalia na]
143766	ATU005 706	ATL8C3 5918:1 440..1	gap2	ATCEA4 C22182 _1	98					945127 12	31	82	0.0007 7	(AC006 569) unknow n protei n [Arabi dopsis thalia na]
143767	ATU005 707	ATL8C4 8062:9 99..1	gap2	ATCEA4 C10806 _1, ATCEA4 S29541	98, 97					922528 40	31	378	2.4e- 29	(AF013 293) contai ns region s of simila rity to Haemop hilus influe nzae permea se (SP:P3 8767) [Arabi dopsis

143768	ATU005 708	ATL8C7 51:685 ..1	gap2	ATCEA4 C711_1	98					g41509 63	31	252	1.9e- 15	thalia nal (Y1862 0) DsPTP1 protei n [Arabi dopsis thalia nal]
143769	ATU005 709	ATL8C3 2403:6 39..13 3	gap2	ATCEA4 C32632 _1	98					g46783 44	31	226	3.8e- 17	(Al049 659) putati ve protei n [Arabi dopsis thalia nal]
143770	ATU005 710	ATL8C3 2455:1 374..1	gap2	ATCEA4 C10896 _1	98					g23234 10	30	362	5.2e- 26	(AF015 913) Skb1Hs [Homo sapien s]
143771	ATU005 711	ATL8C2 601:16 66..36 7	gap2	ATCEA4 S30524	98					g27022 83	30	310	4.8e- 18	(AC003 033) unknow n protei n [Arabi dopsis thalia nal]
143772	ATU005 712	ATL8C3 5137:1 ..800	gap2	ATCEA4 S5526	98					g27919 00	30	219	1.4e- 10	(AJ000 057) PP7 [Arabi dopsis thalia nal]

143773	ATU005 713	ATL8C3 9767:1 ..713	gap2	ATCEA4 C543_1 0, ATCEA4 S13217	98, 97	ATL8C3 9767:6 92..61 0	0.98	g48367 00	30	98	2.2e- 06	(AF132 794) anapha se promot ing comple x subuni t 10 [Homo sapien s]
143774	ATU005 714	ATL8C2 1822:1 120..1	gap2	ATCEA4 C3555_4, ATCEA4 C3555_1, ATCEA4 S29033	98, 94, 88	ATL8C2 1822:1 120..3 43	0.90	g19359 14	30	677	9.6e- 57	(U7734 7) lethal leaf- spot 1 homolo g [Arabi dopsis thalia na]
143775	ATU005 715	ATL8C4 7456:2 142..6 07	gap2	ATCEA4 C56349 _1	98	ATL8C4 7456:2 048..6 07	0.88	g34510 71	30	519	4.7e- 32	(AL031 326) beta adapti n - like protei n [Arabi dopsis thalia na]
143776	ATU005 716	ATL8C1 46:1.. 1639	gap2	ATCEA4 S29309 , ATCEA4 C1225_1, ATCEA4 S31452	98, 97, 94, 93	ATL8C1 46:71. .1283	0.84	g17658 99	30	768	(Y0791 7) Spot 3 protei n [Arabi dopsis thalia na]	

143777	ATU005 717	ATL8C7 61:1.. 676	gap2	ATCEA4 S33564 ATCEA4 C88733 _1	98	ATL8C7 61:75. .262	0.83	g40069 43	30	415	1.5e- 40	(AJL31 392) altern ative oxidase [Arabi dopsis thalia na]
143778	ATU005 718	ATL8C4 8100:1 ..1726	gap2	ATCEA4 S2397	98	ATL8C4 8100:4 39..16 68	0.83	g24628 37	30	751	6.9e- 42	(AF000 657) hypoth etical protein [Arabi dopsis thalia na]
143779	ATU005 719	ATL8C3 9380:8 95..11 9	gap2	ATCEA4 S24429 , ATCEA4 C360_1	98, 97	ATL8C3 9380:8 73..42 1	0.81	g27065 44	30	549	3.5e- 62	(Y1589 9) Sig1 [Sinap is alba]
143780	ATU005 720	ATL8C3 2716:1 38..10 12	gap2	ATCEA4 C4896_1	98	ATL8C3 2716:1 56..97 6	0.65	g31220 38	30	157	9.1e- 08	DIHYDR OPYRIM IDINAS E RELATE D PROTEI N-3 (DRP- 3) (COLLA PSIN RESPON SE MEDIAT OR PROTEI

143781	ATU005 721	ATL8C2 6624:1 868..7 78	gap2	ATCEA4 C9415- 3, ATCEA4 C9415- 1, ATCEA4 S33475 , ATCEA4 S2975	98, 95, 90, 82	ATL8C2 6624:1 868..9 22	0.65	g34349 75	30	252	2.7e- 21	N 4) (CRMP- 4) [Rattus norvegicus]
143782	ATU005 722	ATL8C2 8062:2 83..10 09	gap2	ATCEA4 S26003	98	ATL8C2 8062:2 83..95 0	0.65	g33866 03	30	156	9.7e- 11	(AC004 665) unknown protein [Arabidopsis thaliana]
143783	ATU005 723	ATL8S1 600:1. .564	gap2	ATCEA4 S5402	98	ATL8S1 600:29 ..479	0.44	g33675 68	30	219	4.8e- 18	(AL031 135) protein kinase- like protein [Arabidopsis thaliana]

143784	ATU005 724	ATL8C1 3687:1 ..900	gap2	ATCEA4 C39670 _1	98	ATL8C1 3687:4 64..53 3	0.42	g44553 60	30	170	1.4e- 18	(AL035 524) putati ve protei n [Arabi dopsis thalia na]
143785	ATU005 725	ATL8C2 2713:7 95..1	gap2	ATCEA4 C17331 _1, ATCEA4 C18832 _1	98, 97			g25586 55	30	1363	5.1e- 138	(AC002 354) No defini tion line found [Arabi dopsis thalia na]
143786	ATU005 726	ATL8S7 046:1. .424	gap2	ATCEA4 C323_1 , ATCEA4 S35149 , ATCEA4 S1918	98, 97, 97			g13267 7	30	356	9.4e- 25	50S RIBOSO MAL PROTEI N L15, CHLORO PLAST PRECUR SOR (CL15) [Arabi dopsis thalia na]
143787	ATU005 727	ATL8C3 7526:2 155..1	gap2	ATCEA4 S1794, ATCEA4 C11820 _1, ATCEA4 S26938	98, 97, 85			g42204 77	30	156		(AC006 069) unknow n protei n [Arabi dopsis thalia na]

Accession	Gene	Protein	Accession	Gene	Protein	Accession	Gene	Protein	Accession	Gene	Protein	Accession	Gene	Protein	Accession	Gene	Protein	Accession	Gene	Protein
143793	ATU005 733	ATL8C3 9612:1 606..4 16	gap2	ATCEA4 S24151 , ATCEA4 C1645_1	98, 97	ATL8C3 9612:1 472..6 17	1.00													proteins [Arabidopsis thaliana]
143794	ATU005 734	ATL8C2 0207:3 543..1 196	gap2	ATCEA4 S24153 , ATCEA4 S25854	98, 88	ATL8C2 0207:3 543..1 293	1.00													
143795	ATU005 735	ATL8C3 993:1. .1136	gap2	ATCEA4 C944_1 , ATCEA4 S35622 , ATCEA4 S26876	98, 96, 94	ATL8C3 993:23 0..865	1.00													
143796	ATU005 736	ATL8C1 1483:2 780..2 14	gap2	ATCEA4 C16964 1, ATCEA4 S8111	98, 85	ATL8C1 1483:2 780..2 14	1.00													
143797	ATU005 737	ATL8C1 9208:2 794..3 350	gap2	ATCEA4 S25980 , ATCEA4 S23510	98, 82	ATL8C1 9208:2 912..3 350	1.00													
143798	ATU005 738	ATL8C3 8427:1 ..825	gap2	ATCEA4 S10429 , ATCEA4 S4940	98, 98	ATL8C3 8427:4 53..80 7	1.00													
143799	ATU005 739	ATL8S2 0481:1 16..59 9	gap2	ATCEA4 S6229	98	ATL8S2 0481:1 41..28 4	1.00													

143810	ATU005 750	ATL8C2 6458:1 ..456	gap2	ATCEA4 C6659_1	98	ATL8C2 6458:7 3..456	1.00						
143811	ATU005 751	ATL8C2 2185:1 ..1018	gap2	ATCEA4 C344_1 , ATCEA4 C344_2 , ATCEA4 S32293 , ATCEA4 S24123	98, 93, 88, 84	ATL8C2 2185:2 0..799	1.00						
143812	ATU005 752	ATL8C9 270:1. .469	gap2	ATCEA4 S1607	98	ATL8C9 270:75 ..469	1.00						
143813	ATU005 753	ATL8C4 3094:1 ..707	gap2	ATCEA4 S24554 , ATCEA4 S33423	98, 96	ATL8C4 3094:2 52..55 9	0.99						
143814	ATU005 754	ATL8C4 8479:2 024..2 74	gap2	ATCEA4 C35228 _1	98	ATL8C4 8479:1 598..5 35	0.99						
143815	ATU005 755	ATL8S2 5983:4 70..9	gap2	ATCEA4 S30204	98	ATL8S2 5983:3 20..9	0.99						
143816	ATU005 756	ATL8S1 8201:1 ..487	gap2	ATCEA4 S6201, ATCEA4 C2009_1	98, 83	ATL8S1 8201:4 7..293	0.99						
143817	ATU005 757	ATL8C3 2642:1 577..5 8	gap2	ATCEA4 C1498_1	98	ATL8C3 2642:1 522..2 08	0.99						
143818	ATU005 758	ATL8C3 5760:4 380..3 4	gap2	ATCEA4 S2113	98	ATL8C3 5760:4 380..3 4	0.99						
143819	ATU005 759	ATL8C4 8004:3	gap2	ATCEA4 C15277	97, 97,	ATL8C4 8004:3	0.99	940918 06	100	970	8.3e- 84	(AF052 585)	

		061..1 281		1, ATCEA4 C51413 1, ATCEA4 C15277 3, ATCEA4 C15277 2	94, 88	007..1 510						CONSTA NS- like protei n 2 [Malus domest ica]
143820	ATU005 760	ATL8S9 495:50 6..105	gap2	ATCEA4 S35163	98	ATL8S9 495:42 5..273	0.99					
143821	ATU005 761	ATL8C3 5679:1 248..2 130	gap2	ATCEA4 C1410_ 1, ATCEA4 S35778 , ATCEA4 S31465	98, 91, 88	ATL8C3 5679:1 287..2 053	0.99					
143822	ATU005 762	ATL8C8 19:209 7..136 7	gap2	ATCEA4 C58167 1, ATCEA4 S8899	98, 85	ATL8C8 19:200 0..146 9	0.99					
143823	ATU005 763	ATL8C1 5258:1 666..7 52	gap2	ATCEA4 C324_1	98	ATL8C1 5258:1 634..7 52	0.99					
143824	ATU005 764	ATL8S2 1730:5 52..1	gap2	ATCEA4 S29473 , ATCEA4 C34107 1	98, 91	ATL8S2 1730:4 40..55	0.99					
143825	ATU005 765	ATL8C3 0768:2 869..3 687	gap2	ATCEA4 S7545	97	ATL8C3 0768:2 917..3 687	0.99	g31222 32	100	613	4.0e- 54	MITOCH ONDRIA L HEAT SHOCK 22 KD PROTEI N PRECUR

789	2209:1 ..2765		S1602, ATCEA4 S2280, ATCEA4 S5672	94, 93	2209:3 3..276 5	23	177	087) mitoge n- activa ted protei n kinase homolo gue [Medic ago sativa]
143850	ATU005 790	gap2	ATCEA4 C36994 _1	98	ATL8C1 0196:1 255..2 55	0.98		
143851	ATU005 791	gap2	ATCEA4 C25551 _1, ATCEA4 C25551 _2	98, 98	ATL8C2 696:10 55..17 3	0.98		
143852	ATU005 792	gap2	ATCEA4 C13182 _1, ATCEA4 S26754	98, 86	ATL8C1 9164:4 03..20 8	0.98		
143853	ATU005 793	gap2	ATCEA4 C20079 _1	98	ATL8C4 4607:7 37..14 9	0.98		
143854	ATU005 794	gap2	ATCEA4 C72195 _1, ATCEA4 S14273	98, 90	ATL8C3 8422:5 23..19 7	0.98		
143855	ATU005 795	gap2	ATCEA4 C364_1 _1, ATCEA4 C364_2	98, 85	ATL8C4 1175:3 0..178	0.98		
143856	ATU005	gap2	ATCEA4	98	ATL8C1	0.98		

143879	ATU005 819	ATL8C3 2500:6 82..10 56	gap2	ATCEA4 S28440	98	ATL8C3 2500:7 01..90 7	0.97												
143880	ATU005 820	ATL8C2 519:93 2..242 4	gap2	ATCEA4 C4737 1, ATCEA4 S36077 , ATCEA4 S34470 , ATCEA4 S24239	98, 98, 92, 83	ATL8C2 519:10 03..21 55	0.97												
143881	ATU005 821	ATL8C4 3045:3 469..1 088	gap2	ATCEA4 C76435 1, ATCEA4 C4734 2, ATCEA4 S34083 , ATCEA4 C4734 1, ATCEA4 S2218, ATCEA4 S23015	98, 98, 94, 93, 89, 88	ATL8C4 3045:3 310..1 355	0.97												
143882	ATU005 822	ATL8C1 4495:8 33..16 03	gap2	ATCEA4 C180_1	98	ATL8C1 4495:8 63..16 03	0.97												
143883	ATU005 823	ATL8C4 4926:1 ..432	gap2	ATCEA4 C15241 2, ATCEA4 S9860	98, 85	ATL8C4 4926:5 2..242	0.97												
143884	ATU005	ATL8C2	gap2	ATCEA4	98	ATL8C2	0.97												

143904	ATU005 844	12..86 ATL8C4 2867:3 63..13 82	gap2	ATCEA4 C32614 3, ATCEA4 C47936 1, ATCEA4 C32614 2, ATCEA4 S10929 , ATCEA4 S10927	98, 95, 93, 87, 82	10..89 ATL8C4 2867:3 63..11 95	0.96									
143905	ATU005 845	ATL8C4 4360:5 55..1	gap2	ATCEA4 C120_2	98	ATL8C4 4360:5 36..30 7	0.96									
143906	ATU005 846	ATL8S2 3584:9 8..526	gap2	ATCEA4 C17897 1_	98	ATL8S2 3584:1 00..31 3	0.96									
143907	ATU005 847	ATL8C1 8754:1 ..820	gap2	ATCEA4 C18227 3, ATCEA4 C18227 1, ATCEA4 C18227 2	98, 90, 86	ATL8C1 8754:5 ..820	0.96									
143908	ATU005 848	ATL8C1 7330:2 462..7 92	gap2	ATCEA4 C35328 1, ATCEA4 C10361 5_1	97, 97	ATL8C1 7330:2 397..1 120	0.96	g35818 70	100	121	2.9e- 12	(AL031 541) hypoth etical protei n SCI35. 37 [Strep tomyce s coelic				

143909	ATU005 849	ATL8C1 570:13 8..180 3	gap2	ATCEA4 C15227 1, ATCEA4 S4675	97, 94	ATL8C1 570:24 7..172 9	0.96	g42205 12	100.	1594	4.7e- 166	olor] (AL035 356) putati ve pectat e lyase [Arabi dopsis thalia na]
143910	ATU005 850	ATL8C2 7046:1 28..56 5	gap2	ATCEA4 S3723	98	ATL8C2 7046:1 28..25 1	0.96					
143911	ATU005 851	ATL8C9 395:10 24..39	gap2	ATCEA4 C4457 1, ATCEA4 S9221	98, 82	ATL8C9 395:96 4..39	0.96					
143912	ATU005 852	ATL8C3 9841:1 41..10 53	gap2	ATCEA4 C28035 1, ATCEA4 C16951 1, ATCEA4 S4461	98, 96	ATL8C3 9841:1 41..10 21	0.96					
143913	ATU005 853	ATL8C5 0032:7 58..1	gap2	ATCEA4 C79488 1	98	ATL8C5 0032:7 58..14 4	0.96					
143914	ATU005 854	ATL8C4 4340:1 62..15 20	gap2	ATCEA4 S1700, ATCEA4 C21150 1	98, 93	ATL8C4 4340:1 62..15 20	0.96					
143915	ATU005 855	ATL8C6 312:64 5..1	gap2	ATCEA4 C57814 1	98	ATL8C6 312:64 5..128	0.96					
143916	ATU005 856	ATL8C3 8995:1 635..1	gap2	ATCEA4 C18935 1,	98, 93	ATL8C3 8995:1 630..6	0.96					

143927	ATU005 867	ATL8C3 9646:1 ..558	gap2	ATCEA4 C12072 1	98	ATL8C3 9646:7 5..168	0.95					
143928	ATU005 868	ATL8C2 3516:4 06..12 11	gap2	ATCEA4 C39802 1	98	ATL8C2 3516:5 04..12 11	0.95					
143929	ATU005 869	ATL8C2 1792:3 321..1 485	gap2	ATCEA4 S1374, ATCEA4 C13563 1	98, 96	ATL8C2 1792:3 142..1 485	0.95					
143930	ATU005 870	ATL8S2 9831:1 ..433	gap2	ATCEA4 C45345 1, ATCEA4 S30998	98, 82	ATL8S2 9831:1 15..33 3	0.95					
143931	ATU005 871	ATL8C1 3731:1 85..16 67	gap2	ATCEA4 C19227 1, ATCEA4 C13218 6 1, ATCEA4 S29802 , ATCEA4 S12511	98, 98, 97, 85	ATL8C1 3731:2 14..16 46	0.95					
143932	ATU005 872	ATL8C2 5149:1 ..1543	gap2	ATCEA4 S36295	98	ATL8C2 5149:6 ..1325	0.95					
143933	ATU005 873	ATL8C1 5514:2 623..1 715	gap2	ATCEA4 S7806, ATCEA4 C17018 1	98, 89	ATL8C1 5514:2 553..1 715	0.95					
143934	ATU005 874	ATL8C2 983:39 96..14 6	gap2	ATCEA4 S23836 , ATCEA4 C22009 1, ATCEA4 S34220	97, 96, 95, 91	ATL8C2 983:39 96..48 5	0.95	g34514 74	100	1323	1.5e- 112	(AL031 349) conser ved hypoth etical protei n

143935	ATU005 875	ATL8C2 0402:1 36..43 0	gap2	ATCEA4 S34541	98	ATL8C2 0402:1 98..42 6	0.95					[Schiz osacch aromyc es pombe]
143936	ATU005 876	ATL8C4 5679:1 229..1 433	gap2	ATCEA4 C8377_1	98	ATL8C4 5679:1 265..1 374	0.95					
143937	ATU005 877	ATL8S1 5693:1 ..640	gap2	ATCEA4 C30943 1, ATCEA4 C30943 2, ATCEA4 S22690	98, 97, 83	ATL8S1 5693:1 50..32 2	0.95					
143938	ATU005 878	ATL8C2 8978:1 59..13 69	gap2	ATCEA4 C41813 1	98	ATL8C2 8978:8 98..11 79	0.95					
143939	ATU005 879	ATL8C2 2189:6 42..1	gap2	ATCEA4 S3239	98	ATL8C2 2189:6 42..21 4	0.95					
143940	ATU005 880	ATL8C3 9131:1 ..591	gap2	ATCEA4 C8645_1	98	ATL8C3 9131:1 0..591	0.95					
143941	ATU005 881	ATL8C1 2671:1 112..1	gap2	ATCEA4 C40670 1, ATCEA4 C6816_1	98, 94	ATL8C1 2671:8 74..14 4	0.95					
143942	ATU005 882	ATL8C3 0699:5 575..5 59	gap2	ATCEA4 C1565_2, ATCEA4 S31167	98, 90	ATL8C3 0699:5 176..7 56	0.95					
143943	ATU005	ATL8C4	gap2	ATCEA4	98	ATL8C4	0.95					

143944	883	4646:1 ..1048	gap2	C1081_1	97	4646:1 41..86 6	0.95	g35602 64	100	210	1.3e- 28	(AI031 535) sol1 family protei n [Schiz osacch aromyc es pombel]
	ATU005 884	ATL8C1 1425:1 531..2 50	gap2	ATCEA4 S30679		ATL8C1 1425:1 480..2 64						
143945	ATU005 885	ATL8C1 6996:1 468..3 404	gap2	ATCEA4 S1124, ATCEA4 C12934 _1	97, 95	ATL8C1 6996:1 468..3 404	0.95	g39414 36	100	891	1.3e- 83	(AF062 872) putati ve transc riptio n factor [Arabi dopsis thalia na]
143946	ATU005 886	ATL8C3 716:26 99..88 1	gap2	ATCEA4 S3935, ATCEA4 S15048 , ATCEA4 S30544	97, 91, 91	ATL8C3 716:23 36..14 54	0.95	g22451 27	100	379	1.7e- 37	(Z9734 4) hypoth etical protei n [Arabi dopsis thalia na]
143947	ATU005 887	ATL8C4 6602:5 26..1	gap2	ATCEA4 S14621 , ATCEA4 C328 1	98, 98	ATL8C4 6602:4 32..23 3	0.95					
143948	ATU005 888	ATL8C4 4765:2 793..9	gap2	ATCEA4 S33519	98	ATL8C4 4765:2 793..1	0.95					

143955	ATU005 895	ATL8C4 8774:6 7..838	gap2	S7637 ATCEA4 S2103	98	ATL8C4 8774:6 7..779	0.95													
143956	ATU005 896	ATL8C1 0007:1 677..4 27	gap2	ATCEA4 S9944	98	ATL8C1 0007:1 665..4 27	0.95													
143957	ATU005 897	ATL8C2 4563:9 8..162 9	gap2	ATCEA4 C389_1	98	ATL8C2 4563:9 8..131 4	0.95													
143958	ATU005 898	ATL8C3 8233:7 11..48	gap2	ATCEA4 C2243_1, ATCEA4 S22382	98, 87	ATL8C3 8233:6 74..48	0.95													
143959	ATU005 899	ATL8C3 8268:8 6..163 1	gap2	ATCEA4 C11291_2	98	ATL8C3 8268:8 6..158 1	0.95													
143960	ATU005 900	ATL8C2 4443:8 13..20 12	gap2	ATCEA4 C1131_1	98	ATL8C2 4443:1 168..1 782	0.95													
143961	ATU005 901	ATL8C1 4687:1 116..1 15	gap2	ATCEA4 C1693_1	98	ATL8C1 4687:1 090..2 32	0.95													
143962	ATU005 902	ATL8C1 2395:2 430..5 88	gap2	ATCEA4 C27475_1, ATCEA4 C73034_1, ATCEA4 S16367	98, 89	ATL8C1 2395:2 412..8 15	0.94													
143963	ATU005 903	ATL8C1 2555:9 09..1	gap2	ATCEA4 S4132	98	ATL8C1 2555:9 09..17	0.94													
143964	ATU005 904	ATL8C3 3552:1 ..331	gap2	ATCEA4 S34288	98	ATL8C3 3552:2 41..33 1	0.94													

		6..147 3		1, ATCEA4 S23834		8..122 7						
143978	ATU005 918	ATL8C5 0156:3 26..25 93	gap2	ATCEA4 C29676 1, ATCEA4 S8414, ATCEA4 S883, ATCEA4 S2180, ATCEA4 S13703	98, 98, 91, 87, 85	ATL8C5 0156:3 26..25 93	0.94					
143979	ATU005 919	ATL8C5 031:11 00..10 0	gap2	ATCEA4 S29495	98	ATL8C5 031:11 00..64 3	0.94					
143980	ATU005 920	ATL8C1 5473:4 969..4 247	gap2	ATCEA4 C30282 1 _	98	ATL8C1 5473:4 891..4 414	0.94					
143981	ATU005 921	ATL8C2 2677:1 3..891	gap2	ATCEA4 C18168 1 _	98	ATL8C2 2677:1 42..85 2	0.94					
143982	ATU005 922	ATL8C1 9626:2 64..11 73	gap2	ATCEA4 C6990 1 _	98	ATL8C1 9626:2 71..11 73	0.94					
143983	ATU005 923	ATL8C5 421:11 38..30 5	gap2	ATCEA4 S22603 , ATCEA4 S35088 , ATCEA4 S31334	98, 94, 89	ATL8C5 421:10 95..10 31	0.94					
143984	ATU005 924	ATL8C1 5452:1 087..5 09	gap2	ATCEA4 S2422, ATCEA4 S10360	98, 96	ATL8C1 5452:1 038..5 09	0.94					
143985	ATU005 925	ATL8C3 5864:8	gap2	ATCEA4 C46209	98	ATL8C3 5864:8	0.94					

		02...1	gap2	_1	98, 90	02...11						
143986	ATU005 926	ATL8C1 4998:1 251..1 38	gap2	ATCEA4 C18601 5, ATCEA4 C18601 2	98, 90	ATL8C1 4998:1 216..1 38	0.94					
143987	ATU005 927	ATL8C1 5388:1 ..909	gap2	ATCEA4 C3522_1	98	ATL8C1 5388:3 08..90 9	0.94					
143988	ATU005 928	ATL8C4 5376:1 269..6 19	gap2	ATCEA4 S4365	98	ATL8C4 5376:1 269..7 10	0.94					
143989	ATU005 929	ATL8C8 010:1. .1349	gap2	ATCEA4 C1932_1, ATCEA4 S23739	98, 84	ATL8C8 010:19 5..120 0	0.93					
143990	ATU005 930	ATL8C3 5349:1 305..1	gap2	ATCEA4 C633_1	98	ATL8C3 5349:1 295..3 17	0.93					
143991	ATU005 931	ATL8C1 3001:4 65..37	gap2	ATCEA4 C69769 1	98	ATL8C1 3001:4 61..37	0.93					
143992	ATU005 932	ATL8S2 326:47 3..10	gap2	ATCEA4 S12236	98	ATL8S2 326:47 3..67	0.93					
143993	ATU005 933	ATL8C4 7672:1 08..19 61	gap2	ATCEA4 C30325 1, ATCEA4 S32722 , ATCEA4 C6801_2	98, 91 94, 91	ATL8C4 7672:1 08..16 80	0.93					
143994	ATU005 934	ATL8C3 5623:7 3..204 5	gap2	ATCEA4 C49568 1, ATCEA4	98, 85	ATL8C3 5623:7 3..204 5	0.93					

[illegible]

964	5101:1 58..25 09		S25818 , ATCEA4 S16903		5101:1 58..19 44						
144025	ATU005 965	ATL8C3 0998:1 667..6 01	gap2	ATCEA4 S20250	98	ATL8C3 0998:1 667..7 17	0.92				
144026	ATU005 966	ATL8C4 1798:9 45..10	gap2	ATCEA4 S5752, ATCEA4 C14644 1	98, 82	ATL8C4 1798:9 45..10	0.92				
144027	ATU005 967	ATL8S1 2003:3 66..67 6	gap2	ATCEA4 C1845 1, ATCEA4 S31007 , ATCEA4 S9640, ATCEA4 S15204	98, 96, 96, 83	ATL8S1 2003:3 97..65 8	0.92				
144028	ATU005 968	ATL8C2 2259:1 ..659	gap2	ATCEA4 C16001 2	98	ATL8C2 2259:1 24..65 9	0.92				
144029	ATU005 969	ATL8C3 8405:1 38..74 6	gap2	ATCEA4 S12332 , ATCEA4 S12746 , ATCEA4 S12330	98, 98, 87	ATL8C3 8405:1 85..68 4	0.92				
144030	ATU005 970	ATL8C1 6821:1 9..938	gap2	ATCEA4 S16353 , ATCEA4 S1422	98, 86	ATL8C1 6821:6 80..93 8	0.92				
144031	ATU005 971	ATL8C1 331:38 6..79	gap2	ATCEA4 C7065 1	98	ATL8C1 331:33 8..79	0.92				
144032	ATU005	ATL8C4	gap2	ATCEA4	98,	ATL8C4	0.92,				

972	0711:2 05..15 75		C12703 5 1, ATCEA4 C52907 1, ATCEA4 C21901 1	97, 96	0711:2 30..96 6, ATL8C4 0711:1 573..1 446	0.99					
144033	ATU005 973	gap2	ATCEA4 C365_1	98	ATL8C3 3984:1 915..5 3	0.92					
144034	ATU005 974	gap2	ATCEA4 C11906 4 1	98	ATL8C2 534:7. .710	0.92					
144035	ATU005 975	gap2	ATCEA4 C1242_1, ATCEA4 C1242_5, ATCEA4 S25385 , ATCEA4 S33941	98, 98, 98, 87	ATL8C2 7182:1 96..14 88	0.92					
144036	ATU005 976	gap2	ATCEA4 S31902 , ATCEA4 S29200	98, 82	ATL8S2 5007:1 95..30 6	0.92					
144037	ATU005 977	gap2	ATCEA4 S16244 , ATCEA4 C1965_2, ATCEA4 C1965_1	98, 94, 90	ATL8C4 4320:4 07..84 9	0.92					
144038	ATU005 978	gap2	ATCEA4 C4440_1, ATCEA4	98, 89, 86	ATL8S4 114:1. .563	0.92					

144048	ATU005 988	2265:1 ..1262	gap2	C80122 1, ATCEA4 S26176 , ATCEA4 C25060 1	93, 90	2265:1 90..95 8						
144049	ATU005 989	ATL8C2 821:10 05..1	gap2	ATCEA4 C740_3 , ATCEA4 C740_2 , ATCEA4 S14598	98, 97, 82	ATL8C2 821:10 04..47 9	0.91					
144050	ATU005 990	ATL8C2 884:83 9..131 8	gap2	ATCEA4 C15075 _1	98	ATL8C2 884:10 88..11 86	0.91					
144051	ATU005 991	ATL8C2 776:11 59..18 36	gap2	ATCEA4 C3673_1	98	ATL8C2 776:16 44..18 15	0.91					
144052	ATU005 992	ATL8C4 5950:2 54..21 47	gap2	ATCEA4 S10275 , ATCEA4 S33143 , ATCEA4 S31404	98, 98, 89	ATL8C4 5950:2 54..19 52	0.91					
144053	ATU005 993	ATL8C3 7545:1 36..35 4	gap2	ATCEA4 C13793 _1	98	ATL8C3 7545:2 20..35 4	0.91					
144054	ATU005 994	ATL8C6 647:14 7..557	gap2	ATCEA4 S12158	98	ATL8C6 647:25 3..557	0.91					
144055	ATU005	ATL8C2 794:44 7..151 7	gap2	ATCEA4 S1197	98	ATL8C2 794:88 3..151 7	0.91					
144056	ATU005	ATL8C1	gap2	ATCEA4	98	ATL8C1	0.91					

	995	4563:3 48..50 7		S30695		4563:3 48..50 7										
144056	ATU005 996	ATL8C1 4025:1 ..2207	gap2	ATCEA4 C600_1 , ATCEA4 C600_3 , ATCEA4 C600_5 , ATCEA4 C600_6 , ATCEA4 S34482 , ATCEA4 C600_2 , ATCEA4 S34112	98, 98, 95, 92, 90, 90, 86	ATL8C1 4025:1 07..19 47	0.91									
144057	ATU005 997	ATL8C1 2065:3 187..1 294	gap2	ATCEA4 C22646 1, ATCEA4 S20888	98, 91	ATL8C1 2065:3 167..1 294	0.91									
144058	ATU005 998	ATL8C1 3778:3 2..115 0	gap2	ATCEA4 S13888	98	ATL8C1 3778:4 1..115 0	0.91									
144059	ATU005 999	ATL8C2 1735:1 86..55 0	gap2	ATCEA4 S112	98	ATL8C2 1735:4 30..55 0	0.91									
144060	ATU006 000	ATL8C4 4020:4 276..1	gap2	ATCEA4 C65755 1, ATCEA4 S1061	97, 97	ATL8C4 4020:4 073..2 27	0.91	g36873 89	100	1857	7.6e- 158	(Y1612 4) putati ve cullin protei n [Lycop				

		993..1 52		ATCEA4 C93774 1, ATCEA4 C39255 _1		993..3 52							SOME REGULA TORY SUBUNI T S3 (NUCLE AR ANTIGE N 21D7) [Nicot iana tabacu m]
144077	ATU006 017	gap2	ATL8C2 9160:3 17..91 8	ATCEA4 S36274	98	ATL8C2 9160:3 17..85 7	0.90						
144078	ATU006 018	gap2	ATL8C2 4772:5 88..13 13	ATCEA4 S2028	98	ATL8C2 4772:5 88..13 13	0.90						
144079	ATU006 019	gap2	ATL8S5 570:44 4..46	ATCEA4 C15384 1	98	ATL8S5 570:38 2..46	0.90						
144080	ATU006 020	gap2	ATL8C1 54:79. .715	ATCEA4 C1897 _ 1	98	ATL8C1 54:79. .634	0.90						
144081	ATU006 021	gap2	ATL8C4 9308:2 63..14 37	ATCEA4 C6270 _ 1, ATCEA4 C6270 _ 2, ATCEA4 C6270 _ 3, ATCEA4 S31781	98, 94, 92, 88	ATL8C4 9308:1 416..5 36	0.90						
144082	ATU006 022	gap2	ATL8C9 380:1. .1378	ATCEA4 C27970 _2, ATCEA4 S33272	98, 97	ATL8C9 380:53 0..122 8	0.90						

144083	ATU006 023	ATL8C1 623:15 50..11 4	gap2	ATCEA4 S8335, ATCEA4 C50630 1	98, 98	ATL8C1 623:14 77..11 4	0.90				
144084	ATU006 024	ATL8C3 7468:9 96..32 8	gap2	ATCEA4 C84064 1	98	ATL8C3 7468:9 96..48 1	0.90				
144085	ATU006 025	ATL8C3 8819:1 156..1	gap2	ATCEA4 C2093 1	98	ATL8C3 8819:1 083..9	0.90				
144086	ATU006 026	ATL8C1 6861:8 95..1	gap2	ATCEA4 C134_1	98	ATL8C1 6861:8 46..18	0.90				
144087	ATU006 027	ATL8C1 2289:2 330..1 21	gap2	ATCEA4 C2356_ 1, ATCEA4 C27313 1, ATCEA4 S2776	98, 96, 90	ATL8C1 2289:2 245..1 21	0.90				
144088	ATU006 028	ATL8C4 3244:5 71..28 54	gap2	ATCEA4 C51352 2, ATCEA4 S30201 , ATCEA4 S6812	98, 98, 94	ATL8C4 3244:6 68..28 54	0.90				
144089	ATU006 029	ATL8C3 5325:1 238..2 203	gap2	ATCEA4 C3495_ 1	98	ATL8C3 5325:1 238..2 046	0.90				
144090	ATU006 030	ATL8S2 2691:1 77..58 0	gap2	ATCEA4 C38479 1	98	ATL8S2 2691:1 77..43 5	0.90				
144091	ATU006 031	ATL8C3 874:28 30..1	gap2	ATCEA4 C4609_ 1	98	ATL8C3 874:28 30..74 9	0.90				
144092	ATU006	ATL8C2	gap2	ATCEA4	98,	ATL8C2	0.90				

144093	032	4825:1 938..1 61		C19635 1, ATCEA4 S16719 , ATCEA4 C24234 1	90, 87	4825:1 553..9 59	0.90	937905 75	100	335	4.2e- 28	(AF078 825) RING- H2 finger protei n RHA3b [Arabi dopsis thalia na]
	ATU006 033	ATL8C4 2699:1 087..4 99	gap2	ATCEA4 C33583 _1	97	ATL8C4 2699:1 038..5 12	0.90					
144094	ATU006 034	ATL8C4 484:27 76..17 6	gap2	ATCEA4 S5531, ATCEA4 C7404_1	98, 95	ATL8C4 484:27 12..17 6	0.90					
144095	ATU006 035	ATL8C3 7210:1 150..4 95	gap2	ATCEA4 C61100 1, ATCEA4 S31121	98, 91	ATL8C3 7210:1 136..6 69	0.90					
144096	ATU006 036	ATL8S9 420:50 ..517	gap2	ATCEA4 C46094 1, ATCEA4 S35890	98, 84	ATL8S9 420:28 8..379	0.89					
144097	ATU006 037	ATL8C4 946:24 13..16 33	gap2	ATCEA4 S33324	98	ATL8C4 946:24 13..18 97	0.89					
144098	ATU006 038	ATL8C3 1390:1 ..1397	gap2	ATCEA4 C633_1	98	ATL8C3 1390:1 05..12 00	0.89					
144099	ATU006	ATL8C3	gap2	ATCEA4	98	ATL8C3	0.89					

	039	7467:1 048..1		C3205_1		7467:6 36..15											
144100	ATU006 040	ATL8C1 8505:3 283..1 218	gap2	ATCEA4 C18713 1, ATCEA4 S6790, ATCEA4 S22412	98, 94 98, 85	ATL8C1 8505:2 837..1 258	0.89										
144101	ATU006 041	ATL8C1 6641:1 66..20 15	gap2	ATCEA4 C5729_1, ATCEA4 S15147	98, 94	ATL8C1 6641:1 137..1 821	0.89										
144102	ATU006 042	ATL8C4 2048:8 75..1	gap2	ATCEA4 S16188, ATCEA4 S10402	98, 82	ATL8C4 2048:8 75..51	0.89										
144103	ATU006 043	ATL8C3 2960:1 14..22 47	gap2	ATCEA4 C11118 1, ATCEA4 S33766	97, 94	ATL8C3 2960:1 15..18 81	0.89	g16536 55, g13520 91	100, 99	227, 108	1.2e- 14, 0.0018	(D9091 5) ATP- depend ent Clp protea se proteo lytic subuni t [Synec hocyst is sp.]; PUTATI VE ATP- DEPEND ENT CLP PROTEA SE PROTEO LYTIC					

	051	6646:1 ..2791		C24313 1, ATCEA4 S32124 , ATCEA4 S25266	93, 83	6646:1 50..22 48	59				75	599) spermi dine syntha se [Coffe a arabic a]
144112	ATU006 052	ATL8C2 2431:3 186..5 4	gap2	ATCEA4 C1901_ 1, ATCEA4 S35273	98, 90	ATL8C2 2431:2 729..1 85	0.89					
144113	ATU006 053	ATL8C1 6659:2 34..13 57	gap2	ATCEA4 C9804_ 1	98	ATL8C1 6659:2 34..12 21	0.89					
144114	ATU006 054	ATL8C3 0984:3 037..1 992	gap2	ATCEA4 S25884	98	ATL8C3 0984:3 037..2 091	0.89					
144115	ATU006 055	ATL8C4 1801:1 065..6 9	gap2	ATCEA4 C482_1	98	ATL8C4 1801:4 40..26 4	0.89					
144116	ATU006 056	ATL8C2 1717:1 78..53 7	gap2	ATCEA4 C1806_ 1	98	ATL8C2 1717:1 78..49 3	0.89					
144117	ATU006 057	ATL8C3 3518:3 82..16 46	gap2	ATCEA4 C11916 1, ATCEA4 C11916 2, ATCEA4 C24244 2, ATCEA4 S15169	98, 96, 96, 93	ATL8C3 3518:3 82..16 17	0.89					
144118	ATU006 058	ATL8C9 319:11 68..97	gap2	ATCEA4 C21729 1	98	ATL8C9 319:11 68..97	0.89					

144119	ATU006 059	ATL8C3 5993:2 050..1	gap2	ATCEA4 C8724 1, ATCEA4 S22572	98, 97	ATL8C3 5993:2 050..2 1	0.89				
144120	ATU006 060	ATL8C3 2772:2 61..88 9	gap2	ATCEA4 C34552 1	98	ATL8C3 2772:2 71..88 9	0.89				
144121	ATU006 061	ATL8C4 5931:1 83..38 34	gap2	ATCEA4 S7938	98	ATL8C4 5931:3 93..38 34	0.89				
144122	ATU006 062	ATL8S6 981:48 0..93	gap2	ATCEA4 S34162	98	ATL8S6 981:33 3..93	0.89				
144123	ATU006 063	ATL8C3 1720:3 37..83 8	gap2	ATCEA4 S16361 , ATCEA4 C85273 1	98, 91	ATL8C3 1720:7 08..61 5	0.89				
144124	ATU006 064	ATL8C4 8022:1 035..1	gap2	ATCEA4 C5138 1	98	ATL8C4 8022:6 77..17 0	0.89				
144125	ATU006 065	ATL8C5 414:38 69..22 06	gap2	ATCEA4 S36286 , ATCEA4 C1954 1, ATCEA4 S28804	98, 82, 82, 82	ATL8C5 414:37 98..24 01	0.89				
144126	ATU006 066	ATL8C3 1652:5 45..10 1	gap2	ATCEA4 S11944	98	ATL8C3 1652:5 45..10 1	0.89				
144127	ATU006 067	ATL8C3 7154:9 63..10 3	gap2	ATCEA4 S5917	98	ATL8C3 7154:9 15..10 3	0.89				
144128	ATU006 068	ATL8C1 1315:1	gap2	ATCEA4 C17311	98	ATL8C1 1315:1	0.88				

144142	ATU006 082	ATL8C4 9703:1 430..2 990	gap2	ATCEA4 C89_1	98	ATL8C4 9703:1 534..2 903	0.88					
144143	ATU006 083	ATL8C4 8220:2 228..6 88	gap2	ATCEA4 C1775_1	98	ATL8C4 8220:2 079..6 88	0.88					
144144	ATU006 084	ATL8S2 3277:1 ..540	gap2	ATCEA4 C12214_1	98	ATL8S2 3277:1 50..54 0	0.88					
144145	ATU006 085	ATL8S2 1571:2 27..66	gap2	ATCEA4 C32555_1	98	ATL8S2 1571:1 28..66	0.88					
144146	ATU006 086	ATL8C2 4734:5 449..8 15	gap2	ATCEA4 S1202	98	ATL8C2 4734:5 449..8 15	0.88					
144147	ATU006 087	ATL8C8 483:55 3..1	gap2	ATCEA4 S30432 , ATCEA4 S35680 , ATCEA4 C18212_1	98, 95, 92	ATL8C8 483:37 1..158	0.88					
144148	ATU006 088	ATL8C4 3226:8 424..7 181	gap2	ATCEA4 S10793	98	ATL8C4 3226:8 356..7 181	0.88					
144149	ATU006 089	ATL8C4 3536:8 19..1	gap2	ATCEA4 S34780 , ATCEA4 S32361	98, 97	ATL8C4 3536:8 18..17 7	0.88					
144150	ATU006 090	ATL8C4 9369:1 208..3 59	gap2	ATCEA4 S10764	98	ATL8C4 9369:1 208..3 59	0.88					
144151	ATU006 091	ATL8C1 2104:1 356..1	gap2	ATCEA4 C1269_1,	98, 93, 92	ATL8C1 2104:1 186..7	0.88					

108	4847:1 49..15 90		C92228 1, ATCEA4 S27763 87, 85	93, 92, 92, 87, 85	4847:1 49..13 32						
144169	ATU006 109	gap2	ATL8C4 7541:4 343..2 371	98	ATL8C4 7541:4 262..3 086	0.87					
144170	ATU006 110	gap2	ATL8C3 4953:2 64..10 07	98	ATL8C3 4953:2 64..70 9	0.87					
144171	ATU006 111	gap2	ATL8C8 338:59 42..48 97	98, 93	ATL8C8 338:59 42..55 66	0.87					
144172	ATU006 112	gap2	ATL8C1 7030:1 50..10 23	98, 95, 82	ATL8C1 7030:2 38..10 03	0.87					
144173	ATU006 113	gap2	ATL8C1 7228:1 87..10 57	98	ATL8C1 7228:2 25..10 57	0.87					
144174	ATU006 114	gap2	ATL8C1 3109:4 58..46	98, 96, 92, 91	ATL8C1 3109:1 335..4	0.87					

144180	ATU006 120	ATL8C4 6846:5 78..10 14	gap2	ATCEA4 S36381	98	ATL8C4 6846:7 76..99 6	0.87					
144181	ATU006 121	ATL8C4 710:47 24..37 72	gap2	ATCEA4 C226_2 , ATCEA4 C226_1	98, 87	ATL8C4 710:46 31..41 57	0.87					
144182	ATU006 122	ATL8C1 7891:1 115..1	gap2	ATCEA4 C80622 _1	98	ATL8C1 7891:1 115..1 92	0.86					
144183	ATU006 123	ATL8C1 7202:1 12..22 62	gap2	ATCEA4 C24346 1, ATCEA4 C13750 1	98, 97	ATL8C1 7202:1 13..19 39	0.86					
144184	ATU006 124	ATL8C2 3101:4 08..17 07	gap2	ATCEA4 C6193 1	98	ATL8C2 3101:4 08..17 07	0.86					
144185	ATU006 125	ATL8C4 6621:1 08..22 81	gap2	ATCEA4 C2207_1 , ATCEA4 S30253	98, 86	ATL8C4 6621:4 73..22 81	0.86					
144186	ATU006 126	ATL8C2 0459:1 ..1351	gap2	ATCEA4 C11505 1, ATCEA4 S33761	98, 93	ATL8C2 0459:1 44..10 64	0.86					
144187	ATU006 127	ATL8C4 7852:2 107..3 67	gap2	ATCEA4 C13043 5_1	98	ATL8C4 7852:2 107..7 10	0.86					
144188	ATU006 128	ATL8C1 8868:1 06..38 00	gap2	ATCEA4 S12952	98	ATL8C1 8868:1 06..38 00	0.86					
144189	ATU006 129	ATL8C1 2786:3 84..1	gap2	ATCEA4 C8078_1	98	ATL8C1 2786:3 75..21	0.86					

144190	ATU006 130	ATL8C7 075:98 9..1	gap2	ATCEA4 C21155 _1	98	ATL8C7 075:98 9..42	0.86					
144191	ATU006 131	ATL8C1 9824:1 450..1 _11	gap2	ATCEA4 C14136 _1	98	ATL8C1 9824:1 311..1 _12	0.86					
144192	ATU006 132	ATL8C3 1543:2 45..62 _2	gap2	ATCEA4 S33590 , ATCEA4 C623_1 , ATCEA4 S16322	98, 98, 93	ATL8C3 1543:4 05..48 _6	0.86					
144193	ATU006 133	ATL8C3 2022:2 038..1	gap2	ATCEA4 C1269 _1	98	ATL8C3 2022:1 885..1 _80	0.86					
144194	ATU006 134	ATL8C4 8962:1 ..739	gap2	ATCEA4 C1793_ _1, ATCEA4 S4785, ATCEA4 S7833	98, 89, 82	ATL8C4 8962:4 37..4	0.86					
144195	ATU006 135	ATL8C2 0315:5 90..20	gap2	ATCEA4 C72788 _1	98	ATL8C2 0315:4 49..15 _5	0.86					
144196	ATU006 136	ATL8C4 3549:6 12..12 _4	gap2	ATCEA4 S33741 , ATCEA4 S28468	98, 87	ATL8C4 3549:3 96..31 _0	0.86					
144197	ATU006 137	ATL8C3 6172:5 134..1	gap2	ATCEA4 C500_1 , ATCEA4 S27782	98, 92	ATL8C3 6172:4 931..3 _3	0.86					
144198	ATU006 138	ATL8C1 3040:3 371..8 _11	gap2	ATCEA4 C767_1 , ATCEA4	98, 89	ATL8C1 3040:3 371..9 _66	0.86					

144199	ATU006 139	ATL8C2 9027:3 10..14	gap2	S1906 ATCEA4 C99400 _1	98	ATL8C2 9027:3 10..14 1	0.86												
144200	ATU006 140	ATL8C2 1166:1 42..26 6	gap2	ATCEA4 C4368 _2	98	ATL8C2 1166:1 42..26 6	0.86												
144201	ATU006 141	ATL8C1 9836:6 183..4 420	gap2	ATCEA4 C77564 _1, ATCEA4 C11409 8 1, ATCEA4 S30344	98, 98, 97	ATL8C1 9836:6 183..5 150	0.86												
144202	ATU006 142	ATL8C3 1195:1 161..1	gap2	ATCEA4 S26159 , ATCEA4 C1960 _4, ATCEA4 S7773	98, 97, 82	ATL8C3 1195:1 153..1 11	0.86												
144203	ATU006 143	ATL8C4 7463:1 36..25 09	gap2	ATCEA4 S12673	98	ATL8C4 7463:1 36..25 09	0.86												
144204	ATU006 144	ATL8C4 9371:7 66..1	gap2	ATCEA4 C1808 _2, ATCEA4 S33786	98, 90	ATL8C4 9371:4 45..22 8	0.86												
144205	ATU006 145	ATL8C1 8274:5 13..97 4	gap2	ATCEA4 S119	98	ATL8C1 8274:5 76..97 4	0.86												
144206	ATU006 146	ATL8C5 17:657 0..198	gap2	ATCEA4 C27808 _1	98	ATL8C5 17:636 8..198	0.86												
144207	ATU006 147	ATL8C2 9419:1 ..644	gap2	ATCEA4 C727_1	98	ATL8C2 9419:1 22..43	0.86												

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144217	ATU006 157	ATL8C4 5481:2 289..2 20	gap2	ATCEA4 C6119 _ 1, ATCEA4 C6119 _ 2	98, 85	ATL8C4 5481:2 289..2 20	0.85					
144218	ATU006 158	ATL8C3 0687:1 08..67 0	gap2	ATCEA4 S32200	98	ATL8C3 0687:1 08..55 5	0.85					
144219	ATU006 159	ATL8C3 6490:1 599..1	gap2	ATCEA4 C9437 _ 1, ATCEA4 S31897	98, 95	ATL8C3 6490:1 599..1 73	0.85					
144220	ATU006 160	ATL8C1 2367:1 871..1 423	gap2	ATCEA4 S36372 , ATCEA4 S36307 , ATCEA4 C742 1	98, 82 83, 82	ATL8C1 2367:1 825..1 469	0.85					
144221	ATU006 161	ATL8S8 557:18 0..567	gap2	ATCEA4 S1768	98	ATL8S8 557:23 3..448	0.85					
144222	ATU006 162	ATL8C3 8029:7 24..19 50	gap2	ATCEA4 C80603 _1 _1	98	ATL8C3 8029:7 24..19 36	0.85					
144223	ATU006 163	ATL8C2 336:94 2..185 4	gap2	ATCEA4 C11625 9_1 _4	98	ATL8C2 336:94 2..173 6	0.85					
144224	ATU006 164	ATL8C3 2103:4 771..1 44	gap2	ATCEA4 S5419, ATCEA4 C24192 _1, ATCEA4 C20007 _1	98, 86 94, 86	ATL8C3 2103:3 997..1 44	0.85					
144225	ATU006 165	ATL8C3 2466:3	gap2	ATCEA4 C11725	98, 96	ATL8C3 2466:4	0.85					

175	7261:1 631..2 519	C31722 _1		7261:1 648..2 499						
144236	ATU006 176	gap2	ATCEA4 S942	98	ATL8C3 174:80 7..22	0.85				
144237	ATU006 177	gap2	ATCEA4 S7183	97	ATL8C3 1143:2 88..13 32	0.85	100	73	0.0012	(AF051 225) probab le G2/mit otic- specif ic cyclin [Picea marian a]
144238	ATU006 178	gap2	ATCEA4 C8044_1	98	ATL8C2 5265:8 48..15 52	0.85				
144239	ATU006 179	gap2	ATCEA4 S31477 , ATCEA4 S33202	98, 88	ATL8C1 1741:4 06..15 77	0.85				
144240	ATU006 180	gap2	ATCEA4 S29782	98	ATL8C1 0433:1 47..11 06	0.85				
144241	ATU006 181	gap2	ATCEA4 C11727 .1	98	ATL8C3 74:186 0..205	0.85				
144242	ATU006 182	gap2	ATCEA4 S5225, ATCEA4 S10445 , ATCEA4 C28148 1, ATCEA4 S8336	98, 96, 91, 89	ATL8C3 1508:3 827..7 2	0.85				

144243	ATU006 183	ATL8C3 5559:9 32..1	gap2	ATCEA4 C4885_1	98	ATL8C3 5559:9 28..72	0.85					
144244	ATU006 184	ATL8C6 580:11 15..36 9	gap2	ATCEA4 S2908	98	ATL8C6 580:11 15..36 9	0.85					
144245	ATU006 185	ATL8C1 6145:8 72..10 0	gap2	ATCEA4 C5394_2, ATCEA4 S35757	98, 90	ATL8C1 6145:8 67..11 7	0.85					
144246	ATU006 186	ATL8C4 4896:1 174..7 5	gap2	ATCEA4 C25729_1	98	ATL8C4 4896:1 153..7 5	0.85					
144247	ATU006 187	ATL8C3 5511:1 ..1117	gap2	ATCEA4 S11076	98	ATL8C3 5511:1 92..11 17	0.84					
144248	ATU006 188	ATL8C3 365:32 32..62 13	gap2	ATCEA4 C1883_1, ATCEA4 S8385	98, 82	ATL8C3 365:32 32..60 32	0.84					
144249	ATU006 189	ATL8C1 3223:2 001..1	gap2	ATCEA4 C1171_1, ATCEA4 S14911	98, 97	ATL8C1 3223:1 950..2 58	0.84					
144250	ATU006 190	ATL8C4 5390:1 746..1 40	gap2	ATCEA4 C81835_1	98	ATL8C4 5390:1 257..2 49	0.84					
144251	ATU006 191	ATL8C3 5345:1 89..85 4	gap2	ATCEA4 C2950_1, ATCEA4 S6174	98, 82	ATL8C3 5345:3 31..64 0	0.84					
144252	ATU006 192	ATL8C4 4293:2 03..11 99	gap2	ATCEA4 C26630_1	97	ATL8C4 4293:2 03..11 99	0.84	g48848 68	100	450	2.7e- 36	(AF133 532) water channe l

144253	ATU006 193	ATL8C4 8818:1 052..9	gap2	ATCEA4 S1107, ATCEA4 S35543	98, 87	ATL8C4 8818:9 16..9	0.84	g40380 66	100	785	1.0e- 34	(AC005 897) hypoth etical protein [Arabi dopsis thalia na]	protein [Mesem bryant hemum crysta llinum]
144254	ATU006 194	ATL8C1 3612:1 2383.. 14637	gap2	ATCEA4 S344, ATCEA4 S253, ATCEA4 S178	97, 88, 88	ATL8C1 3612:1 2479.. 14637	0.84	g49268 66	100	1197	1.7e- 121	(AC007 509) putati ve amp- bindin g protein [Arabi dopsis thalia na]	
144255	ATU006 195	ATL8C3 2918:9 12..37 92	gap2	ATCEA4 S4709, ATCEA4 S10729 , ATCEA4 C13382 _1	97, 97, 93	ATL8C3 2918:1 070..3 779	0.84						
144256	ATU006 196	ATL8C2 0609:1 629..6 81	gap2	ATCEA4 S23880 , ATCEA4 C38138 2, ATCEA4 C2607 _ 1	98, 91, 82	ATL8C2 0609:1 628..8 55	0.84						

144267	206	6179:1 747:..3 63		S12144 , ATCEA4 S562, ATCEA4 S283, ATCEA4 S12030 , ATCEA4 S12145	97, 97, 96, 83	6179:1 655:..3 63					
144268	ATU006 207	ATL8C2 6111:8 8..110 7	gap2	ATCEA4 C51251 1, ATCEA4 S18842 , ATCEA4 S35868	98, 90, 83	ATL8C2 6111:8 8..616	0.84				
144269	ATU006 208	ATL8C3 5414:7 04..1	gap2	ATCEA4 C2039 1, ATCEA4 S16928	98, 96	ATL8C3 5414:6 21..19 6	0.84				
144270	ATU006 209	ATL8C1 9628:2 055:..5 4	gap2	ATCEA4 S4902	98	ATL8C1 9628:2 055:..5 4	0.84				
144271	ATU006 210	ATL8S1 3488:1 ..486	gap2	ATCEA4 S32901 , ATCEA4 S35427	98, 86	ATL8S1 3488:8 4..386	0.84				
144272	ATU006 211	ATL8C3 2324:4 29..10 25	gap2	ATCEA4 S285	98	ATL8C3 2324:4 64..10 25	0.84				
144273	ATU006 212	ATL8C7 371:1. .1184	gap2	ATCEA4 C72356 1, ATCEA4 S28809 , ATCEA4	98, 97, 94, 91	ATL8C7 371:16 9..100 0	0.84				

144273	ATU006 213	ATL8C4 9937:1 60..12 16	gap2	S31901 , ATCEA4 C72356 3	98, 86	ATL8C4 9937:7 93..11 58	0.84								
144274	ATU006 214	ATL8C3 349:39 18..26 9	gap2	ATCEA4 C977_5 , ATCEA4 C977_1 , ATCEA4 S35041	98, 94	ATL8C3 349:34 71..78 0	0.84								
144275	ATU006 215	ATL8S3 0639:1 91..52 5	gap2	ATCEA4 C11194 _1	98	ATL8S3 0639:2 01..51 4	0.84								
144276	ATU006 216	ATL8C1 3271:1 263..1	gap2	ATCEA4 C5544_1 , ATCEA4 C5544_4 , ATCEA4 S34153	98, 88	ATL8C1 3271:1 123..2 01	0.84								
144277	ATU006 217	ATL8C1 6264:6 99..21 1	gap2	ATCEA4 C30398 _2, ATCEA4 S19403	98, 91	ATL8C1 6264:5 46..21 1	0.84								
144278	ATU006 218	ATL8S2 3280:1 ..318	gap2	ATCEA4 S1079	98	ATL8S2 3280:1 54..31 8	0.83								
144279	ATU006 219	ATL8C1 5563:2 574..1	gap2	ATCEA4 C83443 _1	98	ATL8C1 5563:2 574..1	0.83								

	692	gap2	ATCEA4 C778_1 , ATCEA4 S31238 , ATCEA4 S3752	98, 88	963	0.83					
144280	ATU006 220	ATL8C4 1343:1 28..15 48	gap2	ATCEA4 C778_1 , ATCEA4 S31238 , ATCEA4 S3752	98, 88	ATL8C4 1343:3 60..12 74	0.83				
144281	ATU006 221	ATL8C3 0152:9 34..21 27	gap2	ATCEA4 S1623	98	ATL8C3 0152:1 628..2 032	0.83				
144282	ATU006 222	ATL8C9 930:13 1..182 3	gap2	ATCEA4 C20266 _1, ATCEA4 C10073 _1	98, 97	ATL8C9 930:65 9..182 3	0.83				
144283	ATU006 223	ATL8C4 7656:4 92..16 61	gap2	ATCEA4 C31002 _1, ATCEA4 C4612_1, ATCEA4 S5362	98, 86	ATL8C4 7656:5 77..15 48	0.83				
144284	ATU006 224	ATL8C1 3604:1 ..681	gap2	ATCEA4 C193_1	98	ATL8C1 3604:1 42..49 2	0.83				
144285	ATU006 225	ATL8C3 6453:4 62..27 9	gap2	ATCEA4 C11104 3_1	98	ATL8C3 6453:4 39..27 9	0.83				
144286	ATU006 226	ATL8C2 812:82 4..173 8	gap2	ATCEA4 C2663_1, ATCEA4 S5580	98, 82	ATL8C2 812:94 0..153 1	0.83				
144287	ATU006 227	ATL8C4 5808:9 1..115 0	gap2	ATCEA4 S33117	98	ATL8C4 5808:9 1..955	0.83				

144294	ATU006 234	ATL8S2 4762:5 49..1	gap2	ATCEA4 S36337	98	ATL8S2 4762:5 00..12 4	0.83										CYCLAS E (RNA- 3'- PHOSPH ATE CYCLAS E) (RNA CYCLAS E) [Schiz osacch aromyc es pombe]
144295	ATU006 235	ATL8C2 0516:1 ..1785	gap2	ATCEA4 C1610 1	98	ATL8C2 0516:1 43..99 7	0.83										
144296	ATU006 236	ATL8C4 558:1. .2158	gap2	ATCEA4 S7371	98	ATL8C4 558:15 21..21 58	0.83										
144297	ATU006 237	ATL8C1 5874:5 3..885	gap2	ATCEA4 C1706 1	98	ATL8C1 5874:1 90..73 0	0.83										
144298	ATU006 238	ATL8C2 3465:9 2..261 5	gap2	ATCEA4 C1687 1, ATCEA4 S27536 , ATCEA4 S5493	98, 89, 84	ATL8C2 3465:4 22..24 41	0.83										
144299	ATU006 239	ATL8C4 9784:1 ..1091	gap2	ATCEA4 C475 2 , ATCEA4	98, 97	ATL8C4 9784:2 12..74 8	0.83										

					ATCEA4 C12797 6 1		1										
144309	ATU006 249	ATL8S2 7755:4 58..18 3	gap2	ATCEA4 S27141	98	ATL8S2 7755:4 04..22 9	0.82										
144310	ATU006 250	ATL8C5 434:91 6..65	gap2	ATCEA4 C32160 1, ATCEA4 S23029	98, 90	ATL8C5 434:91 6..65	0.82										
144311	ATU006 251	ATL8C1 2831:1 07..12 16	gap2	ATCEA4 S7766	98	ATL8C1 2831:1 07..12 16	0.82										
144312	ATU006 252	ATL8C1 0963:1 332..1	gap2	ATCEA4 C31351 1, ATCEA4 S8225, ATCEA4 C23291 1	98, 93, 83	ATL8C1 0963:1 240..5 3	0.82										
144313	ATU006 253	ATL8C3 7686:1 354..1	gap2	ATCEA4 C852_1 , ATCEA4 S17691	98, 88	ATL8C3 7686:1 264..3 41	0.82										
144314	ATU006 254	ATL8C4 2057:6 21..18 42	gap2	ATCEA4 S15016 , ATCEA4 C7853_1	97, 93	ATL8C4 2057:6 51..18 42	0.82	g14197 58	100	1119	4.1e- 103	(X9879 5) gerany lgeran yl pyroph osphat e syntha se [Sinap is alba]					
144315	ATU006 255	ATL8C4 1977:6	gap2	ATCEA4 C62799	98, 88	ATL8C4 1977:6	0.82										

												ASE, ROOT ISOZYM E PRECUR SOR (FNR) [Oryza sativa l; (AL035 527) hypoth etical protei n [Arabi dopsis thalia na]
144324	ATU006 264				ATL8C2 923:88 4..1	gap2		ATCEA4 S32034	98, 96, 17, 88, 87, 86	ATL8C2 923:39 7..83	0.82	
144325	ATU006 265				ATL8C3 0983:8 7..860	gap2		ATCEA4 S26045	98	ATL8C3 0983:8 7..691	0.82	
144326	ATU006 266				ATL8C8 886:60 ..615	gap2		ATCEA4 C86018	98	ATL8C8 886:60 ..421	0.82	
144327	ATU006 267				ATL8C2 031:91 4..148 3	gap2		ATCEA4 C10259 _2	98	ATL8C2 031:93 0..146 3	0.82	

144328	ATU006 268	ATL8C9 697:12 33..49 9	gap2	ATCEA4 C8803_1, ATCEA4 S20298	98, 82	ATL8C9 697:12 33..87 8	0.82					
144329	ATU006 269	ATL8C3 6800:2 24..14 96	gap2	ATCEA4 C5342_1	98	ATL8C3 6800:2 24..14 96	0.82					
144330	ATU006 270	ATL8C1 1276:1 ..608	gap2	ATCEA4 C1624_1	98	ATL8C1 1276:1 46..41 7	0.82					
144331	ATU006 271	ATL8C4 4364:3 595..1 654	gap2	ATCEA4 C46799 1, ATCEA4 C19193 _2	97, 96	ATL8C4 4364:3 571..1 854	0.82	927	100	g47340 07	4.2e- 71	(AC007 178) hypoth etical protei n [Arabi dopsis thalia na]
144332	ATU006 272	ATL8C6 344:50 0..1	gap2	ATCEA4 C11801 3 1	98	ATL8C6 344:50 0..109	0.82					
144333	ATU006 273	ATL8C4 5984:1 264..2 3	gap2	ATCEA4 S5679, ATCEA4 C9813_2	98, 95	ATL8C4 5984:1 178..1 33	0.82					
144334	ATU006 274	ATL8C2 7242:2 946..3 0	gap2	ATCEA4 S3767, ATCEA4 S36137 , ATCEA4 S12099	98, 88, 85	ATL8C2 7242:2 946..3 0	0.82					
144335	ATU006 275	ATL8C3 877:17 22..26 00	gap2	ATCEA4 C90 1, ATCEA4 S33270 , ATCEA4	98, 91, 86, 83	ATL8C3 877:17 22..21 26	0.82					

144336	ATU0006 276	ATL8C1 3529:8 01..13 12	gap2	S21071 , ATCEA4 S25840	98	ATL8C1 3529:8 25..11 54	0.82												
144337	ATU0006 277	ATL8C2 7302:7 28..1	gap2	ATCEA4 C29452 1, ATCEA4 S7479	98, 86	ATL8C2 7302:7 28..51 9	0.82												
144338	ATU0006 278	ATL8C4 7081:1 192..1	gap2	ATCEA4 C11671 7 1, ATCEA4 S26871	98, 91	ATL8C4 7081:9 25..21 0	0.81												
144339	ATU0006 279	ATL8C2 1568:9 3..648	gap2	ATCEA4 C18460 1	98	ATL8C2 1568:9 3..637	0.81												
144340	ATU0006 280	ATL8C2 7957:1 048..2 417	gap2	ATCEA4 C498 1	98	ATL8C2 7957:1 048..2 417	0.81												
144341	ATU0006 281	ATL8C1 6628:9 21..29 84	gap2	ATCEA4 S31882 , ATCEA4 C12595 1 1, ATCEA4 S27721 , ATCEA4 C11851 9 1	98, 92, 90, 88	ATL8C1 6628:1 049..2 910	0.81												
144342	ATU0006 282	ATL8C1 7404:2 99..1	gap2	ATCEA4 S36227	98	ATL8C1 7404:1 58..86	0.81												
144343	ATU0006 283	ATL8C4 7302:1 270..6 5	gap2	ATCEA4 S13421	98	ATL8C4 7302:1 247..6 5	0.81												

144344	ATU006 284	ATL8S2 6793:1 ..613	gap2	ATCEA4 C527_1	98	ATL8S2 6793:4 4..406	0.81					
144345	ATU006 285	ATL8C1 158:18 9..125 3	gap2	ATCEA4 C89422 _1	98	ATL8C1 158:18 9..125 3	0.81					
144346	ATU006 286	ATL8C1 2097:4 421..8 71	gap2	ATCEA4 S6337, ATCEA4 S35209 , ATCEA4 S34882 , ATCEA4 S34476	98, 97, 89 90, 89	ATL8C1 2097:4 421..1 166	0.81					
144347	ATU006 287	ATL8C1 086:26 34..43 3	gap2	ATCEA4 S2519, ATCEA4 C64106 _1, ATCEA4 S35299	97, 82 97, 82	ATL8C1 086:25 05..64 6	0.81	g21911 94	100	573	3.8e- 31	(AF007 271) contai ns weak to the SAPB protei n (TR:E2 36624) [Arabi dopsis thalia na]
144348	ATU006 288	ATL8C4 4284:1 256..7 6	gap2	ATCEA4 S30251 , ATCEA4 S30154	97, 92	ATL8C4 4284:1 215..7 7	0.81	g45388 97	100	1221	1.6e- 115	(AL049 482) AX110P -like protei n [Arabi dopsis thalia na]
144349	ATU006 289	ATL8C3 4948:9	gap2	ATCEA4 C11654	98, 96	ATL8C3 4948:9	0.81					

144350	ATU006 290	26..48 71		5.1, ATCEA4 S12186		26..48 71						
144351	ATU006 291	ATL8S6 616:49 6..115 ATL8C9 574:11 74..1	gap2	ATCEA4 C1679_1	98	ATL8S6 616:38 8..193 ATL8C9 574:11 74..85	0.81					
144352	ATU006 292	ATL8C4 8517:5 09..1	gap2	ATCEA4 C12194_1	98	ATL8C4 8517:4 87..59	0.81					
144353	ATU006 293	ATL8C1 1602:6 437..7 58	gap2	ATCEA4 C5486_3, ATCEA4 C4058_1, ATCEA4 C5486_1, ATCEA4 C5486_2, ATCEA4 S12813, ATCEA4 S9294, ATCEA4 S27104	97, 97, 96, 93, 92, 91, 89, 86, 83, 82	ATL8C1 1602:6 224..1 574	0.81	g16520 82, g21601 49, g19316 53	100, 65 68, 65	383, 336, 745	8.8e- 30, 2.9e- 37, 2.1e- 80	(D9090 2) UDP-3- O-acyl N- acetyl glucosa mine deacet ylase [Synec hocyst is sp.l; (AC000 375) No defini tion, line found [Arabi dopsis thalia nal; (U9597 3) unknow n protei n

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144403	ATU006 343	ATL8C2 0578:4 11..94	gap2	ATCEA4 C11723 3_1	98	ATL8C2 0578:4 08..30 1	0.79				
144404	ATU006 344	ATL8C4 9629:5 045..5 91	gap2	ATCEA4 S33507 , ATCEA4 S35013 , ATCEA4 S35294 , ATCEA4 S28487	98, 93, 90, 90	ATL8C4 9629:5 045..5 91	0.79				
144405	ATU006 345	ATL8C2 7295:1 055..1 989	gap2	ATCEA4 C13347 3_1	98	ATL8C2 7295:1 066..1 989	0.79				
144406	ATU006 346	ATL8C2 3576:3 60..24 29	gap2	ATCEA4 C23859 1, ATCEA4 S6713	98, 88	ATL8C2 3576:3 60..24 29	0.79				
144407	ATU006 347	ATL8S4 144:52 2..1	gap2	ATCEA4 S36334	98	ATL8S4 144:50 7..16	0.79				
144408	ATU006 348	ATL8C4 8954:1 ..1695	gap2	ATCEA4 C373_1	98	ATL8C4 8954:7 ..1683	0.79				
144409	ATU006 349	ATL8C2 7042:1 006..1 47	gap2	ATCEA4 S17026 , ATCEA4 S34714	98, 91	ATL8C2 7042:9 82..14 7	0.79				
144410	ATU006 350	ATL8C1 9144:1 ..283	gap2	ATCEA4 S11961	98	ATL8C1 9144:8 3..283	0.79				
144411	ATU006 351	ATL8C2 4413:1 82..95 2	gap2	ATCEA4 S6589	98	ATL8C2 4413:1 82..95 2	0.79				
144412	ATU006 352	ATL8S1 4243:8	gap2	ATCEA4 S2030,	98, 96, 93	ATL8S1 4243:2	0.79				

144418	ATU006 358	ATL8C2 4345:5 070..2 78	gap2	ATCEA4 S21483 ATCEA4 C29234 1, ATCEA4 C23028 1, ATCEA4 S7697, ATCEA4 C47936 1, ATCEA4 S8215	97, 97, 94, 88, 86	22 ATL8C2 4345:5 070..4 733, ATL8C2 4345:3 773..2 78	0.79, 0.96	g10014 30, g37383 23	100, 60	444, 127	4.4e- 39, 2.5e- 09	(D6399 9) ORF1 [Synec hocyst is sp.1; (AC005 170) hypoth etical protei n [Arabi dopsis thalia na]
144419	ATU006 359	ATL8C2 0150:7 34..1	gap2	ATCEA4 C390_1	98	ATL8C2 0150:7 27..62 0	0.79					
144420	ATU006 360	ATL8C2 2559:2 01..53 3	gap2	ATCEA4 C44389 _1	98	ATL8C2 2559:2 35..49 8	0.79					
144421	ATU006 361	ATL8C5 0109:1 175..2 109	gap2	ATCEA4 C8612_1	98	ATL8C5 0109:1 821..2 028	0.78					
144422	ATU006 362	ATL8C2 5299:9 8..953	gap2	ATCEA4 S4941	98	ATL8C2 5299:9 8..953	0.78					
144423	ATU006 363	ATL8C8 234:23 6..118 4	gap2	ATCEA4 C8622_1, ATCEA4 S10981	98, 93	ATL8C8 234:28 5..118 4	0.78					
144424	ATU006 364	ATL8C3 3976:1 ..485	gap2	ATCEA4 S30282 , ATCEA4 S29171	98, 92, 89, 84	ATL8C3 3976:1 38..24 4	0.78					

144432	ATU006 372	ATL8C2 5119:2 74..71 2	gap2	ATCEA4 S11742 ATCEA4 S36354	98	ATL8C2 5119:3 12..66 8	0.78												
144433	ATU006 373	ATL8C4 5200:1 ..2564	gap2	ATCEA4 S36278	98	ATL8C4 5200:5 5..242 1	0.78												
144434	ATU006 374	ATL8C2 1942:7 01..30 3	gap2	ATCEA4 C1343 1	98	ATL8C2 1942:6 55..30 3	0.78												
144435	ATU006 375	ATL8C4 7787:7 249..3 889	gap2	ATCEA4 C12323 1, ATCEA4 C54663 1	98, 98	ATL8C4 7787:6 976..3 889	0.78												
144436	ATU006 376	ATL8C1 3764:6 3..192 7	gap2	ATCEA4 C68939 1	98	ATL8C1 3764:6 3..192 7	0.78												
144437	ATU006 377	ATL8C3 365:31 29..15 98	gap2	ATCEA4 C2834 1, ATCEA4 S3312, ATCEA4 S2403	98, 92 96, 92	ATL8C3 365:28 00..15 98	0.78												
144438	ATU006 378	ATL8C4 1855:7 72..1	gap2	ATCEA4 C25822 1, ATCEA4 C11211 1, ATCEA4 S18136	98, 82 98, 82	ATL8C4 1855:7 07..15 1	0.78												
144439	ATU006 379	ATL8C6 419:49 0..169 1	gap2	ATCEA4 C94628 1	98	ATL8C6 419:49 0..145 4	0.78												

144440	ATU006 380	ATL8C2 7023:1 799..1	gap2	ATCEA4 C9350_1, ATCEA4 S1021	98, 98	ATL8C2 7023:1 799..7	0.78				
144441	ATU006 381	ATL8C3 3884:7 84..41 88	gap2	ATCEA4 S25931 , ATCEA4 C29384 1	98, 95	ATL8C3 3884:9 97..41 19	0.78				
144442	ATU006 382	ATL8C3 8368:2 212..5 47	gap2	ATCEA4 C56784 _1	98	ATL8C3 8368:2 212..5 47	0.78				
144443	ATU006 383	ATL8C9 251:11 4..544	gap2	ATCEA4 C812_1	98	ATL8C9 251:11 4..281	0.78				
144444	ATU006 384	ATL8C4 7746:4 65..60	gap2	ATCEA4 C39640 1	98	ATL8C4 7746:3 98..60	0.78				
144445	ATU006 385	ATL8C4 8679:3 11..19 21	gap2	ATCEA4 S12685 , ATCEA4 C68549 2, ATCEA4 C68549 1, ATCEA4 S22402	98, 97, 95, 87	ATL8C4 8679:3 11..14 30	0.78				
144446	ATU006 386	ATL8C3 5001:5 209..1 27	gap2	ATCEA4 S6161	98	ATL8C3 5001:5 209..1 27	0.78				
144447	ATU006 387	ATL8C1 342:5. .3735	gap2	ATCEA4 S5911	98	ATL8C1 342:21 0..373 5	0.77				
144448	ATU006 388	ATL8C2 5922:7 1..168 3	gap2	ATCEA4 C5070_1	98	ATL8C2 5922:7 2..168 3	0.77				

144449	ATU006 389	ATL8C4 7871:1 069..2 333	gap2	ATCEA4 S4518, ATCEA4 C6476_1	98, 96	ATL8C4 7871:1 219..1 819	0.77					
144450	ATU006 390	ATL8C3 9947:1 458..1	gap2	ATCEA4 C1806_1	98	ATL8C3 9947:1 458..2 9	0.77					
144451	ATU006 391	ATL8C3 8062:3 44..39 34	gap2	ATCEA4 C23982 1, ATCEA4 C95660 1, ATCEA4 C40768 1, ATCEA4 S12778	98, 98, 97, 83	ATL8C3 8062:5 67..39 34	0.77					
144452	ATU006 392	ATL8S1 4074:5 36..1	gap2	ATCEA4 S36379	98	ATL8S1 4074:5 17..29	0.77					
144453	ATU006 393	ATL8C6 995:17 22..1	gap2	ATCEA4 C1549_1	98	ATL8C6 995:16 36..29	0.77					
144454	ATU006 394	ATL8C4 6514:9 07..28 27	gap2	ATCEA4 S7276, ATCEA4 C6028_1	98, 95	ATL8C4 6514:1 195..2 827	0.77					
144455	ATU006 395	ATL8C4 7368:7 01..12 47	gap2	ATCEA4 C6451_1	98	ATL8C4 7368:1 100..1 243	0.77					
144456	ATU006 396	ATL8C4 0858:1 281..4 66	gap2	ATCEA4 C28787_1	98	ATL8C4 0858:9 72..46 6	0.77					
144457	ATU006 397	ATL8C4 6459:1 704..8 7	gap2	ATCEA4 C13231 2_1, ATCEA4 S30395	98, 93	ATL8C4 6459:1 704..3 34	0.77					

144458	ATU006 398	ATL8S2 6055:4 80..16 7	gap2	ATCEA4 S12515	98	ATL8S2 6055:2 71..16 7	0.77						
144459	ATU006 399	ATL8C4 958:61 ..2729	gap2	ATCEA4 S5896	98	ATL8C4 958:61 ..2729	0.77						
144460	ATU006 400	ATL8C2 0269:2 95..26 35	gap2	ATCEA4 C24245 1, ATCEA4 S23097	97, 96	ATL8C2 0269:2 95..25 12	0.77	g34026 72	100	3465	0.0	(AC004 697) putati ve white protei n [Arabi dopsis thalia na]	
144461	ATU006 401	ATL8C1 9705:5 22..17 19	gap2	ATCEA4 C24908 1, ATCEA4 S24850 , ATCEA4 S32434	98, 94, 89	ATL8C1 9705:5 36..15 71	0.77						
144462	ATU006 402	ATL8C4 2685:1 41..12 51	gap2	ATCEA4 S1800	98	ATL8C4 2685:1 41..12 49	0.77						
144463	ATU006 403	ATL8C2 0345:5 69..12 30	gap2	ATCEA4 C16188 1	98	ATL8C2 0345:1 011..9 48	0.77						
144464	ATU006 404	ATL8C4 845:14 4..215 4	gap2	ATCEA4 S36171	97	ATL8C4 845:31 1..215 4	0.77	g13990 38	100	136	9.0e- 11	(U4076 2) glycer ophosp hodies ter phosph odiesterase [Porre	

144470	ATU006 410	ATL8C2 3659:1 971..1	gap2	ATCEA4 C1712_1	98	ATL8C2 3659:1 195..4 4	0.77						
144471	ATU006 411	ATL8C4 9084:6 62..14 75	gap2	ATCEA4 C27384 1, ATCEA4 C27384 2	98, 97	ATL8C4 9084:6 62..14 75	0.77						
144472	ATU006 412	ATL8C1 2347:1 633..1	gap2	ATCEA4 C2922_1, ATCEA4 C2922_2	98, 95	ATL8C1 2347:1 530..1 93	0.77						
144473	ATU006 413	ATL8C2 3650:8 76..1	gap2	ATCEA4 C1554_2	98	ATL8C2 3650:3 83..13 0	0.77						
144474	ATU006 414	ATL8C2 2254:3 69..28 38	gap2	ATCEA4 C1144_1	98	ATL8C2 2254:3 69..25 71	0.77						
144475	ATU006 415	ATL8C3 3712:1 ..1330	gap2	ATCEA4 C8178_1, ATCEA4 S26120	98, 85	ATL8C3 3712:1 7..133 0	0.76						
144476	ATU006 416	ATL8C2 9363:8 45..11 96	gap2	ATCEA4 S1272	98	ATL8C2 9363:9 33..11 76	0.76						
144477	ATU006 417	ATL8C4 0280:1 ..432	gap2	ATCEA4 C77739 1	98	ATL8C4 0280:8 3..432	0.76						
144478	ATU006 418	ATL8S1 7202:1 ..553	gap2	ATCEA4 S35860	98	ATL8S1 7202:2 05..50 2	0.76						
144479	ATU006 419	ATL8S2 8801:1 ..657	gap2	ATCEA4 C19122 1	98	ATL8S2 8801:2 1..657	0.76						
144480	ATU006	ATL8C4	gap2	ATCEA4	98	ATL8C4	0.76						

420	5205:2 47..45 6	C24247 1		5205:2 47..44 9						
144481	ATU006 421	gap2	ATCEA4 C1571_	98	ATL8S9 2:547. .147	0.76				
144482	ATU006 422	gap2	ATCEA4 C34137 1, ATCEA4 S15119 , ATCEA4 C9535_	98, 97, 93, 92	ATL8C4 3598:1 132..3 7	0.76				
144483	ATU006 423	gap2	ATCEA4 C4056_	97, 91	ATL8C4 6093:1 624..2 768	0.76	g42043 08	100	963	6.5e- 82
144484	ATU006 424	gap2	ATCEA4 S30, ATCEA4 C2375_	98, 82	ATL8C3 1643:1 989..2 497	0.76				
144485	ATU006 425	gap2	ATCEA4 S31153 , ATCEA4 C29018 1	98, 97	ATL8C2 5643:2 81..35 5	0.76				
144486	ATU006 426	gap2	ATCEA4 S31374	98	ATL8C7 028:49 5..161	0.76				

144496	ATU006 436	ATL8C9 83:705 ..7	gap2	ATCEA4 C679_1 , ATCEA4 S3101, ATCEA4 S11637	98, 86, 85	ATL8C9 83:523 ..74	0.75						
144497	ATU006 437	ATL8C1 7270:3 549..1 956	gap2	ATCEA4 S36349	98	ATL8C1 7270:3 502..1 995	0.75						
144498	ATU006 438	ATL8C3 5832:1 520..2 8	gap2	ATCEA4 S6022	98	ATL8C3 5832:1 485..2 8	0.75						
144499	ATU006 439	ATL8C5 324:19 27..41 62	gap2	ATCEA4 C79625 _1, ATCEA4 S35532 , ATCEA4 S32964	97, 88, 83	ATL8C5 324:19 34..41 62	0.75	100	1528	2.7e- 157			ACETYL ORNITH INE AMINOT RANSFE RASE PRECUR SOR (ACOAT) (ACETY LORNIT HINE TRANSA MINASE) (AOTA) [Alnus glutin osa]
144500	ATU006 440	ATL8C1 4146:1 001..1 3	gap2	ATCEA4 C33066 _1	98	ATL8C1 4146:7 94..13 9	0.75						
144501	ATU006 441	ATL8C3 2523:7 01..1	gap2	ATCEA4 S1566, ATCEA4 C15070 _1,	98, 92, 91	ATL8C3 2523:3 72..64	0.75						

144502	ATU006 442	ATL8C2 3100:2 430..3 83	gap2	ATCEA4 C17257 1	98, 97, 95, 95, 95	ATL8C2 3100:2 400..4 91	0.75					
144503	ATU006 443	ATL8C4 6166:1 270..1 555	gap2	ATCEA4 S30728	98	ATL8C4 6166:1 391..1 547	0.75					
144504	ATU006 444	ATL8C4 3687:8 25..63	gap2	ATCEA4 C5179 1	98	ATL8C4 3687:7 63..63	0.75					
144505	ATU006 445	ATL8C2 8679:9 02..11 84	gap2	ATCEA4 C28706 2	98	ATL8C2 8679:9 02..99 6	0.75					
144506	ATU006 446	ATL8C4 8525:1 ..1156	gap2	ATCEA4 C20398 1, ATCEA4 C18010 1	98, 92	ATL8C4 8525:2 00..97 0	0.75					
144507	ATU006 447	ATL8C2 7604:8 02..12 8	gap2	ATCEA4 S29505 , ATCEA4 S35948	98, 93	ATL8C2 7604:8 02..12 8	0.75					
144508	ATU006 448	ATL8C4 8846:1 23..73 3	gap2	ATCEA4 S2132	98	ATL8C4 8846:1 49..73 3	0.75					

144509	ATU006 449	ATL8C4 2185:1 ..850	gap2	ATCEA4 C14861 _1	98	ATL8C4 2185:3 17..85 0	0.75					
144510	ATU006 450	ATL8C4 4434:3 83..82 2	gap2	ATCEA4 C16704 _1	98	ATL8C4 4434:3 84..82 2	0.75					
144511	ATU006 451	ATL8C1 7546:3 63..11 00	gap2	ATCEA4 S21057 , ATCEA4 S25836	98, 92	ATL8C1 7546:4 34..11 00	0.75					
144512	ATU006 452	ATL8C5 726:16 28..77	gap2	ATCEA4 C210_1 , ATCEA4 S33979 , ATCEA4 S33624 , ATCEA4 S28125	97, 92, 91, 82 0	ATL8C5 726:15 63..11 0	0.75	g26187 23	100	1023		(U4907 3) IAA17 [Arabi dopsis thalia na]
144513	ATU006 453	ATL8C1 5243:3 73..98 3	gap2	ATCEA4 S19818 , ATCEA4 C4140_1 , ATCEA4 S31793	98, 97, 94	ATL8C1 5243:5 11..94 6	0.75					
144514	ATU006 454	ATL8C3 1107:2 419..1 27	gap2	ATCEA4 C202_1 , ATCEA4 S24410 , ATCEA4 S5248, ATCEA4 S8557	98, 97, 87, 83	ATL8C3 1107:2 419..1 27	0.75					
144515	ATU006 455	ATL8C1 0338:4	gap2	ATCEA4 C12770	98	ATL8C1 0338:3	0.75					

		09..1		9_1		76..23												
144516	ATU006 456	ATL8C4 313:19 72..21 8	gap2	ATCEA4 S8057	98	ATL8C4 313:17 48..21 8	0.75											
144517	ATU006 457	ATL8C4 4292:4 87..64	gap2	ATCEA4 C70948 1	98	ATL8C4 4292:4 85..64	0.75											
144518	ATU006 458	ATL8C1 3278:1 675..2 92	gap2	ATCEA4 C1452_ 1, ATCEA4 S14614	98, 94	ATL8C1 3278:1 545..4 62	0.75											
144519	ATU006 459	ATL8C2 2421:1 ..1161	gap2	ATCEA4 C656_1 , ATCEA4 S4232	98, 84	ATL8C2 2421:5 13..10 50	0.75											
144520	ATU006 460	ATL8C2 19:997 ..1	gap2	ATCEA4 C27631 1, ATCEA4 S1237, ATCEA4 S33865 , ATCEA4 S13961	98, 98, 95, 86	ATL8C2 19:566 ..190	0.74											
144521	ATU006 461	ATL8C4 2838:5 92..1	gap2	ATCEA4 S30054 , ATCEA4 S32784	98, 89	ATL8C4 2838:5 92..16 9	0.74											
144522	ATU006 462	ATL8C2 9859:5 47..19 21	gap2	ATCEA4 C9370_ 1	97	ATL8C2 9859:6 07..16 77	0.74	g36872 37	100	1314	2.9e- 114	(AC005 169) putati ve Cys3Hi s zinc- finger protei n						

144523	ATU006 463	ATL8C3 2679:4 152..6 65	gap2	ATCEA4 C816_1 , ATCEA4 S20793 , ATCEA4 S15168 , ATCEA4 S16655	98, 91, 90, 83	ATL8C3 2679:4 087..6 65	0.74					[Arabi dopsis thalia na]
144524	ATU006 464	ATL8C3 9805:5 01..1	gap2	ATCEA4 C462_1	98	ATL8C3 9805:5 01..13 0	0.74					
144525	ATU006 465	ATL8S1 7763:3 23..45	gap2	ATCEA4 C21483 1	98	ATL8S1 7763:3 22..45	0.74					
144526	ATU006 466	ATL8C3 9952:2 229..2 27	gap2	ATCEA4 C2114_1	98	ATL8C3 9952:1 653..3 44	0.74					
144527	ATU006 467	ATL8C6 814:20 72..47 0	gap2	ATCEA4 C4058_8, ATCEA4 S30873	98, 96	ATL8C6 814:20 72..54 0	0.74					
144528	ATU006 468	ATL8C4 7983:1 ..2457	gap2	ATCEA4 S1844, ATCEA4 S2463, ATCEA4 C5741_1, ATCEA4 C26976	98, 94, 85, 84	ATL8C4 7983:2 58..24 57	0.74					
144529	ATU006 469	ATL8C5 15:102 ..1446	gap2	ATCEA4 C12190 3 1	98	ATL8C5 15:102 ..1446	0.74					

	480	3183:5 56..1	C1873_1		3183:3 96..164							
144541	ATU006 481	ATL8C2 4989:3 1..446	ATCEA4 C12201 9_1	gap2	ATL8C2 4989:3 1..446	0.74						
144542	ATU006 482	ATL8C2 2413:2 09..20 44	ATCEA4 C21737 1, ATCEA4 C965_1 , ATCEA4 C21737 2	gap2	ATL8C2 2413:2 09..16 85	0.74						
144543	ATU006 483	ATL8C1 7416:2 709..6 13	ATCEA4 S1523	gap2	ATL8C1 7416:2 616..6 13	0.74						
144544	ATU006 484	ATL8C1 2673:1 4..647 2	ATCEA4 S2721, ATCEA4 C11671 2_1, ATCEA4 S32818	gap2	ATL8C1 2673:1 4..571 4	0.74	939151 69	100	166	6.9e- 05	PROBAB LE TRNA (GUANO SINE- 2'-O-) - METHYL TRANSFERASE (TRNA [Aquif ex aeolic us])	
144545	ATU006 485	ATL8C1 7561:9 35..64	ATCEA4 S5271	gap2	ATL8C1 7561:7 29..64	0.74						
144546	ATU006 486	ATL8C2 0256:1 ..211	ATCEA4 S27114	gap2	ATL8C2 0256:3 5..119	0.73						
144547	ATU006 487	ATL8C8 352:20 48..1	ATCEA4 C497_1	gap2	ATL8C8 352:19 61..55 8	0.73						

144548	ATU006 488	ATL8C1 5488:4 734..5 39	gap2	ATCEA4 C25720 1, ATCEA4 C13489 1	98, 97	ATL8C1 5488:4 734..5 39	0.73					
144549	ATU006 489	ATL8C1 7042:1 ..850	gap2	ATCEA4 C25386 1	98	ATL8C1 7042:3 9..850	0.73					
144550	ATU006 490	ATL8C1 9755:5 95..13 14	gap2	ATCEA4 S7609	98	ATL8C1 9755:6 58..13 14	0.73					
144551	ATU006 491	ATL8C3 254:34 3..121 6	gap2	ATCEA4 C5026 1	98	ATL8C3 254:74 3..121 6	0.73					
144552	ATU006 492	ATL8C4 7735:1 503..1	gap2	ATCEA4 S11281 , ATCEA4 C21421 1	98, 98	ATL8C4 7735:1 503..3 8	0.73					
144553	ATU006 493	ATL8C3 4782:1 448..1 061	gap2	ATCEA4 C2220 1, ATCEA4 C66363 1	98, 85	ATL8C3 4782:1 375..1 149	0.73					
144554	ATU006 494	ATL8C2 7630:1 829..1	gap2	ATCEA4 C29067 1	98	ATL8C2 7630:1 829..2 27	0.73					
144555	ATU006 495	ATL8C1 468:32 8..513	gap2	ATCEA4 S34168 , ATCEA4 C12989 6 1	98, 91	ATL8C1 468:48 5..329	0.73					
144556	ATU006 496	ATL8C4 5828:8 46..22 9	gap2	ATCEA4 S26202	98	ATL8C4 5828:8 46..64 1	0.73					
144557	ATU006	ATL8C2	gap2	ATCEA4	98,	ATL8C2	0.73					

	497		1100:1 907:1 71		C12702 6 1, ATCEA4 S32942 , ATCEA4 C12004 9 1	96, 94	1100:1 481:3 73										
144558	ATU006 498	gap2	ATL8C8 938:91 4:1		ATCEA4 C932 1	98	ATL8C8 938:87 3:83	0.73									
144559	ATU006 499	gap2	ATL8C1 5166:1 494:2 31		ATCEA4 S8271, ATCEA4 S4951	98, 97	ATL8C1 5166:9 94:23 1	0.73									
144560	ATU006 500	gap2	ATL8C3 5225:1 521:6 17		ATCEA4 S14095 , ATCEA4 C26836 1	98, 85	ATL8C3 5225:1 521:8 73	0.73									
144561	ATU006 501	gap2	ATL8C7 957:1. .1007		ATCEA4 C7296 1, ATCEA4 S21519	98, 88	ATL8C7 957:43 :629	0.73									
144562	ATU006 502	gap2	ATL8C1 0883:1 018:2 164		ATCEA4 C77419 1 _	97	ATL8C1 0883:1 091:2 161	0.73	g22135 95	100	770	2.2e- 67				(AC000 348) T7N9:1 5 [Arabi dopsis thalia na]	
144563	ATU006 503	gap2	ATL8C1 7407:1 48:26 64		ATCEA4 C29701 1, ATCEA4 S19015 , ATCEA4 S13493 , ATCEA4	98, 97, 96, 95	ATL8C1 7407:1 48:57 6	0.73									

144564	ATU006 504	ATL8C4 9760:4 76..17 64	gap2	ATCEA4 C2096 1	98	ATL8C4 9760:5 70..15 53	0.73	g45103 48	100	1226	1.6e- 125	(AC006 921) unknow n protei n [Arabi dopsis thalia na]
144565	ATU006 505	ATL8C3 3108:1 675..3 22	gap2	ATCEA4 C39890 1	97	ATL8C3 3108:1 570..3 22	0.73	g45103 48	100	1226	1.6e- 125	(AC006 921) unknow n protei n [Arabi dopsis thalia na]
144566	ATU006 506	ATL8C1 9296:1 ..2187	gap2	ATCEA4 S30555 , ATCEA4 S19502 , ATCEA4 C30826 1	98, 90, 83	ATL8C1 9296:3 67..16 01	0.73					
144567	ATU006 507	ATL8C2 1006:1 193..6 3	gap2	ATCEA4 C21806 1, ATCEA4 S31668	98, 94	ATL8C2 1006:1 152..6 3	0.72					
144568	ATU006 508	ATL8C1 5832:3 63..69 4	gap2	ATCEA4 C53108 1	98	ATL8C1 5832:3 63..50 7	0.72					
144569	ATU006 509	ATL8C4 817:39 27..22 47	gap2	ATCEA4 S34	98	ATL8C4 817:39 09..22 47	0.72					
144570	ATU006 510	ATL8C3 2321:9 84..1	gap2	ATCEA4 S36317	98	ATL8C3 2321:8 54..35 2	0.72					
144571	ATU006 511	ATL8C1 643:30 02..36	gap2	ATCEA4 C11755 1,	98, 93, 92, 89	ATL8C1 643:23 97..36	0.72					

		5		ATCEA4 S34090 , ATCEA4 C15095 3_1, ATCEA4 S3194		5											
144572	ATU006 512	ATL8C2 422:35 16..22 0	gap2	ATCEA4 S11428 , ATCEA4 S32542	98, 96	ATL8C2 422:35 16..22 0	0.72										
144573	ATU006 513	ATL8S2 8904:1 ..559	gap2	ATCEA4 C560_1	98	ATL8S2 8904:7 ..402	0.72										
144574	ATU006 514	ATL8C3 1146:1 ..1300	gap2	ATCEA4 S30075	98	ATL8C3 1146:4 9..130 0	0.72										
144575	ATU006 515	ATL8C2 2352:3 281..1 100	gap2	ATCEA4 S1505, ATCEA4 S33072 , ATCEA4 S35787	98, 92, 88	ATL8C2 2352:2 708..1 275	0.72										
144576	ATU006 516	ATL8C2 0923:5 4..104 7	gap2	ATCEA4 C8896_1	98	ATL8C2 0923:6 8..104 7	0.72										
144577	ATU006 517	ATL8C7 755:86 1..66	gap2	ATCEA4 S29906	98	ATL8C7 755:86 1..66	0.72										
144578	ATU006 518	ATL8C3 7935:4 62..97 3	gap2	ATCEA4 C8445_1	98	ATL8C3 7935:4 62..97 3	0.72										
144579	ATU006 519	ATL8C4 5849:1 ..612	gap2	ATCEA4 S7691	98	ATL8C4 5849:1 92..61 2	0.72										
144580	ATU006 520	ATL8C2 7499:5	gap2	ATCEA4 C27241	98	ATL8C2 7499:5	0.72										

[illegible]

	530	1713:1 .1121		C1872_1		1713:2 5..920						
144591	ATU006 531	ATL8C2 0251:1 756..8 87	gap2	ATCEA4 C50676 1, ATCEA4 S6665	98, 87	ATL8C2 0251:1 534..1 032	0.71					
144592	ATU006 532	ATL8S1 0183:1 ..543	gap2	ATCEA4 C1781_1, ATCEA4 S22634 , ATCEA4 S22636	98, 83 97,	ATL8S1 0183:1 17..52 4	0.71					
144593	ATU006 533	ATL8C3 6467:1 ..506	gap2	ATCEA4 C25963 _1	98	ATL8C3 6467:1 07..49 5	0.71					
144594	ATU006 534	ATL8C1 3635:1 578..9 10	gap2	ATCEA4 S1151	98	ATL8C1 3635:1 466..9 10	0.71					
144595	ATU006 535	ATL8C1 8738:4 4..191 6	gap2	ATCEA4 C33569 1, ATCEA4 S3373	98, 87	ATL8C1 8738:1 38..18 38	0.71					
144596	ATU006 536	ATL8C1 6960:3 434..7 9	gap2	ATCEA4 C1063_38, ATCEA4 C1063_40, ATCEA4 C1063_36, ATCEA4 S23371	98, 97, 96, 93	ATL8C1 6960:3 434..3 44	0.71					
144597	ATU006 537	ATL8C4 0545:7 90..32 3	gap2	ATCEA4 S29913	98	ATL8C4 0545:7 90..32 3	0.71					
144598	ATU006	ATL8C3	gap2	ATCEA4	97, 83	ATL8C3	0.71	g38515	100	1700	6.2e-	(AF065)

	538	1950:2 127..4 44		C71145 1, ATCEA4 C7929 1		1950:2 083..4 50		30				170	435) noduli n [Glyci ne max]
144599	ATU006 539	ATL8C7 2:36.. 930	gap2	ATCEA4 S11252	98	ATL8C7 2:930. .36	0.71						
144600	ATU006 540	ATL8C3 8350:1 ..394	gap2	ATCEA4 C98684 _1	98	ATL8C3 8350:1 08..30 1	0.71						
144601	ATU006 541	ATL8C4 5541:7 97..1	gap2	ATCEA4 C325_1 , ATCEA4 S12903	98, 83	ATL8C4 5541:7 41..10 4	0.71						
144602	ATU006 542	ATL8C2 0819:1 ..2018	gap2	ATCEA4 C18612 _1	98	ATL8C2 0819:2 1..201 8	0.71						
144603	ATU006 543	ATL8C2 6967:1 087..2 008	gap2	ATCEA4 S11044 , ATCEA4 C1275_1	98, 96	ATL8C2 6967:1 100..1 977	0.71						
144604	ATU006 544	ATL8C3 2581:3 228..9 96	gap2	ATCEA4 C4112_1, ATCEA4 C4112_2, ATCEA4 C4112_3, ATCEA4 S7977, ATCEA4 S6464	97, 91, 90, 85, 84	ATL8C3 2581:3 228..1 210	0.71	g14980 53	100	868	6.3e- 75	(U6443 6) riboso mal protei n S8 [Zea mays]	
144605	ATU006 545	ATL8C8 769:16 0..929	gap2	ATCEA4 C8243_1	98	ATL8C8 769:16 1..929	0.71						

		09..18 54		1, ATCEA4 C82236 1, ATCEA4 S31309		93..12 26						KINASE , CHLORO PLAST (ATP- AMP TRANSP HOSPHO RYLASE) []
144633	ATU006 573	ATL8C6 72:222 0..1	gap2	ATCEA4 C1373_1	98	ATL8C6 72:210 8..85	0.69					
144634	ATU006 574	ATL8C2 8148:6 12..92 7	gap2	ATCEA4 C17865 1, ATCEA4 S3929	98, 90	ATL8C2 8148:6 12..92 7	0.69					
144635	ATU006 575	ATL8C1 3124:4 205..1 750	gap2	ATCEA4 C465_1 , ATCEA4 S10036	98, 82	ATL8C1 3124:4 205..1 899	0.69					
144636	ATU006 576	ATL8C4 7948:1 022..9 3	gap2	ATCEA4 C18055 1, ATCEA4 S15994	98, 86	ATL8C4 7948:1 022..9 3	0.69					
144637	ATU006 577	ATL8C2 8385:1 ..215	gap2	ATCEA4 C6736_1	98	ATL8C2 8385:1 27..21 5	0.69					
144638	ATU006 578	ATL8C4 47:131 3..296	gap2	ATCEA4 C5223_1, ATCEA4 S33437 , ATCEA4 S33864	98, 97, 91	ATL8C4 47:131 3..711	0.69					
144639	ATU006 579	ATL8C3 0306:1 3..484	gap2	ATCEA4 S7224	98	ATL8C3 0306:1 62..47 4	0.68					

144648	ATU006 588	ATL8C8 38:679 0..341	gap2	ATCEA4 S29592 , ATCEA4 S6763, ATCEA4 S1015	98, 97, 92	ATL8C8 38:679 0..341	0.68						[Solano um tubero sum]
144649	ATU006 589	ATL8C7 690:49 02..59	gap2	ATCEA4 C11769 7 1	98	ATL8C7 690:48 89..59	0.68						
144650	ATU006 590	ATL8S5 333:21 3..651	gap2	ATCEA4 S25033	98	ATL8S5 333:21 3..651	0.68						
144651	ATU006 591	ATL8C4 6606:1 495..2 566	gap2	ATCEA4 C1232 1, ATCEA4 S7832	98, 84	ATL8C4 6606:1 592..2 467	0.68						
144652	ATU006 592	ATL8C4 10:472 0..679 2	gap2	ATCEA4 C2687 1	98	ATL8C4 10:474 8..679 2	0.68						
144653	ATU006 593	ATL8C4 6173:6 47..23 88	gap2	ATCEA4 S5293	98	ATL8C4 6173:8 46..23 88	0.68						
144654	ATU006 594	ATL8C1 7555:8 61..11 6	gap2	ATCEA4 C14484 1 _	98	ATL8C1 7555:8 43..11 6	0.68						
144655	ATU006 595	ATL8C4 2245:1 ..957	gap2	ATCEA4 S34252 , ATCEA4 S4387	98, 89	ATL8C4 2245:5 8..789	0.68						
144656	ATU006 596	ATL8C1 6191:9 52..1	gap2	ATCEA4 C52739 1	98	ATL8C1 6191:9 52..15	0.68						
144657	ATU006 597	ATL8C5 190:69	gap2	ATCEA4 S1947	98	ATL8C5 190:59	0.68						

144669	ATU006 609	ATL8C3 6077:1 578..1 46	gap2	ATCEA4 C35008 _1	98	ATL8C3 6077:1 578..1 50	0.67					
144670	ATU006 610	ATL8C1 1485:2 632..8 978	gap2	ATCEA4 S1812	98	ATL8C1 1485:2 632..8 978	0.67					
144671	ATU006 611	ATL8C1 9825:2 549..3 12	gap2	ATCEA4 C28027 _1, ATCEA4 C10381 8 1, ATCEA4 C28027 2	98, 94, 93	ATL8C1 9825:2 528..3 12	0.67					
144672	ATU006 612	ATL8C4 1649:3 77..12 1	gap2	ATCEA4 C15081 _1	98	ATL8C4 1649:2 92..12 1	0.67					
144673	ATU006 613	ATL8C2 7640:3 62..78 5	gap2	ATCEA4 S6195	98	ATL8C2 7640:3 62..76 2	0.67					
144674	ATU006 614	ATL8C2 6215:1 265..1	gap2	ATCEA4 S31085	98	ATL8C2 6215:1 265..2 5	0.67					
144675	ATU006 615	ATL8C1 674:16 8..117 7	gap2	ATCEA4 C11733 _1, ATCEA4 C95709 1	98, 94	ATL8C1 674:18 9..338	0.67					
144676	ATU006 616	ATL8C1 4159:7 71..48	gap2	ATCEA4 C26412 _1	98	ATL8C1 4159:7 71..48	0.67					
144677	ATU006 617	ATL8C4 096:19 87..56 4	gap2	ATCEA4 C462_1 _1, ATCEA4 S20333	98, 97, 94, 87	ATL8C4 096:15 64..89 1	0.67					

144678	ATU006 618	ATL8C1 6240:4 861..5 26	gap2	ATCEA4 S23976 , ATCEA4 S16847	97	ATL8C1 6240:4 837..5 38	0.67	g20886 55, g32978 24	100, 100	217, 336	1.9e- 07, 2.6e- 24	(AF002 109) hypoth etical protei n [Arabi dopsis thalia na]; (AL031 032) bZIP transc riptio n factor -like protei n [Arabi dopsis thalia na]
144679	ATU006 619	ATL8S1 032:13 5..429	gap2	ATCEA4 S12791 , ATCEA4 S3427, ATCEA4 S12534 , ATCEA4 S11351 , ATCEA4 S5119	98, 96, 87, 86, 85	ATL8S1 032:18 5..385	0.67					
144680	ATU006 620	ATL8C6 500:18 58..64	gap2	ATCEA4 C2249 1,	98, 98, 91	ATL8C6 500:18 58..12	0.67					

		8		ATCEA4 C2249_2, ATCEA4 S12378		61											
144681	ATU006 621	ATL8C5 551:41 0..125 7	gap2	ATCEA4 S24403 , ATCEA4 C1176_1	98, 97	ATL8C5 551:43 9..122 1	0.67										
144682	ATU006 622	ATL8C1 8356:6 39..64	gap2	ATCEA4 S32198	98	ATL8C1 8356:6 39..67	0.67										
144683	ATU006 623	ATL8C4 7473:3 1..184 0	gap2	ATCEA4 S2792	98	ATL8C4 7473:2 14..18 40	0.67										
144684	ATU006 624	ATL8C2 3596:4 61..1	gap2	ATCEA4 C824_1	98	ATL8C2 3596:4 06..78	0.67										
144685	ATU006 625	ATL8C4 5105:7 18..17 2	gap2	ATCEA4 C18213 _1	98	ATL8C4 5105:6 74..17 2	0.66										
144686	ATU006 626	ATL8C2 1796:1 196..3 370	gap2	ATCEA4 C71928 1, ATCEA4 C27632 1	98, 98	ATL8C2 1796:1 893..3 230	0.66										
144687	ATU006 627	ATL8C6 214:99 8..444	gap2	ATCEA4 C22522 1, ATCEA4 C22522 3, ATCEA4 S15426	98, 95, 89	ATL8C6 214:80 5..840	0.66										
144688	ATU006 628	ATL8C4 8231:1 292..1 03	gap2	ATCEA4 C6471_1, ATCEA4 S9274,	98, 91, 82	ATL8C4 8231:6 81..10 3	0.66										

[illegible]

144698	ATU006 638	ATL8C1 4235:1 461..1	gap2	ATCEA4 S4104, ATCEA4 S19911 , ATCEA4 C91817 1, ATCEA4 C77561 1	97, 95, 92, 83	4 ATL8C1 4235:1 370..6 77	0.66	g36081 27	100	949	9.5e- 91	(AC005 314) unknow n protei n [Arabi dopsis thalia na]
144699	ATU006 639	ATL8S9 294:1. .424	gap2	ATCEA4 C29364 1	98	ATL8S9 294:23 6..424	0.66					
144700	ATU006 640	ATL8S2 9908:4 ..501	gap2	ATCEA4 C43753 1, ATCEA4 S9523	98, 90	ATL8S2 9908:5 4..210	0.66					
144701	ATU006 641	ATL8C5 391:84 3..311 6	gap2	ATCEA4 C35004 _2	98	ATL8C5 391:84 3..311 6	0.66					
144702	ATU006 642	ATL8C7 966:27 21..1	gap2	ATCEA4 C590_1	98	ATL8C7 966:25 18..49 6	0.66					
144703	ATU006 643	ATL8C1 2736:2 284..1	gap2	ATCEA4 C19440 1, ATCEA4 C4020 1	98, 90	ATL8C1 2736:2 284..5 29	0.66					
144704	ATU006 644	ATL8C2 6266:1 227..1	gap2	ATCEA4 S36226	98	ATL8C2 6266:1 227..3 47	0.65					
144705	ATU006 645	ATL8S1 1885:1 ..740	gap2	ATCEA4 C1909_1, ATCEA4 S17166	98, 93	ATL8S1 1885:2 10..60 3	0.65					
144706	ATU006	ATL8C8	gap2	ATCEA4	98	ATL8C8	0.65					

144714	ATU006 654	ATL8C2 5193:9 87..38 51	gap2	9 1 ATCEA4 C586_1 , ATCEA4 S30820	98, 92	ATL8C2 5193:9 87..36 55	0.65												
144715	ATU006 655	ATL8C5 372:11 03..18 94	gap2	ATCEA4 C12771 3_1	98	ATL8C5 372:11 03..18 94	0.65												
144716	ATU006 656	ATL8C1 2683:6 6..234 5	gap2	ATCEA4 C29377 _1	98	ATL8C1 2683:6 6..201 2	0.65												
144717	ATU006 657	ATL8C1 2665:2 53..13 32	gap2	ATCEA4 S111	98	ATL8C1 2665:2 53..13 32	0.65												
144718	ATU006 658	ATL8C4 7863:6 45..17 86	gap2	ATCEA4 S36239	98	ATL8C4 7863:1 085..1 699	0.64												
144719	ATU006 659	ATL8C4 0893:1 ..1834	gap2	ATCEA4 C1969_2, ATCEA4 C1969_1	98, 97	ATL8C4 0893:2 23..11 67, ATL8C4 0893:1 566..1 375	0.64, 0.81												
144720	ATU006 660	ATL8C1 2083:3 625..2 793	gap2	ATCEA4 C15670 1, ATCEA4 S13292 , ATCEA4 S6645	98, 90, 89	ATL8C1 2083:3 625..3 438	0.64												
144721	ATU006 661	ATL8C3 5113:6 74..33 16	gap2	ATCEA4 S10807	98	ATL8C3 5113:6 74..33 16	0.64												
144722	ATU006 662	ATL8C1 7085:8	gap2	ATCEA4 S5188	98	ATL8C1 7085:8	0.64												

	ATU006	ATL8C1 1863:1 780..7 4	gap2	ATCEA4 C23186 _1	98	ATL8C1 1863:1 569..7 4	0.64	g45394 08	100	532	1.9e- 31	thalia na]
144738	ATU006 678	ATL8C1 1863:1 780..7 4	gap2	ATCEA4 C23186 _1	98	ATL8C1 1863:1 569..7 4	0.64	g45394 08	100	532	1.9e- 31	(AL049 524) putati ve alpha NAC [Arabi dopsis thalia na]
144739	ATU006 679	ATL8C1 0815:3 399..8 55	gap2	ATCEA4 C15345 3, ATCEA4 C15345 _2	97, 92	ATL8C1 0815:3 399..1 004	0.64					
144740	ATU006 680	ATL8C2 3245:1 639..4 51	gap2	ATCEA4 C1548 _2, ATCEA4 S13220	98, 90	ATL8C2 3245:1 546..6 52	0.64					
144741	ATU006 681	ATL8S9 473:45 0..70	gap2	ATCEA4 S36242	98	ATL8S9 473:45 0..70	0.63					
144742	ATU006 682	ATL8C3 6750:2 134..7 01	gap2	ATCEA4 C92741 1, ATCEA4 S661	98, 91	ATL8C3 6750:2 134..7 01	0.63					
144743	ATU006 683	ATL8C4 9823:6 838..2 057	gap2	ATCEA4 C12152 8 1, ATCEA4 S11237	98, 98	ATL8C4 9823:6 810..2 057	0.63					
144744	ATU006 684	ATL8C2 6428:1 4..181 2	gap2	ATCEA4 C6692 _1, ATCEA4 S20329	98, 82	ATL8C2 6428:4 7..165 0	0.63					
144745	ATU006 685	ATL8S1 0712:2 89..57 8	gap2	ATCEA4 C46548 _1	98	ATL8S1 0712:3 65..46 7	0.63					
144746	ATU006	ATL8C4	gap2	ATCEA4	98,	ATL8C4	0.63					

144760	ATU006 700	ATL8C1 4632:5 73..19 06	gap2	ATCEA4 S7681	98	ATL8C1 4632:1 212..1 906	0.63					
144761	ATU006 701	ATL8C1 5189:2 05..11 73	gap2	ATCEA4 C1946_1, ATCEA4 S18674	98, 96	ATL8C1 5189:2 05..59 0	0.63					
144762	ATU006 702	ATL8C4 869:29 40..11 8	gap2	ATCEA4 C19159 1, ATCEA4 S2058	98, 96	ATL8C4 869:29 40..11 8	0.63					
144763	ATU006 703	ATL8C7 413:93 4..306	gap2	ATCEA4 S4528	98	ATL8C7 413:53 0..306	0.63					
144764	ATU006 704	ATL8C4 1424:1 ..1158	gap2	ATCEA4 C17413 2, ATCEA4 C17413 1	98, 91	ATL8C4 1424:5 5..114 3	0.63					
144765	ATU006 705	ATL8C7 557:92 ..760	gap2	ATCEA4 C1632_2, ATCEA4 S34976	98, 83	ATL8C7 557:29 8..670	0.63					
144766	ATU006 706	ATL8S2 8570:1 17..52 7	gap2	ATCEA4 C10016 _1	98	ATL8S2 8570:1 30..50 2	0.63					
144767	ATU006 707	ATL8C4 6348:1 16..12 91	gap2	ATCEA4 S948, ATCEA4 C59446 1	98, 94	ATL8C4 6348:1 17..93 5	0.63					
144768	ATU006 708	ATL8C3 7644:9 5..626	gap2	ATCEA4 C25826 1	98	ATL8C3 7644:9 5..546	0.63					
144769	ATU006 709	ATL8C3 9620:1 45..16 13	gap2	ATCEA4 S95	98	ATL8C3 9620:1 45..16 13	0.62					

144770	ATU006 710	ATL8C1 3059:4 567..1 644	gap2	ATCEA4 S30575 , ATCEA4 C77577 _1	97, 92	ATL8C1 3059:4 480..1 650	0.62	g45803 93, g45803 90	100, 48	1618, 957	6.2e- 163, 8.0e- 68	(AC007 171) hypoth etical protei n [Arabi dopsis thalia na]; (AC007 171) putati ve diseas e resist ance respon se protei n [Arabi dopsis thalia na]
144771	ATU006 711	ATL8C1 5465:1 ..976	gap2	ATCEA4 C246_1	98	ATL8C1 5465:2 7..946	0.62					
144772	ATU006 712	ATL8S9 014:32 0..1	gap2	ATCEA4 S27443	98	ATL8S9 014:32 0..163	0.62					
144773	ATU006 713	ATL8C4 3680:1 736..1 220	gap2	ATCEA4 S33432	98	ATL8C4 3680:1 736..1 565	0.62					
144774	ATU006 714	ATL8C4 5535:9 24..47	gap2	ATCEA4 C70779 1	98	ATL8C4 5535:3 34..47	0.62					
144775	ATU006 715	ATL8C2 0785:8 17..26 80	gap2	ATCEA4 C18282 1, ATCEA4 C15866	98, 97, 95	ATL8C2 0785:8 34..26 59	0.62					

144776	ATU006 716	ATL8C1 9664:1 ..496	gap2	1, ATCEA4 C17555 1	98, 86	ATL8C1 9664:1 87..68	0.62										
144777	ATU006 717	ATL8C4 4889:3 62..16 59	gap2	ATCEA4 S33446 , ATCEA4 S10243 ATCEA4 C19212 1, ATCEA4 C25432 1, ATCEA4 S30872	98, 92	ATL8C4 4889:1 657..1 397	0.62										
144778	ATU006 718	ATL8C2 1848:3 056..4 706	gap2	ATCEA4 C209_1 , ATCEA4 S20287 , ATCEA4 S8502, ATCEA4 S25010 , ATCEA4 S34849	98, 97, 96, 92, 87	ATL8C2 1848:3 185..4 706	0.62										
144779	ATU006 719	ATL8C4 5969:1 16..42 29	gap2	ATCEA4 S35615	98	ATL8C4 5969:1 16..42 29	0.62										
144780	ATU006 720	ATL8C7 829:15 94..1	gap2	ATCEA4 C73605 _1	98	ATL8C7 829:15 94..32 4	0.62										
144781	ATU006 721	ATL8C4 4463:3 864..1	gap2	ATCEA4 C684_1 , ATCEA4 C63507 1,	98, 98, 92, 88	ATL8C4 4463:3 634..9	0.62										

144791	ATU006 731	ATL8C1 0931:5 554..1 395	gap2	ATCEA4 S11167 , ATCEA4 C43780 1	98, 97	ATL8C1 0931:5 554..1 395	0.61				
144792	ATU006 732	ATL8C4 4897:9 4..290 7	gap2	ATCEA4 S773	98	ATL8C4 4897:9 4..290 7	0.61				
144793	ATU006 733	ATL8C3 8359:1 ..1285	gap2	ATCEA4 C27600 1, ATCEA4 C78301 1	98, 95	ATL8C3 8359:1 02..12 31	0.61				
144794	ATU006 734	ATL8C2 4958:2 46..51 83	gap2	ATCEA4 S2311, ATCEA4 S4196, ATCEA4 S31525 , ATCEA4 S1578, ATCEA4 S5834	98, 98, 98, 97, 86	ATL8C2 4958:2 46..51 83	0.60				
144795	ATU006 735	ATL8C2 5763:1 ..653	gap2	ATCEA4 C8274_1	98	ATL8C2 5763:7 8..653	0.60				
144796	ATU006 736	ATL8C2 9781:4 5..566	gap2	ATCEA4 C53126 _1	98	ATL8C2 9781:2 64..40 0	0.60				
144797	ATU006 737	ATL8C1 2914:4 6..240 2	gap2	ATCEA4 S4514	98	ATL8C1 2914:2 402..4 6	0.60				
144798	ATU006 738	ATL8C3 3596:1 ..400	gap2	ATCEA4 S5424	98	ATL8C3 3596:6 5..197	0.60				
144799	ATU006 739	ATL8C1 6489:1 690..1	gap2	ATCEA4 S12573 ,	98, 86	ATL8C1 6489:1 690..1	0.60				

144831	770	6926:1 ..1315		S1479, ATCEA4 C13299 7 1		6926:2 58..94 5					
	ATU006 771	ATL8C9 662:1. .942	gap2	ATCEA4 C266_1	98	ATL8C9 662:21 9..537	0.59				
144832	ATU006 772	ATL8C8 489:93 4..1	gap2	ATCEA4 C36955 1, ATCEA4 C36955 2	98, 92	ATL8C8 489:93 3..239	0.59				
144833	ATU006 773	ATL8C2 869:1. .3405	gap2	ATCEA4 S36336	98	ATL8C2 869:16 6..332 7	0.59				
144834	ATU006 774	ATL8C5 0000:2 52..10 08	gap2	ATCEA4 C34009 _1	98	ATL8C5 0000:3 13..10 08	0.58				
144835	ATU006 775	ATL8C2 0048:4 1..124 2	gap2	ATCEA4 S12805	98	ATL8C2 0048:5 38..12 42	0.58				
144836	ATU006 776	ATL8S2 3787:1 ..546	gap2	ATCEA4 C14341 1, ATCEA4 S12218	98, 98	ATL8S2 3787:3 8..151	0.58				
144837	ATU006 777	ATL8C3 5206:9 73..1	gap2	ATCEA4 C20032 _1	98	ATL8C3 5206:9 73..71 4	0.58				
144838	ATU006 778	ATL8C1 7120:8 6..473 1	gap2	ATCEA4 C27684 1, ATCEA4 S14319	98, 97	ATL8C1 7120:8 6..442 1	0.58				
144839	ATU006 779	ATL8C4 6588:8 12..18	gap2	ATCEA4 C7967_1	98	ATL8C4 6588:5 80..18	0.58				
144840	ATU006 780	ATL8C2 2543:4	gap2	ATCEA4 C23706	98, 96	ATL8C2 2543:4	0.58				

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144891	ATU006 831	ATL8C3 1976:1 ..1937	gap2	ATCEA4 C7491_1, ATCEA4 S15043	98, 97	ATL8C3 1976:1 43..17 64	0.55					
144892	ATU006 832	ATL8C1 6547:8 67..30	gap2	ATCEA4 C22474 1	98	ATL8C1 6547:8 07..30	0.55					
144893	ATU006 833	ATL8C2 004:40 6..1	gap2	ATCEA4 C2517_1	98	ATL8C2 004:27 4..18	0.55					
144894	ATU006 834	ATL8C1 8907:5 79..31 69	gap2	ATCEA4 S102, ATCEA4 C13959 4 1, ATCEA4 C76410 1	98, 91, 88	ATL8C1 8907:6 40..31 69	0.55					
144895	ATU006 835	ATL8S1 1947:1 ..660	gap2	ATCEA4 S24389	98	ATL8S1 1947:1 21..52 4	0.55					
144896	ATU006 836	ATL8C3 5079:1 57..14 14	gap2	ATCEA4 S3854	98	ATL8C3 5079:1 57..14 14	0.55					
144897	ATU006 837	ATL8C2 5321:1 253..6 76	gap2	ATCEA4 C2037_1, ATCEA4 C2037_5	98, 88	ATL8C2 5321:8 30..67 6	0.55					
144898	ATU006 838	ATL8C3 2399:1 ..486	gap2	ATCEA4 S10836	98	ATL8C3 2399:9 2..452	0.55					
144899	ATU006 839	ATL8C1 5533:8 6..417	gap2	ATCEA4 S1014	98	ATL8C1 5533:2 47..29 5	0.54					
144900	ATU006 840	ATL8C2 2763:6 94..40 3	gap2	ATCEA4 C9919_1	98	ATL8C2 2763:6 46..40 3	0.54					

144901	ATU006 841	ATL8C3 7787:1 ..2370	gap2	ATCEA4 S29661 , ATCEA4 C7433 _1	98, 97	ATL8C3 7787:6 03..22 83	0.54				
144902	ATU006 842	ATL8C2 7298:1 678..7 66	gap2	ATCEA4 C99768 _1	98	ATL8C2 7298:1 678..9 10	0.54				
144903	ATU006 843	ATL8C2 415:58 0..390	gap2	ATCEA4 S2074	98	ATL8C2 415:58 0..390	0.54				
144904	ATU006 844	ATL8C8 782:31 44..16 74	gap2	ATCEA4 S27463 , ATCEA4 S32297 , ATCEA4 C70527 _1	98, 93 95, 93	ATL8C8 782:31 44..17 10	0.54				
144905	ATU006 845	ATL8C1 4477:3 398..2 083	gap2	ATCEA4 S4012	98	ATL8C1 4477:3 398..2 083	0.54				
144906	ATU006 846	ATL8S2 3700:5 81..41 _1	gap2	ATCEA4 C40471 _1	98	ATL8S2 3700:4 68..41 _1	0.54				
144907	ATU006 847	ATL8C1 8123:2 59..11 83	gap2	ATCEA4 S1162	98	ATL8C1 8123:2 59..10 88	0.54				
144908	ATU006 848	ATL8C4 6395:1 131..1 32	gap2	ATCEA4 C2071_1 , ATCEA4 S28771	98, 90	ATL8C4 6395:1 037..3 08	0.54				
144909	ATU006 849	ATL8S2 8676:4 3..463	gap2	ATCEA4 C27755 _1	98	ATL8S2 8676:7 5..146	0.54				
144910	ATU006 850	ATL8C7 31:407	gap2	ATCEA4 S30367	98	ATL8C7 31:407	0.54				

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144929	ATU006 869	ATL8C3 3775:1 420..2 75	gap2	ATCEA4 S34584 ATCEA4 C5810 1	98	ATL8C3 3775:1 384..8 05	0.52												
144930	ATU006 870	ATL8C4 689:11 3..881	gap2	ATCEA4 S31293	98	ATL8C4 689:11 3..830	0.52												
144931	ATU006 871	ATL8C1 5142:5 3..837	gap2	ATCEA4 C76898 1	98	ATL8C1 5142:5 3..837	0.52												
144932	ATU006 872	ATL8C7 710:49 25..30 58	gap2	ATCEA4 C1854 1	98	ATL8C7 710:47 04..30 58	0.52												
144933	ATU006 873	ATL8C1 8186:8 90..12 41	gap2	ATCEA4 C2842 1	98	ATL8C1 8186:1 110..1 225	0.52												
144934	ATU006 874	ATL8C2 4689:1 063..1	gap2	ATCEA4 C30628 1	98	ATL8C2 4689:1 063..1 9	0.52												
144935	ATU006 875	ATL8C3 2645:7 88..36 4	gap2	ATCEA4 S14090	98	ATL8C3 2645:7 88..62 6	0.52												
144936	ATU006 876	ATL8C1 3582:1 065..5 028	gap2	ATCEA4 S253	98	ATL8C1 3582:1 065..5 028	0.52												
144937	ATU006 877	ATL8C1 3820:7 30..22 3	gap2	ATCEA4 C24173 1	98	ATL8C1 3820:7 30..22 3	0.52												
144938	ATU006 878	ATL8C3 9847:7 57..1	gap2	ATCEA4 C5251 1	98	ATL8C3 9847:7 57..45	0.52												

144939	ATU006 879	ATL8C1 7165:6 83..17 14	gap2	ATCEA4 S714	98	9	ATL8C1 7165:6 83..17 14	0.52									
144940	ATU006 880	ATL8S5 841:58 8..116	gap2	ATCEA4 S5839	98		ATL8S5 841:43 1..116	0.51									
144941	ATU006 881	ATL8C2 7987:7 52..26 9	gap2	ATCEA4 S12820 , ATCEA4 S4343	98, 86		ATL8C2 7987:7 47..30 1	0.51									
144942	ATU006 882	ATL8C4 5095:2 291..7 14	gap2	ATCEA4 C56211 1, ATCEA4 C13295 1, 1, ATCEA4 S30844	98, 92		ATL8C4 5095:2 254..7 14	0.51									
144943	ATU006 883	ATL8C4 6636:9 18..27 33	gap2	ATCEA4 S10636 , ATCEA4 C55480 1	98, 89		ATL8C4 6636:9 34..22 96	0.51									
144944	ATU006 884	ATL8C2 6910:1 ..800	gap2	ATCEA4 C5733 1	98		ATL8C2 6910:7 0..800	0.51									
144945	ATU006 885	ATL8C3 7291:1 ..1191	gap2	ATCEA4 C6494 1	98		ATL8C3 7291:8 9..119 1	0.51									
144946	ATU006 886	ATL8S1 0142:1 26..56 1	gap2	ATCEA4 S30187	98		ATL8S1 0142:1 26..56 1	0.51									
144947	ATU006 887	ATL8C1 4122:5 13..13 97	gap2	ATCEA4 C7919 1	98		ATL8C1 4122:5 13..13 91	0.51									
144948	ATU006 888	ATL8C1 3089:1	gap2	ATCEA4 C40514	97, 95,		ATL8C1 3089:1	0.51									(AC002 411)

		132..5 766		2, ATCEA4 S25276	95, 94, 92	132..5 766						Strong simila rity to phosph oribos ylanth ranila te transf erase gb D86 180 from Pisum sativu m. [Arabi dopsis thalia na]
144949	ATU006 889	ATL8C2 6477:5 15..92 8	gap2	ATCEA4 C4210_1, ATCEA4 C2803_2	98, 87	ATL8C2 6477:5 43..75 0	0.51					
144950	ATU006 890	ATL8C2 5163:3 529..3 21	gap2	ATCEA4 C27337 1, ATCEA4 C6554_1, ATCEA4 C27337 2, ATCEA4 S14258	98, 90, 88, 82	ATL8C2 5163:3 529..5 63	0.51					
144951	ATU006 891	ATL8C2 1680:5 17..39	gap2	ATCEA4 C11501 _2	98	ATL8C2 1680:4 74..15 1	0.51					
144952	ATU006 892	ATL8C3 5485:1 521..4	gap2	ATCEA4 S13752	98, 96, 83	ATL8C3 5485:1 369..8	0.51					

		45		ATCEA4 C29202 1, ATCEA4 S22539		13								
144953	ATU006 893	ATL8C1 8091:1 157..1 36	gap2	ATCEA4 S7754	98	ATL8C1 8091:6 81..13 6	0.51							
144954	ATU006 894	ATL8C3 1471:8 96..1	gap2	ATCEA4 C1932 1	98	ATL8C3 1471:7 00..68	0.50							
144955	ATU006 895	ATL8C1 84:277 8..141 5	gap2	ATCEA4 S10979	98	ATL8C1 84:277 8..141 5	0.50							
144956	ATU006 896	ATL8S2 5562:1 ..235	gap2	ATCEA4 C7015_ 4, ATCEA4 S36061 , ATCEA4 S28519 , ATCEA4 C7015_ 2	98, 98, 97, 82	ATL8S2 5562:2 35..20 2	0.50							
144957	ATU006 897	ATL8C3 7661:2 270..1 73	gap2	ATCEA4 C19305 1, ATCEA4 S34440 , ATCEA4 S33677	98, 93, 82	ATL8C3 7661:2 217..8 20	0.50							
144958	ATU006 898	ATL8C2 6189:4 43..10 43	gap2	ATCEA4 S89	98	ATL8C2 6189:4 43..10 43	0.50							
144959	ATU006 899	ATL8C4 5067:1 ..735	gap2	ATCEA4 C14280 1, ATCEA4	98, 97	ATL8C4 5067:1 9..731	0.50							

144987	ATU006 927	5294:1 14..16 37	C11407 4_1		5294:1 75..14 94	15, g25418 76	62	162	31, 1.2e- 27	929) putati ve chloro plast nucleo id DNA bindin g protei n [Arabi dopsis thalia nal; (D2601 5) CND41, chloro plast nucleo id DNA bindin g protei n [Nicot iana tabacu m]
144988	ATU006 928	ATL8S2 2046:3 7..622	ATCEA4 C9529 1	98	ATL8S2 2046:3 7..576	0.48				
144989	ATU006 929	ATL8C1 0369:3 584..2 44	ATCEA4 S2613	98	ATL8C1 0369:3 350..2 44	0.47				
144990	ATU006 930	ATL8C3 8991:1 558..7 7	ATCEA4 S6245	98	ATL8C3 8991:1 558..5 26	0.47				
		ATL8C3 2562:1 ..470	ATCEA4 C26896 1, ATCEA4	98, 85	ATL8C3 2562:2 4..313	0.47				

954	7280:2 205..5 07	S28631 , ATCEA4 S35526		7280:2 205..5 07	50				375) EST gb T43 829 comes from this gene. [Arabi dopsis thalia na]
145015	ATU006 955	gap2	ATCEA4 C8810_1	98	ATL8C2 1531:7 93..87	0.46			
145016	ATU006 956	gap2	ATCEA4 C80546 2, ATCEA4 S14809 , ATCEA4 S16840 , ATCEA4 C80546 3	98, 93, 86, 83	ATL8C4 3562:1 23..77 7	0.46			
145017	ATU006 957	gap2	ATCEA4 C34520 _1	98	ATL8C2 5019:1 219..5 95	0.46			
145018	ATU006 958	gap2	ATCEA4 C5283_1	98	ATL8C3 4653:1 25..69 8	0.46			
145019	ATU006 959	gap2	ATCEA4 C10466 1, ATCEA4 S2728	98, 96	ATL8C1 876:19 98..18 1	0.46			
145020	ATU006 960	gap2	ATCEA4 C23304 1, ATCEA4	98, 94	ATL8C3 7314:1 249..1 09	0.46			

145025	ATU006 965	ATL8S2 9901:5 59..41 8	gap2	ATCEA4 S13914	98	ATL8S2 9901:4 66..41 8	0.45					
145026	ATU006 966	ATL8C3 8460:7 33..14 8	gap2	ATCEA4 C74533 1, ATCEA4 S31015	98, 96	ATL8C3 8460:6 70..14 8	0.45					
145027	ATU006 967	ATL8S2 3649:3 98..1	gap2	ATCEA4 C1889_2, ATCEA4 C1889_5, ATCEA4 C1889_1	98, 89, 88	ATL8S2 3649:3 33..14 8	0.45					
145028	ATU006 968	ATL8C3 8498:7 60..15 20	gap2	ATCEA4 S12098	98	ATL8C3 8498:1 367..1 520	0.45					
145029	ATU006 969	ATL8C3 5371:5 0..167 9	gap2	ATCEA4 C1338_1, ATCEA4 S32883	98, 83	ATL8C3 5371:5 0..164 0	0.45					
145030	ATU006 970	ATL8C3 8672:3 12..14 61	gap2	ATCEA4 C6252_1	98	ATL8C3 8672:4 57..14 61	0.45					
145031	ATU006 971	ATL8C2 3429:4 62..10 933	gap2	ATCEA4 S12669, ATCEA4 S11082	97, 86	ATL8C2 3429:4 62..10 933	0.45	g46894 54, g42637 66, g46894 53	100, 30 98, 30	4833, 1969, 180	0.0, 5.3e- 96, 4.1e- 13	(AC006 267) putati ve polyp rotein [Arabi dopsis thalia nal; (AC006 218) hypoth

145032	ATU006 972	ATL8C8 314:1. .658	gap2	ATCEA4 C14136 1	98	ATL8C8 314:12 8..372	0.45					etical protei n [Arabi dopsis thalia na]; (AC006 267) predic ted protei n of unknow n functi on [Arabi dopsis thalia na]
145033	ATU006 973	ATL8C3 6617:1 908..1 326	gap2	ATCEA4 S12874	98	ATL8C3 6617:1 878..1 326	0.45					
145034	ATU006 974	ATL8C4 1250:4 54..10 55	gap2	ATCEA4 C4552 1, ATCEA4 S7940, ATCEA4 S11453	98, 87, 86	ATL8C4 1250:9 43..10 55	0.45					
145035	ATU006 975	ATL8S3 0402:2 68..1	gap2	ATCEA4 S2701	98	ATL8S3 0402:1 90..30	0.45					
145036	ATU006 976	ATL8C4 5666:1 06..67 4	gap2	ATCEA4 C11604 2_1	98	ATL8C4 5666:1 08..67 4	0.45					
145037	ATU006 977	ATL8C3 6281:1	gap2	ATCEA4 S12509	98	ATL8C3 6281:1	0.45					

145046	ATU006 986	ATL8C4 39:131 2..165 2	gap2	S1182 ATCEA4 C3100_1, ATCEA4 S2022	98, 84	ATL8C4 39:139 9..163 4	0.44										
145047	ATU006 987	ATL8C4 0522:1 135..3 32	gap2	ATCEA4 C20830 _1	98	ATL8C4 0522:1 104..5 06	0.44										
145048	ATU006 988	ATL8C9 656:63 3..131 5	gap2	ATCEA4 S36220	98	ATL8C9 656:63 3..129 7	0.43										
145049	ATU006 989	ATL8C2 3107:1 ..598	gap2	ATCEA4 S24686 , ATCEA4 S24553 , ATCEA4 S32309 , ATCEA4 C4002_1	98, 96, 92, 82	ATL8C2 3107:4 33..97	0.43										
145050	ATU006 990	ATL8C1 8702:3 418..5 350	gap2	ATCEA4 C6272_1	98	ATL8C1 8702:3 560..5 350	0.43										
145051	ATU006 991	ATL8S7 747:46 8..1	gap2	ATCEA4 S2576, ATCEA4 S22214	98, 84	ATL8S7 747:46 8..166	0.43										
145052	ATU006 992	ATL8C1 1802:1 26..71 3	gap2	ATCEA4 C11892 7_1	98	ATL8C1 1802:2 82..30 8	0.43										
145053	ATU006 993	ATL8C2 2249:6 7..164 9	gap2	ATCEA4 C25171 _1, ATCEA4 C25171 2,	98, 97, 96, 89, 88	ATL8C2 2249:9 1..996	0.43										

145054	ATU006 994	ATL8C3 391:17 0..841	gap2	ATCEA4 S33822 , ATCEA4 S34878 , ATCEA4 S16696	98	ATL8C3 391:30 0..561	0.42									
145055	ATU006 995	ATL8C4 8879:6 23..11 25	gap2	ATCEA4 S6824	98	ATL8C4 8879:6 23..11 25	0.42									
145056	ATU006 996	ATL8C4 4852:1 330..6 44	gap2	ATCEA4 C10_1, ATCEA4 S31639	98, 91	ATL8C4 4852:1 271..8 07	0.42									
145057	ATU006 997	ATL8C3 4188:4 0..137 3	gap2	ATCEA4 C49195 _1	97	ATL8C3 4188:1 67..12 72	0.42	g23427 28	100	1287	5.4e- 128	(AC002 341) Cystei ne protei nase isolog [Arabi dopsis thalia na]				
145058	ATU006 998	ATL8C1 1199:8 78..35 6	gap2	ATCEA4 S12099	98	ATL8C1 1199:8 30..35 6	0.42									
145059	ATU006 999	ATL8C4 1807:1 169..1	gap2	ATCEA4 C732_2 , ATCEA4 C732_6 , ATCEA4 S28971 , ATCEA4	98, 96, 95, 84, 83, 83	ATL8C4 1807:9 46..22 1	0.42									

145060	ATU007 000	ATL8C7 215:1. .604	gap2	S32073 , ATCEA4 S31585 , ATCEA4 C732 3	98	ATL8C7 215:28 3..604	0.42					
145061	ATU007 001	ATL8C3 5867:1 073..2 500	gap2	ATCEA4 C14241 _1	98	ATL8C3 5867:1 139..2 119	0.42					
145062	ATU007 002	ATL8C1 5592:6 6..306	gap2	ATCEA4 S3363	98	ATL8C1 5592:1 07..26 6	0.42					
145063	ATU007 003	ATL8C8 785:17 8..139 6	gap2	ATCEA4 C22292 _2	98	ATL8C8 785:43 0..303	0.42					
145064	ATU007 004	ATL8S1 3316:5 40..1	gap2	ATCEA4 C2042_1, ATCEA4 S12993	98, 98	ATL8S1 3316:5 1..160	0.42					
145065	ATU007 005	ATL8C4 8233:2 07..16 87	gap2	ATCEA4 C12481 _1	98	ATL8C4 8233:2 07..15 69	0.41					
145066	ATU007 006	ATL8C4 8805:4 5..102 6	gap2	ATCEA4 C18136 _1	98	ATL8C4 8805:1 92..41 7	0.41					
145067	ATU007 007	ATL8C1 5078:9 11..1	gap2	ATCEA4 C627_2 , ATCEA4 S32532 , ATCEA4 S35138	98, 97, 96, 95	ATL8C1 5078:3 84..18 3	0.41					

145078	017	8474:2 20..70 2	gap2	S8394	98, 92	8474:2 20..70 2						
	ATU007 018	ATL8C3 7793:3 015..1 16	gap2	ATCEA4 C13112 1, ATCEA4 S1332	98, 92	ATL8C3 7793:3 015..1 16	0.40					
145079	ATU007 019	ATL8S9 441:1. .380	gap2	ATCEA4 S2250	98	ATL8S9 441:10 7..380	0.40					
145080	ATU007 020	ATL8C4 8744:2 990..1 480	gap2	ATCEA4 C44015 _1	98	ATL8C4 8744:2 926..1 480	0.40					
145081	ATU007 021	ATL8C3 1409:5 80..1	gap2	ATCEA4 S31915 , ATCEA4 C413 1	98, 97	ATL8C3 1409:4 05..44	0.40					
145082	ATU007 022	ATL8C4 053:28 36..25 41	gap2	ATCEA4 S6960	98							
145083	ATU007 023	ATL8C4 053:52 5..892	gap2	ATCEA4 S32316	98							
145084	ATU007 024	ATL8C2 7194:1 01..35 2	gap2	ATCEA4 S1872	98							
145085	ATU007 025	ATL8C1 6003:2 367..1 838	gap2	ATCEA4 C11866 7_1	98							
145086	ATU007 026	ATL8C3 2471:2 20..61 0	gap2	ATCEA4 C14027 _1	98							
145087	ATU007 027	ATL8C3 153:61 0..1	gap2	ATCEA4 C1199 _1	98							
145088	ATU007 028	ATL8C2 7177:3	gap2	ATCEA4 S12197	98							

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	107	5365:5 7..1		S15911 , ATCEA4 C17526 1															
145168	ATU007 108	ATL8C4 5575:1 886..2 057	gap2	ATCEA4 C6041_1	98														
145169	ATU007 109	ATL8C1 3930:3 718..3 606	gap2	ATCEA4 S3870	98														
145170	ATU007 110	ATL8C6 316:60 1..781	gap2	ATCEA4 C709_1 , ATCEA4 S26935	98, 86														
145171	ATU007 111	ATL8C1 6906:1 16..63 9	gap2	ATCEA4 C322_1	98														
145172	ATU007 112	ATL8C3 7347:1 87..89 7	gap2	ATCEA4 C82315 _1	98														
145173	ATU007 113	ATL8C1 3660:7 32..93 1	gap2	ATCEA4 S33913	98														
145174	ATU007 114	ATL8C2 4261:4 628..4 294	gap2	ATCEA4 S11687	98														
145175	ATU007 115	ATL8C3 7109:6 77..68	gap2	ATCEA4 S36384	98														
145176	ATU007 116	ATL8C4 30:760 ..1110	gap2	ATCEA4 S26064 , ATCEA4 S20207	98, 83														
145177	ATU007 117	ATL8C5 808:42	gap2	ATCEA4 C10790	98														

145189	ATU007 129	ATL8C1 6942:1 ..316	gap2	ATCEA4 C49202 1, ATCEA4 C49202 2	98, 84														
145190	ATU007 130	ATL8C3 704:11 7..679	gap2	ATCEA4 C80120 1	98														
145191	ATU007 131	ATL8C1 3579:1 75..1	gap2	ATCEA4 C32043 1	98														
145192	ATU007 132	ATL8C2 7378:6 54..81 6	gap2	ATCEA4 C456_1 , ATCEA4 S6737, ATCEA4 S24727	98, 85, 83														
145193	ATU007 133	ATL8C1 3560:4 195..3 714	gap2	ATCEA4 S12806	98														
145194	ATU007 134	ATL8C2 46:124 7..171 8	gap2	ATCEA4 C2233_1	98														
145195	ATU007 135	ATL8C1 0523:1 11..1	gap2	ATCEA4 C9356_1	98														
145196	ATU007 136	ATL8C2 4614:1 89..53 1	gap2	ATCEA4 S22381	98														
145197	ATU007 137	ATL8C2 2451:1 715..2 147	gap2	ATCEA4 C14891 _1	98														
145198	ATU007 138	ATL8C2 4130:1 ..1021	gap2	ATCEA4 C572_1	98														
145199	ATU007 139	ATL8C3 6965:1 089..8	gap2	ATCEA4 S3774	98														

145200	ATU007 140	08 ATL8C1 6789:1 60..64 1	gap2	ATCEA4 C37030 _1	98															
145201	ATU007 141	ATL8C2 4639:1 ..375	gap2	ATCEA4 C43365 1	98															
145202	ATU007 142	ATL8C5 59:151 ..1	gap2	ATCEA4 S33538	98															
145203	ATU007 143	ATL8C5 433:10 03..64 4	gap2	ATCEA4 C574_1 , ATCEA4 S33035	98, 98															
145204	ATU007 144	ATL8C3 6932:1 002..1	gap2	ATCEA4 C1032_1	98															
145205	ATU007 145	ATL8C2 464:16 7..618	gap2	ATCEA4 S15296	98															
145206	ATU007 146	ATL8C4 2680:7 49..84 0	gap2	ATCEA4 C5263_1	98															
145207	ATU007 147	ATL8C4 9996:1 63..12 84	gap2	ATCEA4 C5245_1, ATCEA4 S7504, ATCEA4 C25306 _1, ATCEA4 S14594 , ATCEA4 S6020	98, 95, 95, 84, 82															
145208	ATU007 148	ATL8C3 0:977. .292	gap2	ATCEA4 S12400 , ATCEA4 S11814	98, 97															

158	5842:3 84..14 61		C8171_ 1, ATCEA4 S8138, ATCEA4 S30797 , ATCEA4 S34201	91, 88, 87							
145219	ATU007 159	gap2	ATL8C5 403:83 2..460	98							
145220	ATU007 160	gap2	ATL8C2 4002:1 ..81	98							
145221	ATU007 161	gap2	ATL8C4 257:47 3..111 6	98, 88							
145222	ATU007 162	gap2	ATL8C2 3944:1 ..301	98							
145223	ATU007 163	gap2	ATL8C2 3943:1 ..110	98							
145224	ATU007 164	gap2	ATL8C4 5442:1 ..124	98							
145225	ATU007 165	gap2	ATL8C1 4728:1 ..1277	98, 95, 95, 87							
145226	ATU007 166	gap2	ATL8C2 3906:2 20..1	98							
145227	ATU007 167	gap2	ATL8C4 2493:1	98, 82							

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145261	ATU007 201	ATL8C2 3694:1 784..1 473	gap2	ATCEA4 S3238	98														
145262	ATU007 202	ATL8C4 5120:5 27..30 3	gap2	ATCEA4 C3961_4	98														
145263	ATU007 203	ATL8C3 6637:1 ..169	gap2	ATCEA4 S32879	98														
145264	ATU007 204	ATL8C1 5247:3 2..107 7	gap2	ATCEA4 C3961_4, ATCEA4 C3961_7, ATCEA4 C3961_6, ATCEA4 C3961_3, ATCEA4 S34716	98, 98, 97, 95, 87														
145265	ATU007 205	ATL8C3 6615:1 70..82 8	gap2	ATCEA4 C31381_1	98														
145266	ATU007 206	ATL8C5 023:51 3..1	gap2	ATCEA4 S3027	98														
145267	ATU007 207	ATL8C2 2296:6 2..665	gap2	ATCEA4 C2121_1	98														
145268	ATU007 208	ATL8C5 0226:5 64..92	gap2	ATCEA4 S2954	98														

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		6..397 1		_1																
145318	ATU007 258	ATL8S2 5760:1 ..556	gap2	ATCEA4 C631_2 , ATCEA4 C631_1 ATCEA4 S2607	98, 97															
145319	ATU007 259	ATL8C6 753:50 7..150	gap2	ATCEA4 C631_1 ATCEA4 S2607	98															
145320	ATU007 260	ATL8C4 98:203 ..795	gap2	ATCEA4 S15415	98															
145321	ATU007 261	ATL8C2 3240:1 ..158	gap2	ATCEA4 C6778_1	98															
145322	ATU007 262	ATL8C2 0553:3 73..84 5	gap2	ATCEA4 S33669 , ATCEA4 S34106	98, 98															
145323	ATU007 263	ATL8C1 7242:2 159..1	gap2	ATCEA4 S33572 , ATCEA4 S14420	98, 94															
145324	ATU007 264	ATL8C4 9771:3 46..10 7	gap2	ATCEA4 S29892	98															
145325	ATU007 265	ATL8C2 7341:5 92..1	gap2	ATCEA4 C73931 1, ATCEA4 S33222	98, 82															
145326	ATU007 266	ATL8C1 5925:1 11..59 0	gap2	ATCEA4 S28361 , ATCEA4 C911_1 , ATCEA4 S35896	98, 86															
145327	ATU007	ATL8C1	gap2	ATCEA4	98,															

	267	6594:1 015..2 12		S2934, ATCEA4 S17962 , ATCEA4 S22542 ATCEA4 C5841_1	96, 94														
145328	ATU007 268	ATL8C1 4826:3 5..443	gap2	ATCEA4 C8707_1	98														
145329	ATU007 269	ATL8C3 7890:2 85..87 6	gap2	ATCEA4 C8707_1	98														
145330	ATU007 270	ATL8C4 4577:1 ..495	gap2	ATCEA4 C985_1	98														
145331	ATU007 271	ATL8C3 7852:1 913..2 067	gap2	ATCEA4 C99124_1	98														
145332	ATU007 272	ATL8C4 0817:1 107..1 359	gap2	ATCEA4 C9024_1	98														
145333	ATU007 273	ATL8C1 4342:4 51..59 8	gap2	ATCEA4 C903_1	98														
145334	ATU007 274	ATL8C2 8129:2 30..54 6	gap2	ATCEA4 C13512 1, ATCEA4 S30080	98, 88														
145335	ATU007 275	ATL8C4 3156:9 11..14 10	gap2	ATCEA4 C13512 3, ATCEA4 C13512 2, ATCEA4 S34212	98, 96, 94														
145336	ATU007 276	ATL8C4 5840:3 67..1	gap2	ATCEA4 C9505_1	98														

145337	ATU007 277	ATL8C3 7923:4 14..13 5	gap2	ATCEA4 S29990	98														
145338	ATU007 278	ATL8C4 8972:1 004..6 33	gap2	ATCEA4 S29696	98														
145339	ATU007 279	ATL8C3 6430:1 574..1 136	gap2	ATCEA4 C92084 _1	98														
145340	ATU007 280	ATL8C4 4517:4 38..12 06	gap2	ATCEA4 S10002 , ATCEA4 S3952	98, 96														
145341	ATU007 281	ATL8C1 7512:1 ..878	gap2	ATCEA4 C21216 1, ATCEA4 C21216 2	98, 97														
145342	ATU007 282	ATL8C3 5095:3 034..2 599	gap2	ATCEA4 S26431 , ATCEA4 S23876 , ATCEA4 S20986	98, 84, 83														
145343	ATU007 283	ATL8C4 7507:4 41..67 2	gap2	ATCEA4 C10147 4_1	98														
145344	ATU007 284	ATL8C1 7523:4 84..85	gap2	ATCEA4 C6765_1	98														
145345	ATU007 285	ATL8C2 232:22 0..64	gap2	ATCEA4 S13893	98														
145346	ATU007 286	ATL8C2 2317:1 054..1	gap2	ATCEA4 S12986	98														

	328	9657:1 ..312		S3311																
145389	ATU007 329	ATL8C3 8046:1 ..67	gap2	ATCEA4 S1761	98															
145390	ATU007 330	ATL8S1 9719:4 25..35 3	gap2	ATCEA4 S33544	98															
145391	ATU007 331	ATL8C2 3582:1 182..9 40	gap2	ATCEA4 S33260 , ATCEA4 S16060	98, 90															
145392	ATU007 332	ATL8C2 2076:8 93..1	gap2	ATCEA4 S34825	98															
145393	ATU007 333	ATL8S2 0200:1 ..234	gap2	ATCEA4 C46411 1	98															
145394	ATU007 334	ATL8C4 9117:1 ..172	gap2	ATCEA4 S33163	98															
145395	ATU007 335	ATL8C6 40:476 5..470 4	gap2	ATCEA4 C64837 _1	98															
145396	ATU007 336	ATL8C4 7839:3 908..4 210	gap2	ATCEA4 S5201, ATCEA4 S19916	98, 90															
145397	ATU007 337	ATL8S2 1627:1 ..396	gap2	ATCEA4 C10480 1_1	98															
145398	ATU007 338	ATL8S2 6758:5 89..37 6	gap2	ATCEA4 C783_1 , ATCEA4 S33618 , ATCEA4 S25737 , ATCEA4	98, 90, 90, 88, 88, 88, 87, 87, 84, 82															

145458	ATU007 398	ATL8S2 9245:3 47..52 1	gap2	ATCEA4 S35004	98								thalia nal; (AC006 217) putati ve Athila retroe lement ORF1 protei n [Arabi dopsis thalia na]
145459	ATU007 399	ATL8S2 9254:5 51..47 4	gap2	ATCEA4 C29194 _1	98								
145460	ATU007 400	ATL8C3 9549:7 03..1	gap2	ATCEA4 C24695 _1	98								
145461	ATU007 401	ATL8C4 8947:3 178..3 613	gap2	ATCEA4 C82175 _1	98								
145462	ATU007 402	ATL8C2 4906:2 092..2 322	gap2	ATCEA4 C36924 _1, ATCEA4 S31631	98, 96								
145463	ATU007 403	ATL8S2 9821:5 19..76	gap2	ATCEA4 C12214 4 1	98								
145464	ATU007 404	ATL8C1 1321:1 20..52 5	gap2	ATCEA4 C36982 _1	98								
145465	ATU007	ATL8S3	gap2	ATCEA4	98								

	500	0415:5 71..63 6		C13178 _1												
145561	ATU007 501	ATL8C1 3137:1 81..10 91	gap2	ATCEA4 S1097, ATCEA4 S35036	98, 86											
145562	ATU007 502	ATL8C2 2967:1 ..1276	gap2	ATCEA4 C27105 _1	97					g35102 60	100	697	7.9e- 55	(AC005 310) putati ve AP2 domain contai ning protei n [Arabi dopsis thalia na]		
145563	ATU007 503	ATL8C2 5484:6 30..44 2	gap2	ATCEA4 S35212	98											
145564	ATU007 504	ATL8C2 1336:3 80..94 7	gap2	ATCEA4 C2397 _ 1	98											
145565	ATU007 505	ATL8C3 0681:4 83..1	gap2	ATCEA4 C23096 2, ATCEA4 C23096 1, ATCEA4 C4716 _ 1	98, 97, 85											
145566	ATU007 506	ATL8C2 2972:8 92..97 4	gap2	ATCEA4 C4087 _ 1	98											
145567	ATU007 507	ATL8C3 4237:1 21..37	gap2	ATCEA4 S2900	98											

145579	ATU007 519	ATL8C4 836:31 25..11 57	gap2	ATCEA4 C65716 1, ATCEA4 S34226	97, 96			g13403 7	100	526	1.8e- 13	SMALL NUCLEA R RIBONU CLEOPR OTEIN ASSOCI ATED PROTEI NS B AND B' (SM-B AND SM-B') (SNRNP -B) []
145580	ATU007 520	ATL8C4 8852:1 175..1 276	gap2	ATCEA4 C955_1	98							
145581	ATU007 521	ATL8C3 5566:1 024..7 58	gap2	ATCEA4 C15512 1, ATCEA4 S2145	98, 95							
145582	ATU007 522	ATL8C3 0330:2 139..2 081	gap2	ATCEA4 S320	98							
145583	ATU007 523	ATL8S6 838:35 2..438	gap2	ATCEA4 S30854	98							
145584	ATU007 524	ATL8C4 8868:6 72..11 65	gap2	ATCEA4 S30310 , ATCEA4 S16893	98, 82							
145585	ATU007 525	ATL8S6 934:12 5..214	gap2	ATCEA4 S29075	98							
145586	ATU007 526	ATL8C3 4198:2 24..1	gap2	ATCEA4 S1616	98							

145587	ATU007 527	ATL8C1 4799:1 117..6 25	gap2	ATCEA4 S7850, ATCEA4 S30284	98, 93															
145588	ATU007 528	ATL8C2 6498:2 54..58 5	gap2	ATCEA4 C11791 5_1	98															
145589	ATU007 529	ATL8S7 072:17 4..96	gap2	ATCEA4 S36264	98															
145590	ATU007 530	ATL8C1 2062:1 320..9 58	gap2	ATCEA4 C10560 0_1	98															
145591	ATU007 531	ATL8C3 3174:1 ..1329	gap2	ATCEA4 C75 2, ATCEA4 C75 1	98, 83															
145592	ATU007 532	ATL8C3 3175:1 ..1270	gap2	ATCEA4 C75 1, ATCEA4 C75 2	98, 86															
145593	ATU007 533	ATL8C4 8947:2 281..1 298	gap2	ATCEA4 S7767, ATCEA4 C23562 1	98, 93															
145594	ATU007 534	ATL8C3 0317:5 04..56 9	gap2	ATCEA4 S1477	98															
145595	ATU007 535	ATL8C1 1980:3 68..86 9	gap2	ATCEA4 C12094 4_1	98															
145596	ATU007 536	ATL8S7 287:96 ..17	gap2	ATCEA4 S36264	98															
145597	ATU007 537	ATL8C2 1156:3 452..3 894	gap2	ATCEA4 C88702 _1	98															
145598	ATU007	ATL8C3	gap2	ATCEA4	98															

																				response protein (206- d) like [Arabi dopsis thalia na]
145629	ATU007 569	ATL8C2 0953:5 75..31 6	gap2	ATCEA4 S25868	98															
145630	ATU007 570	ATL8C2 5072:1 718..1 278	gap2	ATCEA4 C34731 _2	98															
145631	ATU007 571	ATL8C1 1905:2 27..85 7	gap2	ATCEA4 S299	98															
145632	ATU007 572	ATL8C2 0943:3 63..1	gap2	ATCEA4 S3968	98															
145633	ATU007 573	ATL8C3 4045:5 32..15 4	gap2	ATCEA4 C19076 _1	98															
145634	ATU007 574	ATL8S9 38:413 ..222	gap2	ATCEA4 C75559 _1	98															
145635	ATU007 575	ATL8C7 927:69 ..1	gap2	ATCEA4 C807_1	98															
145636	ATU007 576	ATL8S2 5548:6 06..32 0	gap2	ATCEA4 C20086 _1	98															
145637	ATU007 577	ATL8S1 7774:6 06..45 9	gap2	ATCEA4 S12399	98															

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145718	657	2186:8 10..99 4		S32293 , ATCEA4 C344_1 , ATCEA4 S31906	90, 82														
145719	ATU007 658	ATL8S1 7011:1 ..212	gap2	ATCEA4 S4347	98														
145720	ATU007 659	ATL8C4 3518:6 22..14 2	gap2	ATCEA4 S12893	98														
145721	ATU007 660	ATL8C7 09:244 6..179 6	gap2	ATCEA4 C29779 _1	98														
145722	ATU007 661	ATL8C3 3554:1 87..1	gap2	ATCEA4 C99444 2	98														
145723	ATU007 662	ATL8C7 082:49 8..763	gap2	ATCEA4 S168	98														
145724	ATU007 663	ATL8C4 7285:1 ..100	gap2	ATCEA4 S1244	98														
145725	ATU007 664	ATL8C1 1745:9 77..26 6	gap2	ATCEA4 C11902 8_1	98														
145726	ATU007 665	ATL8C3 3543:5 28..96 5	gap2	ATCEA4 S5008	98														
145727	ATU007 666	ATL8S8 216:59 8..158	gap2	ATCEA4 C85595 1	98														
145728	ATU007 667	ATL8C4 7271:3 22..1	gap2	ATCEA4 S4519	98														
145729	ATU007 668	ATL8C3 8649:4 56..30	gap2	ATCEA4 C32053 1	98														

145750	ATU007 690	ATL8C4 3326:1 ..381	gap2	S3525 ATCEA4 S30589 , ATCEA4 S22285	98, 88															
145751	ATU007 691	ATL8C7 178:1. .142	gap2	ATCEA4 S3015, ATCEA4 S18581 , ATCEA4 S23648	98, 93 94, 93															
145752	ATU007 692	ATL8C2 2222:1 ..623	gap2	ATCEA4 C11540 9 1	98															
145753	ATU007 693	ATL8C1 4890:1 ..833	gap2	ATCEA4 C48777 1	98															
145754	ATU007 694	ATL8C4 7184:1 ..621	gap2	ATCEA4 S23913	98															
145755	ATU007 695	ATL8C2 5724:6 49..1	gap2	ATCEA4 C31555 1	98															
145756	ATU007 696	ATL8C4 3320:1 115..1 487	gap2	ATCEA4 S150	98															
145757	ATU007 697	ATL8C8 342:1. .255	gap2	ATCEA4 S14448	98															
145758	ATU007 698	ATL8C7 856:10 85..32 2	gap2	ATCEA4 C41993 1, ATCEA4 S32740	98, 98															
145759	ATU007 699	ATL8C8 37:667 ..1126	gap2	ATCEA4 S21045	98															
145760	ATU007 700	ATL8C2 2226:5 23..10 39	gap2	ATCEA4 S1139, ATCEA4 S315	98, 96															

145826	ATU007 766	ATL8C1 6784:2 528..3 280	gap2	ATCEA4 S33770 , ATCEA4 C18532 _1, ATCEA4 S19131	97, 96					g29110 71	100	759	3.0e- 61	(AL021 960) hypo- thetical protein [Arabi- dopsis thaliana]	
145827	ATU007 767	ATL8C4 2920:7 22..23 0	gap2	ATCEA4 C25761 _1	98										
145828	ATU007 768	ATL8C2 8196:8 21..97 7	gap2	ATCEA4 C7645 _1	98										
145829	ATU007 769	ATL8C3 4965:9 30..11 73	gap2	ATCEA4 C60816 _1, ATCEA4 S10279	98, 98										
145830	ATU007 770	ATL8S2 481:14 8..339	gap2	ATCEA4 S30825 , ATCEA4 C612_1	98, 96										
145831	ATU007 771	ATL8C3 1602:3 093..3 807	gap2	ATCEA4 C768_1	98										
145832	ATU007 772	ATL8C4 6916:1 503..7 83	gap2	ATCEA4 C36174 _1	98										

145863	802	9418:1 ..357	gap2	S12082	97					gl4029 9	100	1105	4.0e-87	CYTOCHROME C BIOGENESIS PROTEIN CCNA [Nicotiana tabacum]
145864	ATU007 804	ATL8C1 5113:5 89..1	gap2	ATCEA4 C1891_1	98									
145865	ATU007 805	ATL8C7 009:60 4..84	gap2	ATCEA4 S7682	98									
145866	ATU007 806	ATL8C4 27:1.. 365	gap2	ATCEA4 S4512	98									
145867	ATU007 807	ATL8C2 1537:1 392..1 221	gap2	ATCEA4 S27849 , ATCEA4 S27847	98, 84									
145868	ATU007 808	ATL8C2 6000:8 27..54 2	gap2	ATCEA4 C27479 _1	98									
145869	ATU007 809	ATL8C1 1635:9 44..1	gap2	ATCEA4 C14299 1	98									
145870	ATU007 810	ATL8C3 2958:2 880..3 106	gap2	ATCEA4 C27470 _1	98									
145871	ATU007 811	ATL8C1 5123:1 03..46 2	gap2	ATCEA4 C78008 _1	98									
145872	ATU007 812	ATL8C4 676:30 0..1	gap2	ATCEA4 S30578	98									

1459331	ATU007 871	ATL8C1 5207:6 59..87 8	gap2	ATCEA4 C4881_1	98														
1459332	ATU007 872	ATL8C1 7095:3 92..2	gap2	ATCEA4 S1096	98														
1459333	ATU007 873	ATL8C4 2347:2 537..1 827	gap2	ATCEA4 S29701	98														
1459334	ATU007 874	ATL8C1 1057:4 84..82 3	gap2	ATCEA4 C77239_1	98														
1459335	ATU007 875	ATL8C3 4554:1 ..73	gap2	ATCEA4 C1330_6	98														
1459336	ATU007 876	ATL8C4 2324:9 40..14 87	gap2	ATCEA4 C39697_1	98														
1459337	ATU007 877	ATL8C2 905:29 63..32 43	gap2	ATCEA4 C17934_1	98														
1459338	ATU007 878	ATL8C2 1018:1 ..63	gap2	ATCEA4 C98_1	98														
1459339	ATU007 879	ATL8C4 6506:3 45..53 8	gap2	ATCEA4 C10566_9_1	98														
1459340	ATU007 880	ATL8C4 9837:1 648..1	gap2	ATCEA4 C13631_1, ATCEA4 S3504, ATCEA4 S27565 , ATCEA4 C13631_2,	98, 98, 89, 87, 85, 84														

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145995	934	1394:2 81..1		C18509 1, ATCEA4 S9242															
	ATU007 935	ATL8C2 5415:2 93..71 9	gap2	ATCEA4 C2186_ 1, ATCEA4 S4536	98, 90														
145996	ATU007 936	ATL8C4 6160:7 25..98 4	gap2	ATCEA4 S12594	98														
145997	ATU007 937	ATL8C3 4299:5 073..4 664	gap2	ATCEA4 C12326 1, ATCEA4 S2685	98, 98														
145998	ATU007 938	ATL8C3 2382:2 19..53 8	gap2	ATCEA4 S32106	98														
145999	ATU007 939	ATL8C3 5857:5 19..70 5	gap2	ATCEA4 S12167	98														
146000	ATU007 940	ATL8S2 0739:1 ..593	gap2	ATCEA4 C14579 1, ATCEA4 C8143_ 1	98, 97														
146001	ATU007 941	ATL8C8 819:56 1..186	gap2	ATCEA4 S11193	98														
146002	ATU007 942	ATL8S8 523:26 7..27	gap2	ATCEA4 C8643_ 1	98														
146003	ATU007 943	ATL8C1 3008:1 010..2 92	gap2	ATCEA4 C980_1 , ATCEA4 S35926	98, 89, 83														

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146292	ATU008 232	ATL8S1 9787:2 99..1	gap2	ATCEA4 C32615 1, ATCEA4 C32615 2	98, 94															
146293	ATU008 233	ATL8C1 8623:1 90..1	gap2	ATCEA4 C30082 1	98															
146294	ATU008 234	ATL8C3 3003:6 51..30 6	gap2	ATCEA4 C5974_1, ATCEA4 S20167	98, 83															
146295	ATU008 235	ATL8C4 0523:5 9..108 5	gap2	ATCEA4 C21635 1, ATCEA4 C89584 1, ATCEA4 S26427	98, 96, 95															
146296	ATU008 236	ATL8C1 0291:4 226..4 867	gap2	ATCEA4 C12504 1_	98															
146297	ATU008 237	ATL8C4 3533:1 590..1 034	gap2	ATCEA4 C1324_2, ATCEA4 C1324_1	98, 95															
146298	ATU008 238	ATL8C3 1058:3 041..3 397	gap2	ATCEA4 S14609	98															
146299	ATU008 239	ATL8C1 5552:4 058..4 751	gap2	ATCEA4 S11108	98															
146300	ATU008 240	ATL8C3 9731:8 81..97 2	gap2	ATCEA4 S33628	98															

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146425	ATU008 365	ATL8C2 3860:3 28..19 33	gap2	ATCEA4 C12116 _1	97	ATL8C2 3860:6 29..13 48	0.93	g45836 56	99	229	1.1e- 21	7 [Synec hocyst is sp.] (AJ010 592) ubiqui tin- conjug ating enzyme [Guill ardia theta]
146426	ATU008 366	ATL8C3 7435:2 068..5 62	gap2	ATCEA4 C8816 _1	97	ATL8C3 7435:2 047..7 43	0.92	g33778 12	99	116		(AF076 275) contai ns simila rity to heavy- metal- associ ated domain contai ning protei ns (Pfam: HMA.hm , score: 12.02) [Arabi dopsis thalia na]
146427	ATU008 367	ATL8C1 0970:1 ..3866	gap2	ATCEA4 S5527	97	ATL8C1 0970:9 73..38 48	0.91	g22448 77, g22448 78	99, 87	272, 920	1.0e- 22, 5.8e- 65	(Z9733 8) hypoth etical protei

146428	ATU008 368	ATL8C3 7769:2 434..1 031	gap2	ATCEA4 C11638 1_1	97	ATL8C3 7769:2 434..1 241	0.91	g32041 03	99	403	1.0e- 24	(AJ006 761) hypoth etical protei n [Arabi dopsis thalia na] (Z9733 8) hypoth etical protei n [Arabi dopsis thalia na]
146429	ATU008 369	ATL8C3 5578:1 96..15 19	gap2	ATCEA4 S31126	97	ATL8C3 5578:1 96..15 19	0.90	g47689 78	99	648	1.1e- 69	(AF140 489) kiaa00 78 protei n [Oryza sativa]
146430	ATU008 370	ATL8C9 628:99 0..1	gap2	ATCEA4 S36325	97	ATL8C9 628:92 1..95	0.84	g10449 16	99	190	7.9e- 16	(X8960 5) ORF3, myb7 sequen ce [Oryza sativa]
146431	ATU008 371	ATL8C4 5164:5 167..4	gap2	ATCEA4 S29525	97	ATL8C4 5164:5 167..4	0.83	g45672 07	99	457	4.4e- 44	(AC007 168) unknown

146432	ATU008 372	522	gap2	ATCEA4 C11720 1_1	97	ATL8C1 7156:1 619..7 8	0.82	g33341 62	99	273	3.6e- 20	n protei n [Arabi dopsis thalia na]
146433	ATU008 373	ATL8C1 7156:1 695..1	gap2	ATCEA4 S36015 , ATCEA4 C11332 1, ATCEA4 S35337	97, 89 95, 90	ATL8C3 9593:9 53..29 6	0.81	g37470 26	99	178	1.5e- 13	(AF093 244) import protei n Tim9p [Sacch aromyc es cerevi siae]
146434	ATU008 374	ATL8C2 5284:1 806..3 138	gap2	ATCEA4 C6634 1, ATCEA4 S6905	97, 89	ATL8C2 5284:2 181..3 096	0.76	g28268 11	99	391	1.5e- 33	(AJ002 892) AtGRP2 [Arabi dopsis thalia na]
146435	ATU008 375	ATL8C3 6540:2 313..3 596	gap2	ATCEA4 S2233	97	ATL8C3 6540:2 313..3 595	0.66	g46626 33	99	337	7.0e- 27	(AC007 267) hypoth etical protei n [Arabi dopsis thalia

146436	ATU008 376	ATL8C2 492:92 1..1	gap2	ATCEA4 S30545 , ATCEA4 S35327	97, 94	ATL8C2 492:76 1..34	0.65	g45389 81	99	691	8.1e- 71	na] (AL049 487) putati ve protei n [Arabi dopsis thalia na]
146437	ATU008 377	ATL8S1 527:1. .637	gap2	ATCEA4 C156_6 , ATCEA4 C156_2 , ATCEA4 C156_1 , ATCEA4 S29642 , ATCEA4 S13932	97, 96, 95, 94, 93	ATL8S1 527:35 9..615	0.64	g23387 12	99	317	6.0e- 16	(AF013 959) metall othion ein- like protei n [Arabi dopsis thalia na]
146438	ATU008 378	ATL8C3 990:4 51..24 00	gap2	ATCEA4 C12987 1, ATCEA4 C10909 9_1, ATCEA4 C12987 _2	97, 94 97, 94	ATL8C3 9990:9 24..23 70	0.63	g30470 90	99	739	3.5e- 71	(AF058 826) T26D22 .18 gene produc t [Arabi dopsis thalia na]
146439	ATU008 379	ATL8C3 459:88 ..1800	gap2	ATCEA4 C42936 _1	97	ATL8C3 459:14 9..180 0	0.62	g42493 80	99	243	1.2e- 23	(AC005 966) ESTs gb Z37 637, gb AA0 42498 and gb AA0

146440	ATU008 380	ATL8C2 2073:1 379..3 62	gap2	ATCEA4 C59546 _1, ATCEA4 C59546 _2	97, 97	ATL8C2 2073:1 376..3 62	0.61	g16535 16	99	208	1.6e- 17	(D9091 4) hypoth etical protei n [Synec hocyst is sp.]	42269 come from this gene. [Arabi dopsis thalia na]
146441	ATU008 381	ATL8C4 7849:6 28..1	gap2	ATCEA4 C51315 _1	97	ATL8C4 7849:5 69..35	0.61	g46893 66	99	119	4.1e- 09	(AF134 155) RING finger protei n [Arabi dopsis thalia na]	
146442	ATU008 382	ATL8C3 0723:4 0..497 9	gap2	ATCEA4 C13346 0_1, ATCEA4 S24698 , ATCEA4 S34801 , ATCEA4 S17090	97, 93, 92, 90	ATL8C3 0723:4 2..362 1	0.59	g44688 16, g45394 68	99, 30	271, 145	2.6e- 21, 4.4e- 11	(AL035 601) putati ve protei n [Arabi dopsis thalia na]; (AL049 500) putati ve protei n	

146443	ATU008 383	ATL8C1 4432:1 ..1696	gap2	ATCEA4 S34388 , ATCEA4 C22876 1, ATCEA4 S24188 , ATCEA4 C11745 71, ATCEA4 S33335 , ATCEA4 S33658 , ATCEA4 C22876 3	97, 97, 96, 92, 91, 88, 85	ATL8C1 4432:2 48..65 1	0.56	g13393 8	99	667	4.4e- 61	[Arabi dopsis thalia na] CHLORO PLAST 30S RIBOSO MAL PROTEI N S3 [Spina cia olerac ea]
146444	ATU008 384	ATL8C1 6561:1 46..14 05	gap2	ATCEA4 S8018	97	ATL8C1 6561:1 46..12 21	0.56	g45394 17	99	574	1.3e- 53	(AL049 171) putati ve protei n [Arabi dopsis thalia na]
146445	ATU008 385	ATL8C3 953:43 5..1	gap2	ATCEA4 S2183	97	ATL8C3 953:43 5..21	0.53	g31525 85	99	306	2.3e- 30	(AC002 986) Contai ns simila rity to auxin- induce d

146446	ATU008 386	ATL8C2 7440:3 62..74	gap2	ATCEA4 C70692 _1	97	ATL8C2 7440:3 58..14 9	0.52	g45672 26	99	353			protein TM018A 10.6 from A. thalia na BAC gb AF0 13294. [Arabi dopsis thalia na]
146447	ATU008 387	ATL8C1 4808:7 98..49 81	gap2	ATCEA4 C3267 _1, ATCEA4 S3937	97, 86	ATL8C1 4808:1 043..4 406	0.52	g45586 84, g36953 99	99, 31	477, 1357	1.7e- 13, 9.4e- 100		(AC006 586) hypothesis et al protein [Arabi dopsis thalia na]; (AF096 372) contains similarity to Arabidopsis thalia na

146448	ATU008 388	ATL8C3 8783:7 33..1	gap2	ATCEA4 C893_1	97	ATL8C3 8783:6 83..15 5	0.52	g11271 7	99	434	3.3e- 42	21 KD PROTEI N PRECUR SOR (1.2 PROTEI N) [Daucu s carota]
146449	ATU008 389	ATL8C1 7537:1 ..1650	gap2	ATCEA4 C10312 _1	97			g41057 94	99	288	2.4e- 24	(AF049 928) PGP224 [Petun ia x hybrid a]
146450	ATU008 390	ATL8C3 8637:2 15..94 2	gap2	ATCEA4 C21845 _1	97			g21297 42	99	289	8.9e- 26	stress - induce d protei n OZIL precu sor - Arabid opsis thalia na [Arabi dopsis thalia na]

146451	ATU008 391	ATL8C2 3799:1 083..1 773	gap2	ATCEA4 S26413 , ATCEA4 C21941 _1	97, 90				g37023 33	99	661	1.5e- 57	(AC005 397) hypoth etical protei n [Arabi dopsis thalia na]
146452	ATU008 392	ATL8S3 182:59 5..61	gap2	ATCEA4 S32161	97				g48742 79	99	167	2.5e- 10	(AC007 354) ESTs gb T75 618 and gb AA4 04816 come from this gene. [Arabi dopsis thalia na]
146453	ATU008 393	ATL8C1 4384:1 98..67 6	gap2	ATCEA4 S5407	97				g33554 83	99	345	3.8e- 26	(AC004 218) gibber ellin- regula ted protei n (GASA5) -like [Arabi dopsis thalia na]
146454	ATU008 394	ATL8C2 3412:2 982..2 507	gap2	ATCEA4 S6065, ATCEA4 S31104	97, 85				g22752 17	99	393	1.3e- 38	(AC002 337) chloro plast protei

146455	ATU008 395	ATL8C3 7436:1 786..2 312	gap2	ATCEA4 C54532 _1	97							g31352 77	99	159			n CP12 isolog [Arabi dopsis thalia na] (AC003 058) hypoth etical protei n [Arabi dopsis thalia na]
146456	ATU008 396	ATL8S4 712:18 3..613	gap2	ATCEA4 S4437	97							g38343 01	99	540	2.8e- 12		(AC005 679) This gene is cut off. It is contin ued from YAC YUP8H1 2R. [Arabi dopsis thalia na]
146457	ATU008 397	ATL8C2 1449:5 35..87	gap2	ATCEA4 C49519 _1	97							g44903 36	99	221	9.7e- 21		(AL035 656) auxin- induce d protei n-like [Arabi dopsis thalia na]
146458	ATU008	ATL8C3	gap2	ATCEA4	97, 92							g31932	99, 99	595,	3.1e-		(AF069

398	7188:7 36...40		C46509 1, ATCEA4 S33386					85, g31932 98	360	35	298) T14P8. 18 gene product [Arabi dopsis thalia na]; (AF069 298) T14P8. 17 gene product [Arabi dopsis thalia na]
146459	ATU008 399	ATL8C4 6534:8 12...49	gap2	ATCEA4 S3303	97			g40380 34	322	4.3e- 24	(AC005 936) unknown protein [Arabi dopsis thalia na]
146460	ATU008 400	ATL8C1 6377:1 323...3 90	gap2	ATCEA4 C17037 1, ATCEA4 C4962_1	97, 94	ATL8C1 6377:7 11...41 2	0.91	g40564 98, g40564 99	140, 152	2.5e- 09, 5.3e- 13	(AC005 896) unknown protein [Arabi dopsis thalia na]; (AC005 896) unknown

146461	ATU008 401	ATL8C6 351:17 ..399	gap2	ATCEA4 S29951	97	ATL8C6 351:10 6..183	0.87	g33554 79	98	125	1.4e- 09	protei n [Arabi dopsis thalia na] (AC004 218) unknow n protei n [Arabi dopsis thalia na]
146462	ATU008 402	ATL8C2 7384:9 5..149 9	gap2	ATCEA4 C1200_2, ATCEA4 S13523, ATCEA4 C1200_1, ATCEA4 S32282, ATCEA4 S34042	97, 94, 93, 85, 83	ATL8C2 7384:4 19..13 27	0.86	g32818 69	98	920		(AL031 004) RSZp22 splici ng factor [Arabi dopsis thalia na]
146463	ATU008 403	ATL8C3 1708:8 59..97	gap2	ATCEA4 S2799	97	ATL8C3 1708:4 94..22 4	0.63	g46790 18	98	107	0.92	(AF077 202) HSPC01 6 [Homo sapien s]
146464	ATU008 404	ATL8C3 1922:2 323..1	gap2	ATCEA4 S26973, ATCEA4 C11854 8_1	97, 97	ATL8C3 1922:2 323..2 07	0.61	g24627 56	98	1042	1.5e- 108	(AC002 292) putati ve recept or kinase [Arabi

146465	ATU008 405	ATL8C1 7399:2 568..1 28	gap2	ATCEA4 C1593_1	97	ATL8C1 7399:2 176..9 47	0.58	g33722 33	98	743	1.2e- 74	dopsis thalia na] (AF019 248) RNA polyme rase I, II and III 24.3 kDa subuni t [Arabi dopsis thalia na] zinc finger protei n 5 - Arabid opsis thalia na [Arabi dopsis thalia na] PHOTOS YSTEM II REACTI ON CENTRE T PROTEI N [] (AF076 275) No defini tion
146466	ATU008 406	ATL8C4 6186:1 ..643	gap2	ATCEA4 C970_1	97			g13620 18	98	954	3.4e- 70	
146467	ATU008 407	ATL8C1 4725:8 40..1	gap2	ATCEA4 C9126_1, ATCEA4 C57905 _1	97, 89	ATL8C1 4725:7 55..44 7	0.95	g58574 3	97	165	5.4e- 05	
146468	ATU008 408	ATL8C4 8049:1 ..2885	gap2	ATCEA4 C92052 _1, ATCEA4 C14812	97, 96	ATL8C4 8049:2 72..26 67	0.86	g33778 21	97	1297	7.8e- 112	

146469	ATU008 409	ATL8C4 9340:1 530..1	gap2	ATCEA4 C12756 6_1, ATCEA4 S26869 , ATCEA4 S34104	97, 96 96, 96	ATL8C4 9340:1 503..8 9	0.79	g10862 52	97	579	2.2e- 66	sucros e cleava ge protei n - Potato [Solan um tubero sum]	line found [Arabi dopsis thalia na]
146470	ATU008 410	ATL8C4 8844:1 ..5149	gap2	ATCEA4 C19652 1, ATCEA4 C9686_1, ATCEA4 C9686_2, ATCEA4 S18428	97, 97, 91 91, 91	ATL8C4 8844:1 48..51 49	0.67	g42105 04	97	5158	0.0	(AC002 392) putati ve cadmiu m- transp orting ATPase [Arabi dopsis thalia na]	
146471	ATU008 411	ATL8C3 4992:9 0..167 2	gap2	ATCEA4 C37302 1, ATCEA4 C32998 1, ATCEA4 C37302 2	97, 94 96, 94	ATL8C3 4992:2 37..14 04	0.59	g38742 28	97	314	1.7e- 27	(Z4990 9) CDNA EST CEMSF2 1F comes from this gene; CDNA EST EMBL:D 73546 comes	

146472	ATU008 412	ATL8C1 0951:4 11..29 54	gap2	ATCEA4 S6136	97	ATL8C1 0951:8 78..27 65	0.79	g30235 16	96	2281	3.5e- 218	PROBAB LE 1- DEOXYX YLULOS E-5- PHOSPH ATE SYNTHA SE PRECUR SOR (DXP SYNTHA SE) [Arabi	from this gene; cDNA EST EMBL:D 73669 comes from this gene; cDNA EST EMBL:D 70979 comes from this gene; cDNA EST EMBL:D 71075 comes from this gene; cDNA EST EMBL:D 71075 comes from this gene; cDNA E...
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					ATCEA4 S33203 , ATCEA4 C19398 _1		05								n protei n [Arabi dopsis thalia na]
146482	ATU008 422	ATL8C4 8768:2 343..8 45	gap2		ATCEA4 C1958_1	97	ATL8C4 8768:2 281..9 57	0.84				93	1500	5.7e- 154	ORIGIN RECOGN ITION COMPLE X PROTEI N, SUBUNI T 2 [Arabi dopsis thalia na]
146483	ATU008 423	ATL8C1 4496:2 121..1	gap2		ATCEA4 S1530, ATCEA4 C33426 _1	97, 93	ATL8C1 4496:1 800..1 463	0.80				93	507	8.1e- 46	(AF002 109) unknow n protei n [Arabi dopsis thalia na]
146484	ATU008 424	ATL8C2 2313:3 633..1	gap2		ATCEA4 C978_2 , ATCEA4 C978_1 , ATCEA4 S24970 , ATCEA4 S26293 , ATCEA4 S19047	97, 97, 89, 86, 84	ATL8C2 2313:2 902..1 6	0.66				93, 38	2076, 177	1.8e- 168, 3.8e- 13	(AF001 308) AtKAP alpha [Arabi dopsis thalia na]; (AF001 308) hypoth etical protei n [Arabi

146485	ATU008 425	ATL8C4 8728:1 714..9 1	gap2	ATCEA4 S6685	97	ATL8C4 8728:9 61..10 4	0.53	g46169 1	93	229	1.9e- 16	F- ACTIN CAPPIN G PROTEI N BETA SUBUNI T []
146486	ATU008 426	ATL8C9 34:112 ..1450	gap2	ATCEA4 S6757, ATCEA4 S5986, ATCEA4 C8114_1	97, 96, 85	ATL8C9 34:454 ..1383	0.50	g22451 01	93	534	9.8e- 53	(Z9734 3) hypoth etical protei n [Arabi dopsis thalia na]
146487	ATU008 427	ATL8C4 6508:1 935..4 170	gap2	ATCEA4 S1270, ATCEA4 C11881 1_1	97, 91	ATL8C4 6508:2 004..3 554	0.90	g48877 56	92	1451	2.7e- 161	(AC006 533) putati ve protei n kinase [Arabi dopsis thalia na]
146488	ATU008 428	ATL8C5 424:80 7..337 9	gap2	ATCEA4 S1984, ATCEA4 C94579 _1	97, 94	ATL8C5 424:80 7..337 9	0.88	g48678 03	92	1305	1.1e- 142	(AJ133 000) phosph olipas e D2 [Crate rostig ma planta gineum]
146489	ATU008	ATL8C2	gap2	ATCEA4	97	ATL8C2	0.79	g41855	92	412	3.6e-	(AB010

429	4160:1 270..1	S9426		4160:1 041..3 5	99	41	708) Anthoc yanin 5- aromat ic acyltr anser ase [Genti ana triflo ra]				
146490	ATU008 430	gap2	ATCEA4 C5654_1	97	ATL8C3 2966:1 461..5 3	0.75	g24594 45	92	475	1.0e- 51	(AC002 332) putati ve ribonu cleopr otein [Arabi dopsis thalia na]
146491	ATU008 431	gap2	ATCEA4 S12265	97	ATL8C4 3775:2 742..7 1	0.48	g33193 67	92	1220	(AF077 409) No defini tion line found [Arabi dopsis thalia na]	
146492	ATU008 432	gap2	ATCEA4 S30051 , ATCEA4 S30089	97, 91			g47536 52	92	593	1.4e- 72	(AL049 751) short- chain alcohol dehydr ogenas e like protei

146493	ATU008 433	ATL8C1 681:65 47..19 28	gap2	ATCEA4 C31430 1, ATCEA4 C30083 1, ATCEA4 C17013 1	97, 89 90, 89	ATL8C1 681:63 70..25 74	0.87	g1159 22	91	3985	0.0	n [Arabi dopsis thalia na] (AF118 222) contai ns simila rity to ubiqui tin carbox yl- termin al hydrol ase family 2 (Pfam: PF0044 3, score= 48.3, E=3.5e -13, N=2) and (Pfam: PF0044 2, Score= 40.0 E=5.2e -08, N=1) [Arabi dopsis thalia na] IN2-1 PROTEI
146494	ATU008 434	ATL8C1 6200:1	gap2	ATCEA4 S2108,	97, 86	ATL8C1 6200:8	0.80	g13524 60	91	347	7.2e- 29	

146498	ATU008 438	ATL8C4 5342:1 95..18 08	gap2	ATCEA4 S5930	97	ATL8C4 5342:2 37..16 74	0.87	g28326 29	90	760	7.7e- 86	n [Arabi dopsis thalia na]
146499	ATU008 439	ATL8C2 7145:1 ..1376	gap2	ATCEA4 S25188 ATCEA4 C12119 1_1	97, 87	ATL8C2 7145:2 29..12 24	0.82	g29841 57	90	191	3.6e- 20	(AE000 761) riboso mal protei n L13 [Aquif ex aeolic us]
146500	ATU008 440	ATL8C4 2937:2 06..20 25	gap2	ATCEA4 C13644 1, ATCEA4 C26637 1, ATCEA4 S1378	97, 93 96, 93	ATL8C4 2937:3 75..20 06	0.58	g44172 96	90	833	7.2e- 46	(AC007 019) unknow n protei n [Arabi dopsis thalia na]
146501	ATU008 441	ATL8C3 45:1.. 3449	gap2	ATCEA4 C28908 1, ATCEA4 C78696 1_1	97, 96			g22621 51, g48951 95	90, 46	911, 137	1.6e- 74, 1.4e- 10	(AC002 330) predic ted protei n of unknow n

146502	ATU008 442	ATL8C1 2010:1 ..1651	gap2	ATCEA4 C12361 1, ATCEA4 S6432, ATCEA4 S30818 , ATCEA4 C5246_1	97, 91, 90, 86	ATL8C1 2010:8 4..151 7	0.94	g21911 50	89	1301	4.2e- 139	(AF007 269) simila r to mitoch ondria l carrie r family protei n [Arabi dopsis thalia na]
146503	ATU008 443	ATL8C2 9534:1 291..3 312	gap2	ATCEA4 C14187 1, ATCEA4 S36049 , ATCEA4 C13143 1,	97, 96, 91, 89	ATL8C2 9534:1 355..3 032	0.88	g45875 42	89	1137	1.9e- 109	(AC006 577) Belong s to the PF 006 57 Lipase /Acylh

146504	ATU008 444	ATL8C4 6875:1 989..1 48	gap2	ATCEA4 S27670 , ATCEA4 S26180 , ATCEA4 S31128	97, 90, 90	ATL8C4 6875:1 963..1 48	0.55	g31766 69	89	638	1.2e- 74	(AC004 393) End is cut off. [Arabi dopsis thalia na]	ydrola se with GDSL- motif family . ESTs gb T45 815, gb T45 130 and gb Z38 046 come from this gene. [Arabi dopsis thalia na]
146505	ATU008 445	ATL8C3 0404:1 ..1484	gap2	ATCEA4 S35800	97	ATL8C3 0404:3 03..71 6	0.96	g29700 34	88	892	5.9e- 74	(D8853 6) delta 9 desatu rase [Arabi dopsis thalia na]	
146506	ATU008 446	ATL8C3 889:13 89..99	gap2	ATCEA4 C12198 1	97	ATL8C3 889:11 07..99	0.95	g20886 50	88	98	7.0e- 05	(AF002 109) peroxi	

146507	ATU008 447	ATL8C4 5533:1 359..1	gap2	ATCEA4 C9813_1, ATCEA4 S30991	97, 84	ATL8C4 5533:1 169..1 41	0.68	g64346 9	88	645	5.4e- 71	(U1988 6) unknown [Lycop ersico n escule ntum]
146508	ATU008 448	ATL8C4 8537:1 509..9 69	gap2	ATCEA4 C14274 1, ATCEA4 S1963	97, 92	ATL8C4 8537:1 393..1 114	1.00	g45394 19	87	432	9.4e- 31	(AL049 171) putati ve riboso mal protei n [Arabi dopsis thalia na]
146509	ATU008 449	ATL8C4 3137:2 000..3 11	gap2	ATCEA4 S7782	97			g34618 14	88	1128	2.5e- 110	(AC004 138) hypoth etical protei n [Arabi dopsis thalia na]
146510	ATU008 450	ATL8C2 6705:3	gap2	ATCEA4 C1157	97, 93, 91	ATL8C2 6705:3	0.87	g45389 65	87	209	7.3e- 17	(AL049 488)

146511	ATU008 451	537..1	gap2	ATCEA4 S6112, ATCEA4 S9206	97	ATL8C2 4137:5 2..145 2	0.78	g49144 35	87	1170	1.4e- 101	hypoth etical protei n [Arabi dopsis thalia na]
												(AL050 351) NAD(P) H oxidor educta se, isofla vone reduct ase- like protei n [Arabi dopsis thalia na]
146512	ATU008 452	537..1	gap2	ATCEA4 S32084	97	ATL8C3 6967:3 674..6 66	0.92	g22810 90	86	949	1.4e- 92	(AC002 333) hypoth etical protei n [Arabi dopsis thalia na]
												hypoth etical protei n [Arabi dopsis thalia na]
146513	ATU008 453	537..1	gap2	ATCEA4 S36216	97	ATL8C2 3636:4 165..6 97	0.63	g13147 12	86	599	1.4e- 58	(U5461 5) calciu m- depend ent protei n kinase

146514	ATU008 454	ATL8C9 739:11 1..193 3	gap2	ATCEA4 C12028 1, ATCEA4 S35296	97, 95						g23448 92	86	638	4.2e- 46	[Arabi dopsis thalia na] (AC002 388) unknown protein [Arabi dopsis thalia na]
146515	ATU008 455	ATL8C3 8801:1 204..1	gap2	ATCEA4 S5377	97	ATL8C3 8801:5 68..71	0.97				g42621 83	85	656	7.7e- 73	(AC005 508) 51434 [Arabi dopsis thalia na]
146516	ATU008 456	ATL8C4 485:19 1..331 3	gap2	ATCEA4 S26863 , ATCEA4 C11866 2_1, ATCEA4 C5668_2	97, 88 94, 88	ATL8C4 485:15 06..31 16	0.96				g43357 73	85	200	1.1e- 16	(AC006 284) unknown protein [Arabi dopsis thalia na]
146517	ATU008 457	ATL8C1 7298:6 503..3 12	gap2	ATCEA4 C27848 1, ATCEA4 S32365 , ATCEA4 S11853	97, 86 94, 86	ATL8C1 7298:5 671..3 12	0.91				g46462 17	85	2557	1.1e- 180	(AC007 290) putative phospho prote in phosph atase [Arabi dopsis thalia na]

146518	ATU008 458	ATL8C2 6710:6 25..18 85	gap2	ATCEA4 S30027	97	ATL8C2 6710:6 25..14 57	0.90	g45673 02	85	799	8.0e- 80	(AC005 956) unknown protein [Arabi dopsis thalia na]
146519	ATU008 459	ATL8C1 5132:1 ..1181	gap2	ATCEA4 S10717	97	ATL8C1 5132:8 4..111 8	0.69	g46462 33	85	850	1.6e- 90	(AC007 266) putative G9a protein [Arabi dopsis thalia na]
146520	ATU008 460	ATL8C8 435:29 2..111 0	gap2	ATCEA4 S10905 , ATCEA4 S8380, ATCEA4 S29757	97, 95, 88	ATL8C8 435:29 2..996	0.56	g43357 45	85	768	1.8e- 78	(AC006 284) putative hydrol ase (containing an esterase/ lipase/thioesterase active site serine domain (prosite: PS50187) [Arabi dopsis thalia na]

146521	ATU008 461	ATL8C6 889:17 71..25	gap2	ATCEA4 S2533, ATCEA4 S3758, ATCEA4 S16726	97, 88 95, 88	ATL8C6 889:17 42..25	0.92	g48369 12	84	1194	3.2e- 78	(AC007 153) 60811 [Arabi dopsis thalia na]
146522	ATU008 462	ATL8C1 6682:1 ..5447	gap2	ATCEA4 C15554 7_1	97	ATL8C1 6682:2 99..53 84	0.91	g36500 38, g47339 78	84, 37	2690, 563	2.8e- 213, 9.6e- 44	(AC005 396) hypoth etical protei n [Arabi dopsis thalia na]; (AC007 264) hypoth etical protei n [Arabi dopsis thalia na]
146523	ATU008 463	ATL8C2 3605:1 007..1	gap2	ATCEA4 C10289 8_1, ATCEA4 S35213	97, 92	ATL8C2 3605:1 007..1 9	0.90	g24438 76	84	381	2.5e- 35	(AC002 294) Hypoth etical protei n [Arabi dopsis thalia na]
146524	ATU008 464	ATL8C4 9453:1 774..1	gap2	ATCEA4 S1630, ATCEA4 S2674	97, 88	ATL8C4 9453:1 774..1 28	0.64	g13461 80	84	230	1.7e- 11	GLYCIN E-RICH RNA- BINDIN G PROTEI N GRP1A

146525	ATU008 465	ATL8C2 1057:5 9..965	gap2	ATCEA4 C64241 1, ATCEA4 S28259	97, 91	ATL8C2 1057:5 9..862	0.41	g34829 75	84	766	1.8e- 83	[Sinap is alba] (AL031 369) putati ve protei n [Arabi dopsis thalia na]
146526	ATU008 466	ATL8C1 326:27 86..1	gap2	ATCEA4 C17396 1, ATCEA4 S3190	97, 91	ATL8C1 326:27 86..15 2	0.97	g48951 70	83	3455	5.2e- 299	(AC007 662) putati ve plasma membra ne ATPase [Arabi dopsis thalia na]
146527	ATU008 467	ATL8C1 2790:1 019..1	gap2	ATCEA4 S381	97	ATL8C1 2790:1 019..1 9	0.87	g43143 89	83	870	1.1e- 47	(AC006 232) putati ve transc riptio n factor [Arabi dopsis thalia na]
146528	ATU008 468	ATL8C3 2449:1 083..1	gap2	ATCEA4 S3715	97			g22448 96	83	505	2.7e- 56	(Z9733 8) simila r to HSR201 protei n N.tab

146529	ATU008 469	ATL8C5 318:10 26..26 53	gap2	ATCEA4 C6424 1	97	ATL8C5 318:10 32..26 23	0.94	g26513 10	82	1015	7.5e- 99	Cum [Arabi dopsis thalia na] (AC002 336) putati ve PTR2-B peptid e transp orter [Arabi dopsis thalia na]
146530	ATU008 470	ATL8C4 7977:1 81..41 37	gap2	ATCEA4 C20934 1, ATCEA4 C13464 1	97, 94	ATL8C4 7977:3 83..40 71	0.91	g17305 60	82	2570	3.1e- 232	ALPHA- GLUCAN PHOSPH ORYLAS E, H ISOZYM E (STARC H PHOSPH ORYLAS E H) [Vicia faba]
146531	ATU008 471	ATL8C3 8067:1 ..2490	gap2	ATCEA4 S13977 , ATCEA4 C31942 1, ATCEA4 S14561	97, 82 89, 82	ATL8C3 8067:3 49..19 93	0.89	g44552 33	82	1598	1.4e- 157	(AL035 523) hypothe tical protein n [Arabi dopsis thalia na]
146532	ATU008 472	ATL8C4 2933:3 423..8	gap2	ATCEA4 S253, ATCEA4	97, 83	ATL8C4 2933:3 423..1	0.61	g32427 13	82	2490	6.1e- 257	(AC003 040) putati

146533	ATU008 473	22	gap2	S178	97	ATCEA4 S31528	ATL8C9 875:22 7..193 2	0.55	g38610 36	82	127	8.8e- 12	ve transp osase [Arabi dopsis thalia na]
146534	ATU008 474	ATL8C4 3378:5 466...5 94	gap2	ATCEA4 S1519	97	ATL8C4 3378:5 396..5 94	0.46	g28800 43, g36953 97	82, 71	926, 1422			(AJ235 272) PUTRES CINE- ORNITH INE ANTIPO RTER (pote) [Ricke ttsia prowaz ekil] (AC002 340) putati ve 3- hydrox yisobu tyryl- coenzy me A hydrol ase [Arabi dopsis thalia na]; (AF096 372) No defini tion line found [Arabi dopsis thalia

146535	ATU008 475	ATL8C4 7217:3 81..15 03	gap2	ATCEA4 S36269	97	ATL8C4 7217:3 92..14 72	0.91	g15815 92	81	1458	2.3e- 147	na] gibber ellin 20- oxidas e [Arabi dopsis thalia na]
146536	ATU008 476	ATL8C4 8671:5 ..2676	gap2	ATCEA4 C25445 1, ATCEA4 S5979	97, 92	ATL8C4 8671:5 ..2347	0.86	g37860 00	81	626	5.6e- 48	(AC005 499) hypoth etical protei n [Arabi dopsis thalia na]
146537	ATU008 477	ATL8C4 9148:2 602..1	gap2	ATCEA4 C6610- 1, ATCEA4 S32394	97, 97	ATL8C4 9148:2 602..2 29	0.84	g35401 97	81	748	3.7e- 76	(AC004 260) Unknow n protei n [Arabi dopsis thalia na]
146538	ATU008 478	ATL8C2 6535:1 ..408	gap2	ATCEA4 S2739	97	ATL8C2 6535:5 9..408	0.63	g38736 77	81	243	4.5e- 16	(Z7117 8) Simila rity with yeast hypoth etical protei n (Swiss Prot access ion number

146539	ATU008 479	ATL8C3 9493:1 189..1	gap2	ATCEA4 C42187 _1	97	ATL8C3 9493:1 111..1 26	0.57	g49031 39	81	169	2.1e- 17	P43577) [Caeno rhabdi tis elegan s]
												456) extens ive homolo gy to FT (FLOWE RING LOCUS T, AB0275 04) and TSF (TWIN SISTER OF FT, AB0275 06) genes of Arabid opsis thalia na; simila r to mammal ian phopha tidyle thanol amine bindin g protei n

146540	ATU008 480	ATL8C2 1355:1 293..2 300	gap2	ATCEA4 C93298 1, ATCEA4 C21193 1	97, 93	ATL8C2 1355:1 481..2 221	0.53	g13620 93	81	442	2.8e- 44	(PEBP) and hippoc ampal cholin ... [J] hypoth etical protei n (clone TPP15) - tomato (fragm ent) [Solan um lycope rsicum]
146541	ATU008 481	ATL8C2 6858:5 00..19 21	gap2	ATCEA4 S551	97			g35823 33	81	603	1.7e- 61	(AC005 496) hypoth etical protei n [Arabi dopsis thalia na]
146542	ATU008 482	ATL8C1 8017:1 ..2215	gap2	ATCEA4 C70452 1, ATCEA4 C88598 1, ATCEA4 S18146	97, 94 97, 94	ATL8C1 8017:9 1..147 0	0.79	g46219 3	80	79	0.012	GOLIAT H PROTEI N (G1 PROTEI N) [Droso phila melano gaster]
146543	ATU008 483	ATL8C1 6277:1 59..33	gap2	ATCEA4 C11830 1,	97, 95	ATL8C1 6277:1 59..29	0.75	g46783 01	80	1293	2.3e- 120	(AL049 655) pectat

146544	ATU008 484	63	ATCEA4 C5291_1	97	ATL8C6 714:21 59..71 0	0.73	g37859 72	80	2014	5.2e- 177	(AC005 560) putati ve auxin transp ort protei n [Arabi dopsis thalia na]
146545	ATU008 485	ATL8S4 612:57 4..1	ATCEA4 C9316_1	97	ATL8S4 612:35 7..23	0.50	g22528 28	80	278	9.3e- 22	(AF013 293) No defini tion line found [Arabi dopsis thalia na]
146546	ATU008 486	ATL8C2 5987:1 33..97 9	ATCEA4 C6155_1, ATCEA4 C92510 _1	97, 88			g28424 91	80	341	2.6e- 35	(AL021 749) putati ve protei n [Arabi dopsis thalia na]
146547	ATU008 487	ATL8C3 8085:1	ATCEA4 C1778	97, 84	ATL8C3 8085:1	0.85	g33090 84	79	691	3.6e- 66	(AF076 252)

		229..1		1, ATCEA4 C1779_1		221..3 0											calcin eurin B-like protei n 2 [Arabi dopsis thalia na]
146548	ATU008 488	ATL8C1 7961:1 878..1	gap2	ATCEA4 C5492_1	97	ATL8C1 7961:1 664..4 3	0.82	g30244 34	79	1335							26S PROTEA SE REGULA TORY SUBUNI T 6A HOMOLO G (TAT- BINDIN G PROTEI N HOMOLO G 1) (TBP- 1) [Brass ica rapa]
146549	ATU008 489	ATL8C4 7127:4 208..6 048	gap2	ATCEA4 C12972 7_1_	97	ATL8C4 7127:4 208..5 987	0.65	g34452 04	79	403							(AC004 786) putati ve GTP- bindin g protei n [Arabi dopsis thalia na]
146550	ATU008 490	ATL8C2 2742:1	gap2	ATCEA4 C31915	97	ATL8C2 2742:1	0.59	g34513 21,	79, 42	527, 165							(AL031 323) 4.4e- 59,

		321...3 035			_1		358...2 997		g15822 6				1.4e- 10	putative transcription or splicing factor [Schizosaccharomyces pombe]; (L04930) RNA-binding protein [Drosophila melanogaster]
146551	ATU008 491	ATL8C1 7452:5 37...16 95	gap2	ATCEA4 C9888_1	97	ATL8C1 7452:1 648...1 139	0.43		g15466 98	79	701	1.2e- 73	(X98808) peroxidase ATP3a [Arabidopsis thaliana]	
146552	ATU008 492	ATL8C2 447:77 ...1674	gap2	ATCEA4 C2542_1, ATCEA4 S9934	97, 85	ATL8C2 447:46 7...158 0	0.40		g21601 66	79	606	1.1e- 55	(AC000132) No definition line found [Arabidopsis thaliana]	

146553	ATU008 493	ATL8C6 606:14 5..138 6	gap2	ATCEA4 C19550 1, ATCEA4 S23163 , ATCEA4 S9063	97, 96, 86				g40069 02	79	243	2.6e- 24	na] (Z9970 8) putati ve protei n [Arabi dopsis thalia na]
146554	ATU008 494	ATL8C1 1038:8 98..1	gap2	ATCEA4 C3399_ 2, ATCEA4 C11509 1_ 1	97, 93	ATL8C1 1038:6 05..30	0.93		g44544 59	78	1013	1.1e- 107	(AC006 234) unknow n protei n [Arabi dopsis thalia na]
146555	ATU008 495	ATL8C4 8882:3 34..14 08	gap2	ATCEA4 C8916_ 1, ATCEA4 C13239 4_ 1	97, 92	ATL8C4 8882:4 17..12 79	0.84		g73173 7	78	175	1.1e- 15	SOL3 PROTEI N [Sacch aromyc es cerevi siae]
146556	ATU008 496	ATL8C1 0026:2 113..6 82	gap2	ATCEA4 S5013, ATCEA4 S10757 , ATCEA4 S7038	97, 92, 87	ATL8C1 0026:1 892..6 82	0.76		g44270 03	78	480		(AF127 664) NBD- like protei n [Arabi dopsis thalia na]
146557	ATU008 497	ATL8C4 5434:1 581..1	gap2	ATCEA4 C8841_ 1, ATCEA4 S32573	97, 92, 82	ATL8C4 5434:1 525..1 43	0.41		g49144 50	78	570	3.7e- 34	(AL050 398) H+- transp orting

146558	ATU008 498	ATL8C3 0062:1 ..2616	gap2	ATCEA4 C8841_3	97, 96, 84	ATL8C3 8187:1 665..34	0.97	g16849 13	78	1973	4.9e-206	(U7788) receptor-like protein kinase [Ipomoea nil]
146559	ATU008 499	ATL8C3 8187:1 721..1	gap2	ATCEA4 C29825_1	97	ATL8C3 8187:1 665..34	0.97	g41917 84	77	1527	2.2e-120	(AC005917) putative WD-40 repeat protein [Arabidopsis thaliana]
146560	ATU008 500	ATL8C1 6625:1 494..3823	gap2	ATCEA4 C57919_1, ATCEA4 C5818_1, ATCEA4 S1848, ATCEA4 S9993	97, 93, 93, 87	ATL8C1 6625:1 616..3772	0.95	g32647 57	77	1645	6.2e-137	(AF071888) zeaxanthin epoxidase [Prunus armeniaca]
146561	ATU008 501	ATL8C4 4122:1 ..785	gap2	ATCEA4 C10844_1, ATCEA4	97, 96, 94	ATL8C4 4122:2 ..466	0.85	g13505 48	77	133	9.5e-09	(L47609) heat shock-

146566	ATU008 506	ATL8C4 8563:8 41..1	gap2	ATCEA4 C34121 1, ATCEA4 S27126 , ATCEA4 S35750 , ATCEA4 C24050 1, ATCEA4 C36345 1, ATCEA4 C4482_ 2, ATCEA4 S7418	91, 88, 87, 85, 83	ATL8C4 8563:8 33..32 4	0.67	g27608 32	76	620	3.8e- 42	ve coat er alpha subuni t [Arabi dopsis thalia na]; (AL022 223) putati ve protei n [Arabi dopsis thalia na]
146567	ATU008 507	ATL8C4 3962:1 ..656	gap2	ATCEA4 S4953, ATCEA4 S17692 , ATCEA4 C247_1	97, 90, 88	ATL8C4 3962:2 17..60 2	0.58	g11741 62	76	440	(U4497 6) ubiqui tin- conjug ating enzyme [Arabi dopsis thalia na]	
146568	ATU008	ATL8C3	gap2	ATCEA4	97	ATL8C3	0.84	g33341	75	363	5.6e-	G1/S-

	508	5199:1 454..1		C32652 _1		5199:1 422..7 6		44		32	SPECIF IC CYCLIN C-TYPE [Oryza sativa]
146569	ATU008 509	ATL8C2 5597:2 107..2 85	gap2	ATCEA4 C11270 81, ATCEA4 C30991 _1	97, 91	ATL8C2 5597:1 689..5 47	0.58	g12369 61	75	4.8e- 64	(U5020 1) prunas in hydrol ase precu sor [Prunu s seroti na]
146570	ATU008 510	ATL8C4 1895:3 545..1	gap2	ATCEA4 S1860, ATCEA4 C16823 _1	97, 94	ATL8C4 1895:3 068..7	0.99	g30251 89	74	2.6e- 50	HYPOTH ETICAL 67.1 KD. PROTEI N SIL177 0 [Synec hocyst is sp.]
146571	ATU008 511	ATL8C4 578:29 40..49 5	gap2	ATCEA4 S11947	97	ATL8C4 578:29 39..49 5	0.95	g45393 94	74	8.0e- 65	(AL035 526) putati ve protei n [Arabi dopsis thalia na]
146572	ATU008 512	ATL8C3 7880:1 965..1	gap2	ATCEA4 C70701 2, ATCEA4	97, 93, 91, 89	ATL8C3 7880:1 778..2 34	0.94	g40380 34	74	1.2e- 11	(AC005 936) unknow n

146573	ATU008 513	ATL8C3 8906:4 72...25 99	gap2	ATCEA4 C28582 _1	97	ATL8C3 8906:4 72...20 60	0.92	g28424 93	74	438	2.3e- 48	(AL021 749) predic ted protei n [Arabi dopsis thalia na]
146574	ATU008 514	ATL8C1 3178:1 352...1	gap2	ATCEA4 C12033 3_1, ATCEA4 S11327	97, 95	ATL8C1 3178:1 133...9 6	0.83	g31766 64	74	127	4.5e- 16	(AC004 393) Contai ns simila rity to beta scruin gb Z47 541 from Limulu s polyph emus. ESTs gb T04 493 and gb AA5 85955 come from this gene. [Arabi dopsis

146575	ATU008 515	ATL8C3 1026:1 548..1	gap2	ATCEA4 S33147	97	ATL8C3 1026:1 548..8 0	0.75	g45196 71	74	374	6.5e- 22	thalia na] (AB017 693) transf actor [Nicot iana tabacu m]
146576	ATU008 516	ATL8C5 60:125 0..1	gap2	ATCEA4 C7617_ 1	97	ATL8C5 60:114 0..190	0.73	g37023 36	74	1080	2.0e- 110	(AC005 397) putati ve 3- methyl -2- oxobut anoate hydrox y- methyl - transf erase [Arabi dopsis thalia na]
146577	ATU008 517	ATL8C3 0739:1 403..1	gap2	ATCEA4 C577_ 1	97	ATL8C3 0739:9 31..30 6	0.54	g30235 35	74	1161	2.0e- 121	MOLYBD OPTERI N BIOSYN THESIS CNX2 PROTEI N (MOLYB DENUM COFACT OR BIOSYN THESIS ENZYME CNX2) [Arabi

146578	ATU008 518	ATL8C2 7512:1 015..4 5	gap2	ATCEA4 C58350 _1	97	ATL8C2 7512:5 87..15 6	0.40	g22448 50	74	141		dopsis thalia na]
146579	ATU008 519	ATL8C3 3011:1 ..375	gap2	ATCEA4 C70084 2, ATCEA4 S18074	97, 87			g45593 65	74	146	7.4e- 12	(Z9733 7) hypoth etical protei n [Arabi dopsis thalia na]
146580	ATU008 520	ATL8C4 3237:1 ..925	gap2	ATCEA4 S13342	97	ATL8C4 3237:7 9..876	0.93	g23471 98	73	1024	3.7e- 72	(AC002 338) hypoth etical protei n [Arabi dopsis thalia na]
146581	ATU008 521	ATL8C1 7553:1 26..47 09	gap2	ATCEA4 S253, ATCEA4 C36870 _1	97, 96	ATL8C1 7553:4 15..31 83	0.87	g49143 30, g47739 10	73, 38	749, 308	1.0e- 74, 2.3e- 22	(AC005 489) F14N23 .16 [Arabi dopsis thalia na]; (AF147 259) No defini

146582	ATU008 522	ATL8C2 3716:1 597..2 22	gap2	ATCEA4 S3439, ATCEA4 S23516	97, 88	ATL8C2 3716:1 522..2 22	0.76	940084 46	73	153	3.0e- 09	(AL034 488) predic ted using Genefi nder; cDNA EST EMBL:C 08771 comes from this gene; cDNA EST EMBL:C 07412 comes from this gene [Caeno rhabdi tis elegan s]
146583	ATU008 523	ATL8C3 5486:5 89..16 70	gap2	ATCEA4 S8770	97	ATL8C3 5486:6 76..16 49	0.71	945393 89	73	1665	1.5e- 157	(AL035 526) putati ve protei n kinase [Arabi dopsis thalia

146584	ATU008 524	ATL8C3 8224:1 74..11 50	gap2	ATCEA4 C279_6 , ATCEA4 S32713	97, 96	ATL8C3 8224:5 73..35 7	0.59	g22448 01	73	142	5.1e- 06	na] (Z9733 6) hypoth etical protei n [Arabi dopsis thalia na]
146585	ATU008 525	ATL8C2 4710:1 ..1154	gap2	ATCEA4 S6695, ATCEA4 C51773 _1	97, 92	ATL8C2 4710:9 3..101 5	0.54	g45444 09	73	1011	4.6e- 99	(AC006 955) putati ve transc riptio n factor [Arabi dopsis thalia na]
146586	ATU008 526	ATL8C9 488:24 37..42 87	gap2	ATCEA4 C5492_1	97	ATL8C9 488:25 39..42 10	0.92	g30244 34	72	1263	4.9e- 117	26S PROTEA SE REGULA TORY SUBUNI T 6A HOMOLO G (TAT- BINDIN G PROTEI N HOMOLO G 1) (TBP- 1) [Brass ica rapa]
146587	ATU008	ATL8C1	gap2	ATCEA4	97,	ATL8C1	0.87	g43370	72	1042	6.3e-	(AF119

527	6112:7 6..145 0		C1874_1, ATCEA4 S35366 , ATCEA4 S1733, ATCEA4 S15263	95, 93 95, 93	6112:1 32..13 66		11			102	572) zinc- bindin g peroxi somal integr al membra ne protei n [Arabi dopsis thalia na]	
146588	ATU008 528	ATL8C1 9084:2 165..4 66	gap2	ATCEA4 S3466, ATCEA4 S3293	97, 94	ATL8C1 9084:2 165..4 66	0.83	g48266 82	72	334	1.4e- 26	cystin osis, nephro pathic [Homo sapien s]
146589	ATU008 529	ATL8C1 3073:1 86..17 60	gap2	ATCEA4 C13007 _1	97	ATL8C1 3073:3 09..16 40	0.82	g44552 37	72	807	5.8e- 71	(AL035 523) ubiqui tin activa ting enzyme -like protei n [Arabi dopsis thalia na]
146590	ATU008 530	ATL8C3 6884:1 006..1	gap2	ATCEA4 S30682	97	ATL8C3 6884:1 006..4 08	0.75	g33353 61	72	525	1.9e- 46	(AC003 028) putati ve acyltr ansfer ase [Arabi

146595	ATU008 535	ATL8C6 408:21 86..1	gap2	ATCEA4 C4292_1	97	ATL8C6 408:21 36..23 2	0.88	g25831 20	70	1271	4.3e- 134	etical protei n [Arabi dopsis thalia na]
146596	ATU008 536	ATL8C1 8592:1 732..2 97	gap2	ATCEA4 S26563 , ATCEA4 C73637 1, ATCEA4 S30474	97, 90, 89	ATL8C1 8592:1 663..5 45	0.85	g42622 34	70	1043	4.3e- 97	(AC006 200) unknow n protei n [Arabi dopsis thalia na]
146597	ATU008 537	ATL8C4 9783:1 374..3 247	gap2	ATCEA4 C7830_1	97	ATL8C4 9783:1 374..2 989	0.68	g41917 96	70	799	2.0e- 58	(AC005 917) putati ve senesc ence- associ ated protei n 5 [Arabi dopsis thalia na]

146598	ATU008 538	ATL8C2 3855:1 554..3 544	gap2	ATCEA4 S32980 , ATCEA4 S35471	97, 95	ATL8C2 3855:1 856..2 898	0.66	g38779 51	70	211	6.4e- 20	(Z8155 5) predic ted using Genefi nder [Caeno rhabdi tis elegan s]
146599	ATU008 539	ATL8C4 8814:1 457..1	gap2	ATCEA4 C38575 _1	97	ATL8C4 8814:1 336..4 48	0.57	g22448 13	70	1274	4.6e- 131	(Z9733 6) acylam inoacy l-peptid ase homolo g [Arabi dopsis thalia na]
146600	ATU008 540	ATL8C3 752:1. .3286	gap2	ATCEA4 C11921 6 1, ATCEA4 S35061	97, 95	ATL8C3 752:48 9..286 9	0.50	g48742 84	70	1142	3.8e- 116	(AC007 212) putati ve mitoch ondria l protei n [Arabi dopsis thalia na]
146601	ATU008 541	ATL8S2 5358:5 92..22 2	gap2	ATCEA4 C70268 _1	97			g17233 24	70	133	1.5e- 09	HYPOTH ETICAL 11.9 KD PROTEI N YCF20

146602	ATU008 542	ATL8C6 67:180 5..1	gap2	ATCEA4 S5064	97					g34618 16	70	736	1.9e- 55	(AC004 138) hypoth etical protein [Arabi dopsis thalia na]	(ORF10 8) [Porph yra purpur ea]
146603	ATU008 543	ATL8C2 793:11 8..340 0	gap2	ATCEA4 C574_1	97					g33193 58	69	2214	3.6e- 138	(AF077 407) Arabid opsis thalia na CLC-d chlori de channe l protei n (GB:Z7 1450) [Arabi dopsis thalia na]	(AF077 407) Arabid opsis thalia na CLC-d chlori de channe l protei n (GB:Z7 1450) [Arabi dopsis thalia na]
146604	ATU008 544	ATL8C3 8050:1 ..2001	gap2	ATCEA4 C11769 3_1, ATCEA4 C4210 1	97, 89					g45077 03	69	129	9.5e- 09	tumor suppre ssing subtra nsfera ble candid ate 1 [Homo sapien]	tumor suppre ssing subtra nsfera ble candid ate 1 [Homo sapien]

146605	ATU008 545	ATL8C3 8958:1 362..1	gap2	ATCEA4 C29972 1, ATCEA4 C90777 1, ATCEA4 S19259	97, 92 97, 92	ATL8C3 8958:5 6..127 8	0.68	g37382 88	69	1109	1.4e- 113	(AC005 309) auxin- respon- sive GH3- like protei n [Arabi dopsis thalia na]
146606	ATU008 546	ATL8C4 4475:2 463..1	gap2	ATCEA4 C24980 1, ATCEA4 S2649, ATCEA4 C5618 1, ATCEA4 S10459	97, 92, 88, 88	ATL8C4 4475:2 373..3 0	0.56	g46782 97	69	707	2.2e- 63	(AL049 655) protei n disulf ide- isomer ase- like protei n [Arabi dopsis thalia na]
146607	ATU008 547	ATL8S2 6585:7 79..25 2	gap2	ATCEA4 C27614 1, ATCEA4 C43253 1 1	97, 84	ATL8S2 6585:7 06..37 6	0.48	g22449 18	69	501	(Z9733 9) hypoth etical protei n [Arabi dopsis thalia na]	
146608	ATU008 548	ATL8C2 3175:1 280..1	gap2	ATCEA4 C1760 1, ATCEA4 S34095	97, 82			g31725 38	69	920	1.5e- 85	(AF067 789) tSNARE AtTLG2 P [Arabi

146609	ATU008 549	ATL8C2 2373:2 308..1	gap2	ATCEA4 S27401	97					943098 68	69	1595	1.7e- 151	(AC006 527) putati ve retrot ranspo son- like orf [Arabi dopsis thalia na]
146610	ATU008 550	ATL8C3 2075:1 70..88 6	gap2	ATCEA4 S6444	97		ATL8C3 2075:2 37..72 4	0.98		g42621 61	68	786	1.6e- 79	(AC005 275) SYR1- like syntax in [Arabi dopsis thalia na]
146611	ATU008 551	ATL8C1 1979:1 355..1	gap2	ATCEA4 C14599 1, ATCEA4 S29671 , ATCEA4 S33948 , ATCEA4 S33094	97, 97, 92, 89		ATL8C1 1979:1 329..2 7	0.90		g39143 86	68	137	9.9e- 15	ALLERG EN MF1 [Malas sezia furfur]
146612	ATU008 552	ATL8C4 8761:1 ..3329	gap2	ATCEA4 S4724	97		ATL8C4 8761:3 91..32 42	0.86		g28323 00, g21349 62	68, 41	610, 342	1.1e- 67, 2.3e- 13	(AF044 285) adenos ine- 5'- phosph osulfa te-

146613	ATU008 553	ATL8C5 350:1. .874	gap2	ATCEA4 S2670, ATCEA4 S1871	97, 86	ATL8C5 350:20 4..760	0.76	g35229 38	68	1028	4.8e- 107	(AC004 411) unknown protein [Arabi dopsis thalia na]	kinase [Catha ranthu s roseus]; cyclop hilin- like protei n Cyp- 60 - human [Homo sapien s]
146614	ATU008 554	ATL8C1 5548:1 60..37 55	gap2	ATCEA4 S3713, ATCEA4 S16437 , ATCEA4 C9278 - 1, ATCEA4 C9278 - 2, ATCEA4 S28427	97, 94, 94, 90, 86	ATL8C1 5548:3 521..3 248, ATL8C1 5548:1 401..2 962, ATL8C1 5548:1 60..10 33	0.44, 0.67, 0.90	g35999 68, g45842 57	68, 53	890, 146	4.2e- 95, 2.5e- 10	(AF032 123) clp protea se [Arabi dopsis thalia na]; (Y1847 2) SINA2p [Vitis vinife ra]	
146615	ATU008 555	ATL8C4 1405:1 144..1	gap2	ATCEA4 C76966 1, ATCEA4	97, 96	ATL8C4 1405:1 112..4 52	0.82	g38941 76	67	204	4.6e- 12	(AC005 312) putati ve NAM	

146616	ATU008 556	ATL8C3 2629:7 29..22 5	gap2	ATCEA4 S6184	97	ATL8C3 2629:6 58..23 1	0.82	g24354 06	67	582	2.5e- 49	(no apical merist em) protei n [Arabi dopsis thalia na]
146617	ATU008 557	ATL8C2 5615:4 18..18 27	gap2	ATCEA4 S10327 , ATCEA4 C83289 1	97, 94	ATL8C2 5615:6 20..10 69	0.75	g22320 57	67	133	5.0e- 08	(AF000 177) CaSm [Homo sapien s]
146618	ATU008 558	ATL8C2 6683:1 037..1	gap2	ATCEA4 S1739	97	ATL8C2 6683:5 73..13 4	0.75	g45393 70	67	695	8.5e- 81	(AL049 525) UDP- galact ose 4- epimer ase- like protei n [Arabi dopsis thalia na]
146619	ATU008 559	ATL8C3 4553:1 ..6534	gap2	ATCEA4 S7066, ATCEA4 S33464	97, 97	ATL8C3 4553:2 84..65 34	0.49	g43780 66	67	3415	1.7e- 294	(AF098 806) polypr otein

146628	ATU008 568	ATL8C6 158:1. .986	gap2	ATCEA4 C12233 8_1	97				g54371 2	66	1106	2.1e- 113	1- AMINOC YCLOPR OPANE- 2- CARBOX YLATE SYNTHA SE 2 (ACC SYNTHA SE 2) (S- ADENOS YL-L- METHIO NINE METHYL THIOAD ENOSIN E- LYASE 2) [Arabi dopsis thalia na]
146629	ATU008 569	ATL8C4 8118:6 28..1	gap2	ATCEA4 C26991 _2	97				g44553 64	66	351	5.6e- 27	(AL035 524) senesc ence- associ ated protei n-like [Arabi dopsis thalia na]
146630	ATU008 570	ATL8C1 6723:1 969..6 20	gap2	ATCEA4 C61_8	97	ATL8C1 6723:1 787..7 89	0.99		g42188 7, g40359 4	65, 61	279, 133	8.8e- 16, 1.5e- 09	vicili n, 47K - garden pea [Pisum]

146631	ATU008 571	ATL8C1 9306:1 ..1989	gap2	ATCEA4 C70309 1, ATCEA4 C70309 2, ATCEA4 C5244_1	97, 91 93, 91	ATL8C1 9306:3 4..197 4	0.95	g54906 0	65	990	2.2e- 66	T- COMPLE X PROTEI N 1, ETA SUBUNI T (TCP- 1-ETA) (CCT- ETA) [Mus muscul us]	sativu m]; (U0113 1) phaseo lin [Phase olus vulgar is]
146632	ATU008 572	ATL8C4 0624:4 6..100 7	gap2	ATCEA4 C23215 1_	97	ATL8C4 0624:8 2..885	0.88	g27361 47	65	510	4.7e- 58	(AF021 804) fatty acid hydrox ylase Fahlp [Arabi dopsis thalia na]	
146633	ATU008 573	ATL8C1 9010:1 ..3906	gap2	ATCEA4 S29781	97	ATL8C1 9010:1 85..37 96	0.86	g31360 48	65	868	1.2e- 69	(AL023 592) putati ve helica se [Schiz osacch aromyc	

146634	ATU008 574	ATL8C1 6669:1 ..2142	gap2	ATCEA4 C1033_1, ATCEA4 S708	97, 97	ATL8C1 6669:2 0..212 6	0.84	g21601 66	65	58	2.1e- 06	es pombe] (AC000 132) No defini tion line found [Arabi dopsis thalia na]
146635	ATU008 575	ATL8C4 2214:1 41..13 73	gap2	ATCEA4 S30517	97	ATL8C4 2214:1 41..12 67	0.80	g28092 46	65	541	3.4e- 49	(AC002 560) F2401. 15 [Arabi dopsis thalia na]
146636	ATU008 576	ATL8C2 498:50 ..778	gap2	ATCEA4 C11308 1, ATCEA4 S27473	97, 94	ATL8C2 498:46 3..685	0.73	g37023 26	65	428	4.9e- 44	(AC005 397) hypoth etical protei n [Arabi dopsis thalia na]
146637	ATU008 577	ATL8C1 4118:4 244..1 292	gap2	ATCEA4 C10898 4 1, ATCEA4 C12701 _1	97, 93	ATL8C1 4118:1 292..3 263, ATL8C1 4118:4 112..3 642	0.91, 0.85	g45672 38	64	508	3.1e- 52	(AC007 070) hypoth etical protei n [Arabi dopsis thalia na]
146638	ATU008 578	ATL8C1 9881:3 31..20	gap2	ATCEA4 S26406	97, 94	ATL8C1 9881:3 33..20	0.85	g41917 80	64	701	7.5e- 68	(AC005 917) putati

		74		ATCEA4 C21777 _1		74							ve cytoki nin oxidas e [Arabi dopsis thalia na]
146639	ATU008 579	ATL8C1 3298:1 ..1049	gap2	ATCEA4 C12327 7_1, ATCEA4 S35973	97, 93	ATL8C1 3298:2 98..78 0	0.84	g35229 54	64	189	7.6e- 14	(AC004 411) IAA20 [Arabi dopsis thalia na]	
146640	ATU008 580	ATL8C4 8510:7 83..1	gap2	ATCEA4 C17295 _2	97	ATL8C4 8510:4 57..25 2	0.83	g30804 39	64	183	5.1e- 06	(AL022 605) putati ve protei n [Arabi dopsis thalia na]	
146641	ATU008 581	ATL8C4 8270:1 ..696	gap2	ATCEA4 C12620 _1	97	ATL8C4 8270:2 70..36 7	0.57	g45080 78	64	252	1.7e- 15	(AC005 882) 64134 [Arabi dopsis thalia na]	
146642	ATU008 582	ATL8C1 0449:1 33..79 6	gap2	ATCEA4 S3569	97			g44552 97	64	508		(AL035 528) hypoth etical protei n [Arabi dopsis thalia na]	
146643	ATU008	ATL8C9	gap2	ATCEA4	97	ATL8C9	1.00	g44551	63	876	3.8e-	(AL035)	

583	855:16 75..45 7	S10534		855:15 67..83 6	83				82	521) putati ve protei n [Arabi dopsis thalia na]		
146644	ATU008 584	ATL8C7 775:98 3..1	gap2	ATCEA4 S1437	97			g54897 6	64	97	0.013	SUPPRE SSOR PROTEI N SRP40 [Sacch aromyc es cerevi siae]
146645	ATU008 585	ATL8C2 2435:2 70..15 78	gap2	ATCEA4 C52206 2, ATCEA4 S35463 , ATCEA4 C52206 1, ATCEA4 S11598	97, 93, 90, 89			g18815 85	64	206	3.7e- 10	(U7248 9) remori n [Solan um tubero sum]
146646	ATU008 586	ATL8C1 7001:6 796..3 319	gap2	ATCEA4 C44198 _1	97			g38314 46, g31281 73	64, 54	1350, 652	2.1e- 137, 1.2e- 64	(AC005 819) putati ve beta- ketoac yl-CoA syntha se [Arabi dopsis thalia na]; (AC004 521)

146647	ATU008 587	ATL8C8 696:1. .1274	gap2	ATCEA4 C72638 _1	97	ATL8C8 696:16 5..114 7	0.94	g21296 98	63	679	1.3e- 51	prote n kinase ATN1 (EC 2.7.1. -) - Arabid opsis thalia na [Arabi dopsis thalia na]
146648	ATU008 588	ATL8C3 383:33 87..45 4	gap2	ATCEA4 C22990 3, ATCEA4 S21010 , ATCEA4 C22990 2, ATCEA4 S16311	97, 94, 93, 84 2	ATL8C3 383:31 27..80 2	0.92	g28297 92	63	1397	1.7e- 117	SOLUBL E GLYCOG EN (STARC H) SYNTHA SE PRECUR SOR (SS I) [Solan um tubero sum]
146649	ATU008 589	ATL8C2 4530:8 57..1	gap2	ATCEA4 C13044 _1	97	ATL8C2 4530:8 05..68 3	0.90	g32362 46	63	828	3.1e- 87	(AC004 684) putati ve expans in protei

146650	ATU008 590	ATL8C2 6762:7 1..129 4	gap2	ATCEA4 C86018 _1	97	ATL8C2 6762:7 1..123 7	0.90	g33675 20	63	267	9.1e- 24	n [Arabi dopsis thalia na] (AC004 392) Simila r to protei n kinase APK1A, tyrosi ne- serine - threon ine kinase gb D12 522 from A. thalia na. [Arabi dopsis thalia na]
146651	ATU008 591	ATL8C7 16:973 ..1	gap2	ATCEA4 S30702 , ATCEA4 S31360	97, 84	ATL8C7 16:892 ..142	0.82	g22752 04	63	916	5.7e- 63	(AC002 337) DNA bindin g protei n isolog [Arabi dopsis thalia na]
146652	ATU008 592	ATL8C1 3164:3 756..1	gap2	ATCEA4 C60052 1,	97, 97, 96,	ATL8C1 3164:3 498..5	0.76	g31529 40	63	48	0.0069	(AF065 483) sortin

								ATCEA4 C22062 2, ATCEA4 C10651 1, ATCEA4 S31682 , ATCEA4 C22062 1, ATCEA4 S18968	89, 82 83, 82	20								g nexin 1 [Homo sapien s]
146653	ATU008 593	ATL8C3 7510:2 110..1	gap2					ATCEA4 S12639	97	ATL8C3 7510:2 109..2 78	0.69		g42180 11	63	998			(AC006 135) putati ve protei n kinase [Arabi dopsis thalia na]
146654	ATU008 594	ATL8C6 082:13 88..1	gap2					ATCEA4 S6260, ATCEA4 S31266	97, 94	ATL8C6 082:12 43..54	0.54		g37023 24	63	148	0.0075		(AC005 397) hypoth etical protei n [Arabi dopsis thalia na]
146655	ATU008 595	ATL8C3 0131:3 355..1 873	gap2					ATCEA4 C12104 4 1, ATCEA4 C33020 _1	97, 90	ATL8C3 0131:3 110..2 005	0.52		g29095 21	63	106	1.9e- 05		(AL021 932) hypoth etical protei n Rv0446 c [Mycob acteri

146656	ATU008 596	ATL8C4 7548:6 40..12 22	gap2	ATCEA4 C14617 2, ATCEA4 S33940 , ATCEA4 C14617 3_	97, 93 95, 93						g43357 24	63	531	1.9e- 37	(AC006 248) putati ve RING- H2 finger protei n [Arabi dopsis thalia na]	um tuberc ulosis]
146657	ATU008 597	ATL8C4 1698:1 ..1533	gap2	ATCEA4 S253	97						g47739 12	63	568	1.8e- 47	(AF147 259) No defini tion line found [Arabi dopsis thalia na]	(AF147 259) No defini tion line found [Arabi dopsis thalia na]
146658	ATU008 598	ATL8C4 8148:1 78..13 26	gap2	ATCEA4 C1690_1, ATCEA4 S8295, ATCEA4 S32248	97, 87 91, 87						g28292 75	63	563	1.0e- 48	(AF044 265) nucleo side diphos phate kinase 3 [Arabi dopsis thalia na]	(AF044 265) nucleo side diphos phate kinase 3 [Arabi dopsis thalia na]
146659	ATU008 599	ATL8C2 0039:7 50..23	gap2	ATCEA4 S35125 , ATCEA4 C14680	97, 96						g36872 39	63	290		(AC005 169) putati ve clathr	(AC005 169) putati ve clathr

146660	ATU008 600	ATL8C2 0864:2 42..14 19	gap2	ATCEA4 S34434 , ATCEA4 S1326	97, 95	ATL8C2 0864:6 09..13 51	0.92	g26217 67	62	220	2.1e- 18	(AE000 848) conser ved protei n [Metha nobact erium thermo autotr ophicu m]	in coat assemb ly protei n [Arabi dopsis thalia na]
146661	ATU008 601	ATL8C3 8394:1 ..1800	gap2	ATCEA4 C31919 _1	97	ATL8C3 8394:1 61..14 74	0.90	g45393 44	62	1286	5.3e- 125	(AL035 539) putati ve protei n [Arabi dopsis thalia na]	
146662	ATU008 602	ATL8C3 018:90 0..12	gap2	ATCEA4 C4766_1, ATCEA4 S33364	97, 90	ATL8C3 018:70 4..183	0.80	g22447 97	62	294	8.1e- 34	(Z9733 6) hypoth etical protei n [Arabi dopsis thalia na]	
146663	ATU008 603	ATL8C1 5867:1	gap2	ATCEA4 C69775	97	ATL8C1 5867:6	0.78	g44551 72	62	548	4.3e- 54	(AL035 521)	

146664	ATU008 604	ATL8C4 4274:4 02..1	gap2	ATCEA4 C3872_1	97	ATL8C4 4274:3 90..17 4	0.76	g31324 75	62	341	2.3e- 11	putative protein [Arabis dopsis thaliana]
146665	ATU008 605	ATL8C8 909:1. .992	gap2	ATCEA4 C9770_1	97	ATL8C8 909:18 2..882	0.75	g32818 53	62	349	2.9e- 27	putative protein [Arabis dopsis thaliana]
146666	ATU008 606	ATL8C4 0905:2 16..16 26	gap2	ATCEA4 S10949	97	ATL8C4 0905:2 16..15 51	0.69	g48352 35, g19463 68	62, 44	283, 118	7.1e- 33, 9.1e- 09	putative protein [Arabis dopsis thaliana]; (U9321 5) unknown protein

146667	ATU008 607	ATL8C2 6651:5 361..1	gap2	ATCEA4 S27366	97	ATL8C2 6651:5 197..7 7	0.66	g49143 72	62	2574	1.1e- 219	n [Arabi dopsis thalia na]
146668	ATU008 608	ATL8C2 1210:5 68..50 16	gap2	ATCEA4 C4679 1, ATCEA4 S23663 , ATCEA4 C21331 _1	97, 97, 96	ATL8C2 1210:5 68..49 14	0.65	g88257 0	62	80	0.020	(U2837 7) ORE_o2 65; altern ate name ygiE; orfb of M77129 [Esche richia colij]
146669	ATU008 609	ATL8C9 536:11 37..1	gap2	ATCEA4 C4187 1, ATCEA4 C76868 _1	97, 95			g33373 67	62	941	6.8e- 95	(AC004 481) hypoth etical protei n [Arabi dopsis thalia na]
146670	ATU008 610	ATL8C1 7704:1 265..1	gap2	ATCEA4 C30508 1, ATCEA4 C13781 0 1	97, 96			g35823 40	62	410	6.9e- 47	(AC005 496) unknow n protei n

146671	ATU008 611	ATL8C3 4582:1 ..3007	gap2	ATCEA4 S31531	97					g21911 87	62	4816	0.0	[Arabi dopsis thalia na]
146672	ATU008 612	ATL8C3 1568:8 5..120 9	gap2	ATCEA4 C427_1 , ATCEA4 C427_2	97, 94	ATL8C3 1568:8 9..117 5	0.80			g37591 77	61	707	2.4e- 80	(AF007 271) contai ns simila rity to a DNAJ- like domain [Arabi dopsis thalia na]
146673	ATU008 613	ATL8C3 5299:2 715..1 194	gap2	ATCEA4 C90902 _1, ATCEA4 C90902 _2	97, 92					g36680 91	61	321	1.8e- 28	(AB018 408) 3- phosph oserin e phosph atase [Arabi dopsis thalia na]
146674	ATU008 614	ATL8C2 807:16 75..24 29	gap2	ATCEA4 C19353 _2, ATCEA4 C19353	97, 88					g33866 14	61	555	1.8e- 43	(AC004 667) hypoth etical protei n [Arabi dopsis thalia na]
														(AC004 665) putati ve transc

146675	ATU008 615	ATL8C2 5914:2 049..1	gap2	ATCEA4 S3109, ATCEA4 C53825 1, ATCEA4 C31431 1	97, 93 95, 93	ATL8C2 5914:2 049..1 42	0.84	g30969 35	60	459	6.7e- 35	(AL023 094) putati ve protei n [Arabi dopsis thalia na]
146676	ATU008 616	ATL8C2 0616:1 055..1	gap2	ATCEA4 C706_1	97	ATL8C2 0616:1 016..2 99	0.83	g49143 15	60	558	6.7e- 43	(AC005 489) F14N23 .1 [Arabi dopsis thalia na]
146677	ATU008 617	ATL8C4 9058:1 435..1	gap2	ATCEA4 S5481	97	ATL8C4 9058:1 388..2 07	0.80	g22526 34	60	1844	1.2e- 170	(U9597 3) hypoth etical protei n [Arabi dopsis thalia na]
146678	ATU008 618	ATL8C1 6637:7 79..21 72	gap2	ATCEA4 S29669	97	ATL8C1 6637:7 79..21 72	0.80	g17231 50	60	179	5.2e- 16	HYPOTH ETICAL 50.2 KD GTP- BINDIN G PROTEI N

146679	ATU008 619	ATL8C1 0983:5 88..27 30	gap2	ATCEA4 C45434 _1	97	ATL8C1 0983:5 88..26 94	0.78	g28424 90	60	1060	8.6e- 68	MG329 [Mycoplasma genitalium] (AL021749) heat-shock protein [Arabidopsis thaliana]
146680	ATU008 620	ATL8C2 434:20 16..1	gap2	ATCEA4 S26843 , ATCEA4 S32787 , ATCEA4 S35738	97, 94, 89	ATL8C2 434:16 67..18 8	0.78	g29110 40	60	2738	5.2e- 276	(AL021961) receptor protein kinase - like protein [Arabidopsis thaliana]
146681	ATU008 621	ATL8C4 0704:2 052..9 08	gap2	ATCEA4 S13199	97	ATL8C4 0704:2 029..9 30	0.72	g22135 92	60	900	5.1e- 95	(AC000348) T7N9.1 2 [Arabidopsis thaliana]
146682	ATU008 622	ATL8C1 3181:3 95..20 60	gap2	ATCEA4 C11888 4 1, ATCEA4 S2242	97, 88	ATL8C1 3181:1 012..1 434	0.71	g42638 20	60	310	7.6e- 33	(AC006067) hypothetical protein [Arabidopsis]

146688	ATU008 628	ATL8C4 9858:1 ..512	gap2	ATCEA4 S11602 , ATCEA4 C5339 _1	97, 94	30..60 5		g22528 28	59	545	1.8e- 48	(AF013 293) No defini tion line found [Arabi dopsis thalia na]	unknown protei n [Arabi dopsis thalia na]
146689	ATU008 629	ATL8C3 6846:1 ..1401	gap2	ATCEA4 C12000 4_1, ATCEA4 S35203	97, 92	ATL8C3 6846:3 19..12 52	0.99	g16985 48	58	744	2.3e- 80	(U5897 1) calmod ulin- bindin g protei n [Nicot iana tabacu m]	unknown protei n [Arabi dopsis thalia na]
146690	ATU008 630	ATL8C1 7766:1 ..964	gap2	ATCEA4 C93285 _1, ATCEA4 S35233	97, 90	ATL8C1 7766:7 4..942	0.94	g26421 54	58	293	8.0e- 34	(AC003 000) unknown protei n [Arabi dopsis thalia na]	unknown protei n [Arabi dopsis thalia na]
146691	ATU008 631	ATL8S2 8271:5 32..1	gap2	ATCEA4 C27863 _1, ATCEA4	97, 88	ATL8S2 8271:4 85..25 6	0.93	g30467 05	58	377	6.1e- 39	(AL022 198) riboso mal	unknown protei n [Arabi dopsis thalia na]

146692	ATU008 632	ATL8C4 831:15 90..1	gap2	ATCEA4 S36280	97	ATL8C4 831:15 09..16 9	0.92	g11704 10	58	1763	1.2e- 134	HOMEOB OX PROTEI N HAT3.1 [Arabi dopsis thalia na]
146693	ATU008 633	ATL8C4 9539:2 51..18 12	gap2	ATCEA4 C6266 1	97	ATL8C4 9539:2 78..18 05	0.85	g32420 62	58	1359	9.0e- 115	(Z9705 8) NRT2;1 P [Arabi dopsis thalia na]
146694	ATU008 634	ATL8C1 3750:1 04..25 83	gap2	ATCEA4 C43907 1, ATCEA4 S35687	97, 96	ATL8C1 3750:1 023..2 426	0.85	g38776 55	58	449	6.0e- 36	(Z7251 1) possib le zinc finger protei n; CDNA EST EMBL:M 89115 comes from this gene; CDNA EST EMBL:D

146695	ATU008 635	ATL8C1 9761:1 ..611	gap2	ATCEA4 C1159 1	97	ATL8C1 9761:2 18..10 8	0.70	g11733 09	58	596	2.1e- 33	71533 comes from this gene; cDNA EST EMBL:D 72314 comes from this gene; cDNA EST EMBL:D 75164 comes from this gene; cDNA EST EMBL:C 1.... []
146696	ATU008 636	ATL8C1 1865:1 319..1 27	gap2	ATCEA4 S365	97	ATL8C1 1865:1 211..1 27	0.68	g47577 62	58	286	7.0e- 31	androg en recept or associ ated

146700	ATU008 640	ATL8C4 0037:6 83..1	gap2	ATCEA4 S35369 , ATCEA4 C37855 _1	97, 95	ATL8C4 0037:5 74..81	0.99	g28298 98	57	211	3.3e- 19	(AC002 311) Hypoth etical protei n [Arabi dopsis thalia na]
146701	ATU008 641	ATL8C6 777:1. .2775	gap2	ATCEA4 C7189 _ 1, ATCEA4 C85554 _1, ATCEA4 S10641 , ATCEA4 C29252 _1	97, 97, 92, 91	ATL8C6 777:13 2..266 9	0.97	g42042 65, g43253 82	57, 31	723, 388	2.0e- 66, 4.4e- 30	(AC005 223) 45643 [Arabi dopsis thalia na]; (AF129 075) T- COMPLE X PROTEI N 1, THETA SUBUNI T (TCP- 1- THETA) [Homo sapien s]
146702	ATU008 642	ATL8C3 6084:2 183..1	gap2	ATCEA4 C8538 _ 1, ATCEA4 S29587	97, 92	ATL8C3 6084:1 599..3 16	0.83	g45126 60	57	692	8.6e- 73	(AC006 931) hypoth etical protei n [Arabi

647	0494:1 347..1	ATU008 648	ATL8C4 1967:2 075..3 03	gap2	ATCEA4 C21764 1, ATCEA4 C37660 1, ATCEA4 C58277 1	97, 91, 90	0494:1 208..3 54	02	40	6) MtN3 [Medic ago trunca tula]
146708				gap2	ATCEA4 C21764 1, ATCEA4 C37660 1, ATCEA4 C58277 1	97, 91, 90		g46462 26	594	(AC007 235) hypoth etical protei n [Arabi dopsis thalia na]
146709	ATL8C4 0077:8 96..1	ATU008 649		gap2	ATCEA4 C6102 1	97		g22136 15	576	(AC000 103) F21J9. 9 [Arabi dopsis thalia na]
146710	ATL8C1 3219:7 82..24 98	ATU008 650		gap2	ATCEA4 S153	97		g45804 69	318	(AC006 081) putati ve zinc finger protei n [Arabi dopsis thalia na]
146711	ATL8C2 1307:2 185..9 76	ATU008 651		gap2	ATCEA4 C11479 8_2	97	ATL8C2 1307:2 014..1 123	g22451 44	651	(Y1084 6) O- acetyl serine (thiol) lyase [Brass ica]

146712	ATU008 652	ATL8C3 1628:1 977..1	gap2	ATCEA4 S2673, ATCEA4 C19123 _1	97, 95	ATL8C3 1628:1 895..1 59	0.94	g45860 56	56	1608	1.2e- 149	juncea [AC007 020) unknown protein [Arabi dopsis thalia na]
146713	ATU008 653	ATL8C4 4149:9 37..1	gap2	ATCEA4 C5295_1, ATCEA4 S26984, ATCEA4 S5558	97, 96, 87	ATL8C4 4149:8 59..62	0.90	g37696 71	56	141	4.7e- 08	(AF095 284) Tic22 [Pisum sativu m]
146714	ATU008 654	ATL8C2 6946:1 630..3 095	gap2	ATCEA4 C4691_1	97	ATL8C2 6946:1 630..3 069	0.90	g45035 21	56	515	4.3e- 47	murine mammar y tumor integr ation site 6 (oncog ene homolo g) [Homo sapien s]
146715	ATU008 655	ATL8C4 6609:1 488..1	gap2	ATCEA4 C41125 _1	97	ATL8C4 6609:1 090..2 53	0.88	g41153 83	56	2058	1.0e- 138	(AC005 967) recept or- like protei n kinase [Arabi dopsis thalia

146716	ATU008 656	ATL8C3 6880:5 644..3 455	gap2	ATCEA4 C1984_1	97	ATL8C3 6880:4 652..3 455	0.84	g27958 04	56	220	5.6e- 22	na] (AC003 674) unknown protein [Arabi dopsis thalia na]
146717	ATU008 657	ATL8C7 497:1. .1285	gap2	ATCEA4 S27465 , ATCEA4 C70762 _1	97, 92	ATL8C7 497:95 ..1105	0.77	g31222 34	56	226	9.3e- 23	EUKARY OTIC TRANSL ATION INITIA TION FACTOR 2 BETA SUBUNI T (EIF- 2- BETA) (P38) [Triti cum aestiv um]
146718	ATU008 658	ATL8C4 0039:8 12..1	gap2	ATCEA4 C36943 1, ATCEA4 S12849	97, 94	ATL8C4 0039:8 12..33 3	0.75	g33351 69	56	486	5.8e- 44	(AF067 857) embryo - specif ic protei n 1 [Arabi dopsis thalia na]
146719	ATU008 659	ATL8C4 6552:1 ..1957	gap2	ATCEA4 S3631	97	ATL8C4 6552:6 15..16 72	0.70	g35229 56	56	389	6.7e- 35	(AC004 411) putati ve

146720	ATU008 660	ATL8C1 5146:5 21..16 61	gap2	ATCEA4 C9136_2, ATCEA4 S30767 , ATCEA4 C9136_1	97, 91 92, 91	ATL8C1 5146:5 60..12 96	0.69	g41153 86	56	825	1.1e- 59	(AC005 967) unknown protein [Arabi dopsis thalia na]
146721	ATU008 661	ATL8C4 5171:1 06..17 91	gap2	ATCEA4 S8179	97			g36412 52	56	1822	2.5e- 163	(AF053 127) leucin e-rich recept or- like protei n kinase [Malus domest ica]
146722	ATU008 662	ATL8C4 8935:1 ..1306	gap2	ATCEA4 S7547, ATCEA4 C5514_1, ATCEA4 C63010 _1, ATCEA4 S10765 , ATCEA4	97, 93, 92, 90, 89, 84			g16657 77	56	812	3.3e- 65	(D8744 4) Simila r to S.cere visiae EMP70 protei n precu sor (S2511

146723	ATU008 663	ATL8C2 2782:4 53..10 65	gap2	ATCEA4 S4964	97					g46782 76	56	908	5.3e- 91	(AL049 660) putati ve protei n [Arabi dopsis thalia na]	0) [Homo sapien s]
146724	ATU008 664	ATL8C3 6560:1 ..802	gap2	ATCEA4 C35325 _1	97					g24594 32	56	1056	2.3e- 100	(AC002 332) CONSTA NS- like protei n [Arabi dopsis thalia na]	
146725	ATU008 665	ATL8C1 4741:1 044..1 710	gap2	ATCEA4 C11384 _1, ATCEA4 S9447	97, 83					g14190 90	56	608	5.3e- 46	(X9496 8) 37kDa chloro plast inner envelo pe membra ne polype ptide precu sor [Nicot iana tabacu m]	
146726	ATU008 666	ATL8C4 5325:2	gap2	ATCEA4 C15554	97	ATL8C4 5325:1	0.94			g36500 38	55	1755	1.5e- 143	(AC005 396)	

146727	ATU008 667	019..1		7_1		97	ATCEA4 S4152	ATL8C1 3617:2 746..1 961	0.91	g28978 75	55	421	6.2e- 42	(U9027 4) histon e acetyl transf erase HAT B [Zea mays]	hypoth etical protei n [Arabi dopsis thalia na]
146728	ATU008 668	ATL8C3 2458:1 ..1298	gap2	ATCEA4 C80449 _1		97		ATL8C3 2458:1 80..94 3	0.85	g45672 55	55	476	4.0e- 29	(AC007 070) hypoth etical protei n [Arabi dopsis thalia na]	hypoth etical protei n [Arabi dopsis thalia na]
146729	ATU008 669	ATL8C4 218:13 37..1	gap2	ATCEA4 S34799 , ATCEA4 S35361 , ATCEA4 S24693 , ATCEA4 S5688	97, 94, 93, 82			ATL8C4 218:13 37..69	0.85	g38818 73	55	242	2.6e- 17	(Z8324 6) predic ted using Genefi nder; cDNA EST EMBL:M 79771 comes from this gene [Caeno rhabdi	predic ted using Genefi nder; cDNA EST EMBL:M 79771 comes from this gene [Caeno rhabdi

146730	ATU008 670	ATL8C5 178:72 7..1	gap2	ATCEA4 C35783 1, ATCEA4 C35783 3, ATCEA4 S33087 , ATCEA4 S33724 , ATCEA4 S15382	97, 96, 93, 83, 83	ATL8C5 178:72 3..46	0.73	g45889 16	55	245	3.6e- 25	(AF119 095) flavon ol syntha se [Malus domest ica]
146731	ATU008 671	ATL8C1 9397:1 09..95 0	gap2	ATCEA4 C35643 1, ATCEA4 S2562	97, 83	ATL8C1 9397:1 82..87 5	0.68	g31641 32	55	1009	1.1e- 82	(D7860 1) cytoch rome P450 monoox ygenase [Arabi dopsis thalia na]
146732	ATU008 672	ATL8C1 2121:3 329..1	gap2	ATCEA4 C1330 7, ATCEA4 S5505, ATCEA4 S33255 , ATCEA4 C1330 4	97, 97, 90, 89	ATL8C1 2121:3 194..1 04	0.66	g41974 5	55	410	1.4e- 23	polyga lactur onase (EC 3.2.1. 15) - avocad o []
146733	ATU008 673	ATL8C3 3281:1 ..1107	gap2	ATCEA4 C9428 1	97	ATL8C3 3281:6 3..103 0	0.59	g16970 5	55	1106	1.1e- 109	(M6473 7) ATP:py ruvate phosph

146734	ATU008 674	ATL8C1 962:19 4..126 5	gap2	ATCEA4 C1779_1, ATCEA4 C1778_1	97, 82	ATL8C1 962:80 1..106 8	0.52	g33090 86	55	508	3.1e- 31	(AF076 253) calcin eurin B-like protei n 3 [Arabi dopsis thalia na]
146735	ATU008 675	ATL8C4 3519:2 46..14 04	gap2	ATCEA4 C23306 _1	97	ATL8C4 3519:2 76..10 01	0.52	g37765 74	55	971		(AC005 388) Simila r to T11J7. 13 [Arabi dopsis thalia na]
146736	ATU008 676	ATL8C4 20:85. .897	gap2	ATCEA4 C5321_1, ATCEA4 C12129 0_1	97, 93			g45103 99	55	290	3.8e- 30	(AC006 587) putati ve zinc finger protei n [Arabi dopsis thalia na]
146737	ATU008 677	ATL8S1 5515:5 75..1	gap2	ATCEA4 C12312 _1	97			g48862 71	55	239	2.5e- 17	(AL050 300) putati ve protei n

146738	ATU008 678	ATL8C4 2689:1 ..379	gap2	ATCEA4 C44308 _1	97						g13378 8	55	228	2.3e- 18	[Arabi dopsis thalia na]
146739	ATU008 679	ATL8C3 6894:9 28..69	gap2	ATCEA4 S11565	97			ATL8C3 6894:7 89..69	0.99		g45103 49	54	127	1.4e- 25	(AC006 921) putati ve bZIP transc riptio n factor [Arabi dopsis thalia na]
146740	ATU008 680	ATL8C4 9782:1 ..2228	gap2	ATCEA4 S2996, ATCEA4 S34723 , ATCEA4 S29628 , ATCEA4 S18542	97, 94, 93, 83			ATL8C4 9782:5 0..222 8	0.92		g24659 23	54	1011	1.6e- 83	(AF024 648) recept or- like serine /threo nine kinase [Arabi dopsis thalia na]
146741	ATU008 681	ATL8C2 4055:2 86..11 52	gap2	ATCEA4 S3995	97			ATL8C2 4055:2 88..11 52	0.88		g44903 04	54	1350	4.6e- 132	(AL035 678) putati ve

146746	ATU008 686	ATL8C2 1809:2 39..23 52	gap2	ATCEA4 C8425_1	97	ATL8C2 1809:2 39..22 99	0.73	g11695 85	54	609	2.8e- 57	FRUCTO SE- 1,6- BISPHO SPHATA SE, CYTOSO LIC (D- FRUCTO SE- 1,6- BISPHO SPHATE 1- PHOSPH OXYDRO LASE) (FBPAS E) [Brass ica napus]
146747	ATU008 687	ATL8C9 815:15 40..21 49	gap2	ATCEA4 S5821	97	ATL8C9 815:15 40..20 97	0.66	g45859 97	54	703	4.1e- 71	AC005 287) Hypoth etical protei n [Arabi dopsis thalia na]
146748	ATU008 688	ATL8C4 9447:1 84..22 67	gap2	ATCEA4 C38469_1	97			g43888 26	54	187	2.3e- 18	AC006 528) hypoth etical protei n [Arabi dopsis thalia na]

146749	ATU008 689	ATL8C4 0599:1 ..446	gap2	ATCEA4 S30096	97					g28943 79	54	205	8.7e- 19	na] (Y1457 3) ring finger protei n [Horde um vulgar e]
146750	ATU008 690	ATL8C1 6976:1 369..2 734	gap2	ATCEA4 S31836 , ATCEA4 C15766 5_1	97, 96					g29470 63	54	378	2.3e- 14	(AC002 521) putati ve Ser/Th r protei n kinase [Arabi dopsis thalia na]
146751	ATU008 691	ATL8C3 1864:5 28..11 17	gap2	ATCEA4 C34496 1, ATCEA4 S16298	97, 84					g40564 93	54	437	2.3e- 32	(AC005 896) unknow n protei n [Arabi dopsis thalia na]
146752	ATU008 692	ATL8C2 5189:1 036..1 12	gap2	ATCEA4 C48645 1, ATCEA4 S6289	97, 91					g48875 43	54	467	2.1e- 30	(AJ012 278) ATP- depend ent Clp protea se subuni t ClpP [Arabi

146753	ATU008 693	ATL8C3 2454:1 53..16 56	gap2	ATCEA4 C49050 1, ATCEA4 S20425 , ATCEA4 C49050 3_	97, 92 94, 88	ATL8C3 2454:2 11..85 5	0.97	g48877 61	53	1090	3.4e- 104	dopsis thalia na] (AC006 533) putati ve indole -3- acetat e beta- glucos yltran sferas e [Arabi dopsis thalia na]
146754	ATU008 694	ATL8C2 0302:1 ..1190	gap2	ATCEA4 C17340 2, ATCEA4 C17340 1_	97, 92	ATL8C2 0302:1 05..11 65	0.96	g39252 77	53	234	3.2e- 23	(AL032 643) simila r to Unchar acteri zed protei n family UPF003 4, Double - strand ed RNA bindin g motif; cDNA EST yk489b 3.5 comes from

146755	ATU008 695	ATL8C3 0440:1 ..712	gap2	ATCEA4 C70764 _1	97	ATL8C3 0440:1 37..69 6	0.95	g25015 55	53	389	4.7e- 31	POSSIB LE APOSPO RY- ASSOCI ATED PROTEI N C [Penni setum ciliar el]	this gene; CDNA EST yk439g 7.5 comes from this gene [Caeno rhabdi tis elegan s]
146756	ATU008 696	ATL8C2 8633:1 ..743	gap2	ATCEA4 C10932 _1, ATCEA4 C22257 _1	97, 97	ATL8C2 8633:1 01..71 5	0.87	g16537 02	53	476	1.7e- 29	(D9091 5) dihydr olipoa mide acetyl transf erase compon ent (E2) of pyruva te dehydr ogenas e comple	

146757	ATU008 697	ATL8C2 1507:1 ..2500	gap2	ATCEA4 S29787 , ATCEA4 S34792	97, 87	ATL8C2 1507:1 385..2 302	0.86	g47585 60	53	94	0.0027	x [Synec hocyst is sp.] prp8, U5 snRNP- specific 40 kDa protein [Homo sapien s]
146758	ATU008 698	ATL8C2 0850:3 601..2 315	gap2	ATCEA4 C54983 _1	97	ATL8C2 0850:3 601..2 315	0.85	g28296 4	53	754	5.1e- 84	transf orming protei n (myb) homolo g (clone myb.Ph 3) - garden petuni a [Petun ia x hybrid a]
146759	ATU008 699	ATL8C3 7742:4 3..756	gap2	ATCEA4 C27922 _1, ATCEA4 S30788 , ATCEA4 C19347 _1	97, 82 97, 82	ATL8C3 7742:2 34..69 4	0.85	g42637 12	53	365	1.2e- 22	(AC006 223) putati ve riboso mal protei n S12 [Arabi dopsis thalia na]

146760	ATU008 700	ATL8C1 8776:1 ..985	gap2	ATCEA4 C48026 1, ATCEA4 C73651 1	97, 93	ATL8C1 8776:2 62..96 0	0.84	g21045 36	53	545	1.9e- 56	(AF001 308) predic ted glycos yl transf erase [Arabi dopsis thalia na]
146761	ATU008 701	ATL8C4 8040:1 920..1	gap2	ATCEA4 C799 1 , ATCEA4 S35939	97, 83	ATL8C4 8040:1 867..5 1	0.82	g10843 35	53	1094	2.4e- 88	calciu m- depend ent protei n kinase (EC 2.7.1. -) 2 - Arabid opsis thalia na [Arabi dopsis thalia na]
146762	ATU008 702	ATL8C2 5239:1 35..18 25	gap2	ATCEA4 C11672 1, ATCEA4 S2039	97, 92	ATL8C2 5239:1 93..18 25	0.81	g26226 29	53	146	5.1e- 11	(AE000 911) arseni cal pump- drivin g ATPase [Metha nobact erium thermo autotr ophicu m]

146763	ATU008 703	ATL8C4 9845:1 591..1	gap2	ATCEA4 S36264	97	ATL8C4 9845:1 285..2 34	0.76	g32016 19	53	599	3.0e- 57	(AC004 669) dihydr oxypol ypreny lbenzo ate methyl transf erase [Arabi dopsis thalia na]
146764	ATU008 704	ATL8C2 0378:1 372..9 0	gap2	ATCEA4 S25834	97	ATL8C2 0378:1 228..1 09	0.75	g44159 19	53	724	1.1e- 54	(AC006 282) hypoth etical protei n [Arabi dopsis thalia na]
146765	ATU008 705	ATL8C2 2203:2 215..1	gap2	ATCEA4 C933_1	97	ATL8C2 2203:2 045..1 179	0.67	g97617 8, g19316 54	53, 41	67, 747	6.9e- 06, 9.1e- 81	(L4718 3) revers e transc riptas e [Arabi dopsis thalia na]; (U9597 3) BRCA1- associ ated RING domain protei n isolog

146766	ATU008 706	ATL8C4 753:26 86..10 08	gap2	ATCEA4 C74290 1, ATCEA4 S34044 , ATCEA4 S31353	97, 88 91, 88	ATL8C4 753:25 34..12 40	0.60	g45875 13	53	880	1.1e- 93	[Arabi dopsis thalia na] (AC007 060) Contai ns eukary otic protei n kinase domain PF1000 69. [Arabi dopsis thalia na]
146767	ATU008 707	ATL8S7 001:60 8..1	gap2	ATCEA4 C12197 2, ATCEA4 C12197 _1	97, 95	ATL8S7 001:58 3..33	0.45	g18711 84	53	161	0.031	(U9043 9) unknow n protei n [Arabi dopsis thalia na]
146768	ATU008 708	ATL8C4 1971:9 59..1	gap2	ATCEA4 S5946	97	ATL8C4 1971:8 11..31 3	0.40	g43252 82	53	79	1.2e- 06	(AF123 310) NAC domain protei n NAM [Arabi dopsis thalia na]
146769	ATU008 709	ATL8C1 0365:1 240..7 67	gap2	ATCEA4 C21824 2, ATCEA4 C21824	97, 82 93, 82			g44544 66	53	177		(AC006 234) unknow n protei

146770	ATU008 710	ATL8C5 431:22 29..97 3	gap2	ATCEA4 C21824 _1	3, ATCEA4 C21824 _1	97, 89				g38314 41	53	62	8.1e- 06	n [Arabi dopsis thalia na] (AC005 819) hypoth etical protei n [Arabi dopsis thalia na]
146771	ATU008 711	ATL8C3 0972:1 642..1	gap2	ATCEA4 C49002 _1	ATCEA4 S32195 , ATCEA4 S34949	97				g38366 11	53	647	1.9e- 62	(AC004 665) unknow n protei n [Arabi dopsis thalia na]
146772	ATU008 712	ATL8C2 1791:1 940..1	gap2	ATCEA4 S324	ATCEA4 S324	97				g44327 94	53	2478	1.2e- 248	(AC006 437) putati ve Tnp2 Taml transp oson protei n [Arabi dopsis thalia na]
146773	ATU008 713	ATL8C1 2759:2 038..9 70	gap2	ATCEA4 S29582	ATCEA4 S29582	97	ATI8C1 2759:1 994..9 70	0.94		g48039 44	52	808	3.2e- 71	(AC006 264) putati ve C2- domain protei

146774	ATU008 714	ATL8C2 529:26 95..11 9	gap2	ATCEA4 C20845 2, ATCEA4 S30927	97, 94	ATL8C2 529:26 22..19 0	0.93	g46789 39	52	900	3.5e- 59	(AL049 711) putati ve protei n [Arabi dopsis thalia na]
146775	ATU008 715	ATL8C2 7256:2 809..8 97	gap2	ATCEA4 C3130 1	97	ATL8C2 7256:2 501..8 97	0.93	g40637 51	52	373		(AC005 851) putati ve white protei n [Arabi dopsis thalia na]
146776	ATU008 716	ATL8C1 7092:2 395..2 98	gap2	ATCEA4 C4553 4, ATCEA4 S24355 , ATCEA4 S1639, ATCEA4 C4553 1, ATCEA4 C4553 6, ATCEA4	97, 94, 93, 89, 88, 85, 85	ATL8C1 7092:2 336..3 03	0.91	g44907 39, g38938 22	52, 50	338, 1215	2.4e- 08, 7.8e- 111	(AL035 708) putati ve protei n [Arabi dopsis thalia na]; (U9649 8) ATPase beta subuni

146777	ATU008 717	ATL8C1 0946:9 93..1	gap2	ATCEA4 C8118 1, ATCEA4 C56655 _1	97, 85	ATL8C1 0946:8 80..59 9	0.88	g30045 60	52	413	1.4e- 23	t [Nicot iana sylv tris]
146778	ATU008 718	ATL8C4 8493:2 25..93 5	gap2	ATCEA4 C15036 _1	97	ATL8C4 8493:2 70..49 3	0.87	g16193 00	52	341	1.5e- 29	(X9526 9) LRR protei n [Lycop ersico n escule ntum]
146779	ATU008 719	ATL8C2 1635:1 343..1	gap2	ATCEA4 S24878	97	ATL8C2 1635:1 139..1 25	0.85	g45393 47	52	354	7.7e- 33	(AL035 539) putati ve growth regula tor protei n [Arabi dopsis thalia na]
146780	ATU008 720	ATL8C1 2811:1 ..2228	gap2	ATCEA4 S30265	97	ATL8C1 2811:1 75..18 98	0.83	g18391 88	52	912	8.5e- 70	(U8608 1) root hair defect ive 3

146781	ATU008 721	ATL8C1 0803:6 075..9 8	gap2	ATCEA4 C28569 1, ATCEA4 S30769 , ATCEA4 S6064, ATCEA4 S6061	97, 92, 86, 86	ATL8C1 0803:6 073..1 03	0.80	g43097 60	52	1150	1.8e- 113	[Arabi dopsis thalia na] (AC006 217) unknown n protei n [Arabi dopsis thalia na]
146782	ATU008 722	ATL8C7 22:135 3..1	gap2	ATCEA4 S11636	97	ATL8C7 22:124 8..35	0.73	g41159 20	52	928	5.9e- 101	(AF118 222) simila r to the subtil ase family of serine protea ses (Pfam: PF0008 2, score; 45.8, E=1.1e -11, n=2) [Arabi dopsis thalia na]
146783	ATU008 723	ATL8C4 1319:8 59..23 2	gap2	ATCEA4 S29996	97	ATL8C4 1319:7 76..37 3	0.72	g28946 07	52	475	1.6e- 38	(AL021 889) NAM (no apical merist em) -

146784	ATU008 724	ATL8C4 3928:1 ..872	gap2	ATCEA4 C13109 1, ATCEA4 S31776 , ATCEA4 S1297	97, 84, 83	ATL8C4 3928:1 57..85 5	0.59	g28326 29	52	401		like protei n [Arabi dopsis thalia na]
146785	ATU008 725	ATL8C7 360:1. .1381	gap2	ATCEA4 S29623	97			g26233 09	52	528	1.5e- 45	(AC002 409) simila r to tgacg- specif ic DNA- bindin g protei n [Arabi dopsis thalia na]
146786	ATU008 726	ATL8C4 6197:9 20..1	gap2	ATCEA4 S3594	97	ATL8C4 6197:7 85..7	0.96	g26227 14	51	209	1.2e- 16	(AE000 918) phosph onopyr uvate decarb oxylas e [Metha nobact

146787	ATU008 727	ATL8C2 5596:8 76..1	gap2	ATCEA4 S30990	97	ATL8C2 5596:8 76..39 4	0.94	g26485 68	51	138	1.8e- 09	(AE000 967) conser ved hypoth etical protei n [Archaeoglobus fulgidus]
146788	ATU008 728	ATL8C3 0984:3 05..19 31	gap2	ATCEA4 C13101 51, ATCEA4 C30551 1	97, 95	ATL8C3 0984:3 05..17 65	0.81	g11294 7	51	210	1.5e- 10	AAC- RICH MRNA CLONE AAC3 PROTEIN [Dictyostelium discoideum]
146789	ATU008 729	ATL8C2 7731:5 74..26 97	gap2	ATCEA4 C9573 1	97	ATL8C2 7731:5 74..24 58	0.81	g30045 64	51	337	(AC003 673) putative receptor Ser/Th r protein kinase [Arabidopsis thaliana]	

734	4658:1 ..577		C25604 _1					05		10	638) putati ve protei n [Arabi dopsis thalia na]
146795	ATU008 735	ATL8C2 7261:1 5..216 2	gap2	ATCEA4 C13714 _1, ATCEA4 S3279	97, 97			g24628 32	51	1212	(AF000 657) simila r to Bacill us CotA [Arabi dopsis thalia na]
146796	ATU008 736	ATL8C3 7711:1 489..1	gap2	ATCEA4 S2199	97			g48357 83	51	804	(AC007 296) Strong simila rity to []
146797	ATU008 737	ATL8C1 0447:1 053..2 15	gap2	ATCEA4 C10430 _1, ATCEA4 S32017	97, 83	ATL8C1 0447:1 006..2 15	0.96	g22447 52	50	615	(Z9733 5) hypoth etical protei n [Arabi dopsis thalia na]
146798	ATU008 738	ATL8C2 0485:6 06..1	gap2	ATCEA4 S36370 , ATCEA4 C1887 _ 3, ATCEA4 C1887 _ 2	97, 90 95, 90	ATL8C2 0485:5 25..23 6	0.95	g33095 75	50	364	(AF060 553) calciu m sensor homolo g [Arabi dopsis

146799	ATU008 739	ATL8C6 494:34 55..1	gap2	ATCEA4 C31360 2, ATCEA4 C10756 6 1, ATCEA4 C31360 1, ATCEA4 S13360 , ATCEA4 S9145	97, 96, 95, 91, 85	ATL8C6 494:33 00..16 7	0.95	g24972 81	50	1057	2.1e- 60	thalia na]
146800	ATU008 740	ATL8C4 127:1. .1368	gap2	ATCEA4 S3850	97	ATL8C4 127:91 ..894	0.94	g54205 8	50	48	0.0042	HSR203 J protei n - common tobacc o [Nicot iana tabacu m]
146801	ATU008 741	ATL8C3 1828:1 630..2 51	gap2	ATCEA4 S10557 , ATCEA4 C51411 1, ATCEA4 S1592	97, 93, 86	ATL8C3 1828:1 426..4 49	0.89	g46226 0	50	803	1.5e- 74	COPROP ORPHYR INOGEN III OXIDAS E PRECUR SOR (COPRO PORPHY RINOGE NASE) (COPRO GEN OXIDAS E) [Glyci ne

146802	ATU008 742	ATL8C9 486:15 6..162 3	gap2	ATCEA4 S11242 , ATCEA4 S31774 , ATCEA4 S12273	97, 82 90, 82	ATL8C9 486:22 2..144 6	0.88	g45671 99	50	555	1.7e- 44	(AC007 168) unknown protein [Arabi dopsis thalia na]
146803	ATU008 743	ATL8C3 0729:1 411..2 94	gap2	ATCEA4 C64263 1, ATCEA4 S27482	97, 84	ATL8C3 0729:1 227..4 94	0.84	g62959 2	50	478	2.4e- 46	hypoth etical protein - rape []
146804	ATU008 744	ATL8C4 4379:2 798..5 24	gap2	ATCEA4 C7382 1	97	ATL8C4 4379:2 750..5 58	0.83	g45585 52	50	2336	1.7e- 226	(AC007 138) putati ve P- glycop rotein -like protein [Arabi dopsis thalia na]
146805	ATU008 745	ATL8C3 9595:1 ..1143	gap2	ATCEA4 C64821 1, ATCEA4 C93604 1	97, 93	ATL8C3 9595:7 8..104 7	0.78	g36872 24	50	690	5.2e- 57	(AC005 169) putati ve N- acetyl - gamma- glutam yl- phosph ate reduct ase [Arabi dopsis]

146806	ATU008 746	ATL8C2 5821:8 83..1	gap2	ATCEA4 C45177 _1	97	ATL8C2 5821:7 56..50 8	0.78	g14048 9	50	143	9.7e- 16	GNS1 PROTEI N [Sacch aromyc es cerevi siae]
146807	ATU008 747	ATL8C3 1315:1 962..3 355	gap2	ATCEA4 C41720 _1	97	ATL8C3 1315:2 026..2 322	0.55	g11701 91	50	546	3.5e- 45	HOMEOB OX PROTEI N HD1 [Brass ica napus]
146808	ATU008 748	ATL8C4 8209:1 283..1	gap2	ATCEA4 C15583 6 1, ATCEA4 C16659 _1, ATCEA4 S24618 , ATCEA4 S10326	97, 93, 88, 83	ATL8C4 8209:6 70..55	0.50	g42061 22	50	782	1.4e- 76	(AF097 667) protei n phosph atase 2C homolo g [Mesem bryant hemum crysta llinum]
146809	ATU008 749	ATL8C3 3428:6 78..1	gap2	ATCEA4 C922_1 , ATCEA4 S13240	97, 84			g42205 15	50	457	8.8e- 50	(AL035 356) putati ve protei n [Arabi dopsis thalia na]
146810	ATU008 750	ATL8C4 7598:1	gap2	ATCEA4 C80742	97			g28092 46	50	471	2.2e- 39	(AC002 560)

146811	ATU008 751	799..2 30	gap2	ATCEA4 S6950	97					g22447 56	50	475	1.3e- 25	(Z9733 5) hypoth etical protei n [Arabi dopsis thalia na]	F2401. 15 [Arabi dopsis thalia na]
146812	ATU008 752	ATL8C2 3807:1 415..1	gap2	ATCEA4 C10510 1, ATCEA4 C30827 1, ATCEA4 S10685	97, 90, 83					g33416 93	50	126	1.4e- 11	(AC003 672) unknow n protei n [Arabi dopsis thalia na]	(AC003 672) unknow n protei n [Arabi dopsis thalia na]
146813	ATU008 753	ATL8C2 0145:1 ..3023	gap2	ATCEA4 C12207 7 1, ATCEA4 S33982	97, 95	ATL8C2 0145:1 54..28 56				g33373 52	49	1662		(AC004 481) putati ve chroma tin struct ural protei n Supt5h p [Arabi dopsis thalia na]	(AC004 481) putati ve chroma tin struct ural protei n Supt5h p [Arabi dopsis thalia na]
146814	ATU008 754	ATL8C3 4606:1 200..2	gap2	ATCEA4 C26526 1,	97, 90, 87	ATL8C3 4606:1 301..2				g45390 10	49	643	1.7e- 53	(AL049 481) putati	(AL049 481) putati

146819	ATU008 759	ATL8C2 0301:1 699..1	gap2	ATCEA4 C4753 1, ATCEA4 S30376	97, 92	ATL8C2 0301:3 51..14	0.69	g18903 13	49	563	3.3e- 56	n of unknown function [Arabi dopsis thalia na]
146820	ATU008 760	ATL8C1 7309:1 ..2479	gap2	ATCEA4 C18918 1, ATCEA4 S4551, ATCEA4 S29904 , ATCEA4 C94571 1, ATCEA4 S5752, ATCEA4 C13390 6 1	97, 91, 84, 83, 83, 82	ATL8C1 7309:2 58..24 79	0.60	g31842 81	49	872	2.6e- 173	(AC004 136) putati ve cytoch rome P450 [Arabi dopsis thalia na]
146821	ATU008 761	ATL8C4 5505:3 15..74 8	gap2	ATCEA4 C10299 1, ATCEA4 S6507	97, 95	ATL8C4 5505:3 98..68 2	0.51	g37460 60	49	245	1.4e- 23	(AC005 311) unknown protein [Arabi dopsis thalia na]
146822	ATU008	ATL8C5	gap2	ATCEA4	97,	ATL8C5	0.42	g36082	49	423	2.1e-	(AB017

762	274:53 0..1		SI6174 , ATCEA4 C425_1 , ATCEA4 C4477_2	96, 83	274:29 9..75		63		22	565) Dof zinc finger protei n [Arabi dopsis thalia na]
146823	ATU008 763	gap2	ATCEA4 C10379 0_1, ATCEA4 C19887 _1	97, 97			g32985 38	49	379	5.3e- 38 (AC004 681) hypoth etical protei n [Arabi dopsis thalia na]
146824	ATU008 764	gap2	ATCEA4 C10352 6_1	97	ATL8C2 8495:5 35..12	0.99	g40068 61	48	1210	2.8e- 113 (Z9970 7) tubuli n-like protei n [Arabi dopsis thalia na]
146825	ATU008 765	gap2	ATCEA4 S13404	97	ATL8S1 7121:2 30..16 5	0.98	g41071 03	48	87	2.1e- 06 (AB015 143) AHP3 [Arabi dopsis thalia na]
146826	ATU008 766	gap2	ATCEA4 S10341	97	ATL8C4 5280:8 30..55 5	0.88	g28946 05	48	156	1.9e- 12 (AL021 889) putati ve protei n [Arabi dopsis

146827	ATU008 767	ATL8C1 3643:1 ..2222	gap2	ATCEA4 S36106	97	ATL8C1 3643:1 7..123 6	0.81	g45875 99	48	316	6.6e- 27	thalia nal (AC006 951) hypoth etical protei n [Arabi dopsis thalia nal]
146828	ATU008 768	ATL8C1 6764:2 276..1	gap2	ATCEA4 S2482	97	ATL8C1 6764:1 918..2 53	0.68	g43712 85	48	750	7.5e- 54	(AC006 260) hypoth etical protei n [Arabi dopsis thalia nal]
146829	ATU008 769	ATL8C4 3868:5 6..793	gap2	ATCEA4 S6483	97	ATL8C4 3868:2 08..58 8	0.56	g28646 26	48	972		(AL021 811) cytoch rome p450 - like protei n [Arabi dopsis thalia nal]
146830	ATU008 770	ATL8C3 3030:1 ..1204	gap2	ATCEA4 C53731 _1	97			g10765 24	48	634	5.4e- 60	chloro plast outer envelo pe protei n OEP86 precu sor - garden

146831	ATU008 771	ATL8S3 643:51 3..1	gap2	ATCEA4 C3131_1	97							g38314 64	48	419	7.8e- 40	(AC005 700) hypoth etical protei n [Arabi dopsis thalia na]	pea [Pisum sativu m]
146832	ATU008 772	ATL8C4 430:12 15..22 2	gap2	ATCEA4 S33009	97							g26513 11	48	100	2.5e- 06	(AC002 336) hypoth etical protei n [Arabi dopsis thalia na]	
146833	ATU008 773	ATL8C1 5577:4 68..17 90	gap2	ATCEA4 S585, ATCEA4 C13174 8_1	97, 93							g45126 67	48	1133	7.1e- 97	(AC006 931) putati ve MAP kinase [Arabi dopsis thalia na]	
146834	ATU008 774	ATL8C5 913:64 ..683	gap2	ATCEA4 C14060 2, ATCEA4 C14060 1_1	97, 87							g14832 22	48	651		(X9909 7) peroxi dase [Arabi dopsis thalia na]	
146835	ATU008 775	ATL8C4 4884:1 466..1	gap2	ATCEA4 C12200 4_1	97							g26335 44	48	159	0.0001 1	(Z9911 0) y]cL	

146836	ATU008 776	ATL8C1 0709:9 54..1	gap2	ATCEA4 S8360	97	ATL8C1 0709:5 56..34 , ATL8C1 0709:9 54..75 9	0.99, 0.73	g45593 27	47	453	2.0e- 35	[Bacillus subtilis] (AC007087) hypothetical protein [Arabidopsis thaliana] (AC005882) 64134 [Arabidopsis thaliana] (AC004484) unknown protein [Arabidopsis thaliana] (Y15179) F1-ATP synthase, beta subunit [Sorghum bicolor] (Z9733)
146837	ATU008 777	ATL8S7 528:65 4..200	gap2	ATCEA4 C12620 1, ATCEA4 S29683	97, 97	ATL8S7 528:32 3..206	0.99	g45080 78	47	186	2.0e- 18	(AC005882) 64134 [Arabidopsis thaliana] (AC004484) unknown protein [Arabidopsis thaliana] (Y15179) F1-ATP synthase, beta subunit [Sorghum bicolor] (Z9733)
146838	ATU008 778	ATL8C4 5482:9 81..1	gap2	ATCEA4 C6119 2, ATCEA4 C10599 1	97, 85	ATL8C4 5482:9 14..71	0.94	g30753 98	47	1119	8.6e- 97	(AC004484) unknown protein [Arabidopsis thaliana] (Y15179) F1-ATP synthase, beta subunit [Sorghum bicolor] (Z9733)
146839	ATU008 779	ATL8C2 0196:3 14..12 88	gap2	ATCEA4 S1639, ATCEA4 C4553 1	97, 96	ATL8C2 0196:3 14..12 11	0.93	g43885 34	47	712	2.0e- 70	(Y15179) F1-ATP synthase, beta subunit [Sorghum bicolor] (Z9733)
146840	ATU008	ATL8C4	gap2	ATCEA4	97,	ATL8C4	0.88	g22447	47	1643	6.7e-	(Z9733)

	780	9609:2 752..1		C4245_1, ATCEA4 S2788, ATCEA4 S676	91, 90	9609:1 970..1 18		92			177	6) ankyri n homolo g. [Arabi dopsis thalia na]
146841	ATU008 781	ATL8C2 5635:1 ..1187	gap2	ATCEA4 C25151 2, ATCEA4 S26537	97, 92	ATL8C2 5635:1 105..1 013	0.87	g45859 74	47	562	2.3e- 56	(AC005 287) Hypoth etical protei n [Arabi dopsis thalia na]
146842	ATU008 782	ATL8C1 2641:7 98..16 38	gap2	ATCEA4 S9364	97	ATL8C1 2641:7 98..14 15	0.73	g48368 83	47	573	5.1e- 52	(AC007 260) lcl pr t_seq No defini tion line found [Arabi dopsis thalia na]
146843	ATU008 783	ATL8C1 0260:1 273..1	gap2	ATCEA4 C9822_1	97	ATL8C1 0260:1 223..2 93	0.70	g47550 83	47	107		(AF038 554) densit y regula ted protei n drpl [Homo sapien s]
146844	ATU008 784	ATL8C2 126:1.	gap2	ATCEA4 C24760	97	ATL8C2 126:30	0.62	g28092 51	47	305	1.1e- 30	(AC002 560)

		.778		_1		1..671							F21B7. 20 [Arabi dopsis thalia na]
146845	ATU008 785	ATL8C4 8136:6 47..1	gap2	ATCEA4 S1763, ATCEA4 C6956_ 1, ATCEA4 S6881	97, 97, 86	ATL8C4 8136:6 12..19 1	0.56	g41153 75	47	581	3.0e- 57	(AC005 967) hypoth etical protei n [Arabi dopsis thalia na]	
146846	ATU008 786	ATL8C4 3076:1 072..1	gap2	ATCEA4 C34636 _1	97	ATL8C4 3076:9 42..18	0.54	g44067 80	47	632	3.4e- 48	(AC006 532) putati ve multis pannin g membra ne protei n [Arabi dopsis thalia na]	
146847	ATU008 787	ATL8C2 6136:2 196..4 51	gap2	ATCEA4 C93 1, ATCEA4 C93 6, ATCEA4 S8002, ATCEA4 S27625 , ATCEA4 S4905	97, 94, 87, 86, 83	ATL8C2 6136:2 160..7 57	0.49	g11302 6	47	1249	4.7e- 129	ISOCIT RATE LYASE (ISOCI TRASE) (ISOCI TRATAS E) (ICL) [Brass ica napus]	
146848	ATU008 788	ATL8C4 9975:1	gap2	ATCEA4 C47185	97	ATL8C4 9975:2	0.44	g30804 50	47	304	2.4e- 31	(AL022 605)	

146849	ATU008 789	..939	gap2	ATCEA4 C21697 _1	97	58..93 9					g36436 05	47	89	8.8e- 07	(AC005 395) hypoth etical protein [Arabi dopsis thalia na]
146850	ATU008 790	ATL8C4 8546:1 11..10 86	gap2	ATCEA4 C18855 _2	97	ATL8C4 8546:5 28..64 1	1.00				g45859 76	46	526	2.0e- 43	(AC005 287) Unknown protein [Arabi dopsis thalia na]
146851	ATU008 791	ATL8C7 819:1. .1490	gap2	ATCEA4 S2301, ATCEA4 C10011 1_1	97, 95	ATL8C7 819:56 3..130 1	0.94				g35401 82	46	226	1.7e- 17	(AC004 122) Unknown protein [Arabi dopsis thalia na]
146852	ATU008 792	ATL8C1 7870:1 ..825	gap2	ATCEA4 C36924 _1	97	ATL8C1 7870:7 4..825	0.77				g24438 76	46	224	2.9e- 27	(AC002 294) Hypoth etical protein [Arabi na]

146853	ATU008 793	ATL8C3 0914:1 ..1671	gap2	ATCEA4 S32890 ATCEA4 S30472	97, 88	ATL8C3 0914:2 60..14 37	0.73	g32427 08	46	598	8.4e- 72	dopsis thalia nal (AC003 040) putati ve serine /threo nine protei n kinase [Arabi dopsis thalia nal]
146854	ATU008 794	ATL8C3 3121:1 ..996	gap2	ATCEA4 C33060 _1	97	ATL8C3 3121:9 6..809	0.70	g46789 34	46	502	1.7e- 40	(AL049 711) putati ve protei n [Arabi dopsis thalia nal]
146855	ATU008 795	ATL8C3 1570:2 807..1 64	gap2	ATCEA4 S7600	97	ATL8C3 1570:2 551..1 64	0.59	g42180 05	46	84	0.31	(AC006 135) putati ve vicili n storag e protei n (globu lin- like) [Arabi dopsis thalia nal]
146856	ATU008	ATL8C1	gap2	ATCEA4	97	ATL8C1	0.58	g31526	46	252	3.3e-	(AC004